

SECRET

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Seq. No.          6
Contig ID         3_1.R1040
5'-most EST      CPR6164_700155735_FL
Method            BLASTX
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NCBI GI g4105772
 BLAST score 804
 E value 6.0e-86
 Match length 183
 % identity 53
 NCBI Description (AF049917) PGP9B [Petunia x hybrida]

Seq. No. 7
 Contig ID 4_1.R1040
 5'-most EST ssr700556639.h1
 Method BLASTX
 NCBI GI g2655008
 BLAST score 867
 E value 5.0e-93
 Match length 374
 % identity 45
 NCBI Description (AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon
 esculentum]

Seq. No. 8
 Contig ID 4_2.R1040
 5'-most EST jC-gmle01810053b07a1
 Method BLASTX
 NCBI GI g2642640
 BLAST score 1554
 E value 1.0e-173
 Match length 339
 % identity 85
 NCBI Description (AF032473) ADP-glucose pyrophosphorylase large subunit 2
 [Citrullus lanatus]

Seq. No. 9
 Contig ID 4_3.R1040
 5'-most EST jC-gmf102220050f03d1

Seq. No. 10
 Contig ID 4_4.R1040
 5'-most EST uC-gmf1minsoy075b06b1
 Method BLASTX
 NCBI GI g2655008
 BLAST score 313
 E value 1.0e-28
 Match length 101
 % identity 54
 NCBI Description (AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon
 esculentum]

Seq. No. 11
 Contig ID 5_1.R1040
 5'-most EST LIB3106-062-Q1-K1-E6
 Method BLASTN
 NCBI GI g1663540
 BLAST score 277
 E value 1.0e-154
 Match length 461
 % identity 90
 NCBI Description Glycine max clone RLG3 disease resistance protein homolog

0563401 1010000

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Seq. No.          13
Contig ID         6_2.R1040
5'-most EST      jC-gmro02910008h06a1
Method            BLASTN
NCBI GI           g1431621
BLAST score       178
E value           4.0e-95
Match length      527
% identity        84
NCBI Description   T.repens mRNA for protein kinase
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Seq. No.	15
Contig ID	6_5.R1040
5'-most EST	jC-gmf102220050g09a1
Method	BLASTN
NCBI GI	g313143
BLAST score	109
E value	3.0e-54
Match length	153
% identity	93
NCBI Description	A.medicago MSK-1 mRNA for protein kinase

64

BLAST score 64
 E value 2.0e-27
 Match length 116
 % identity 89
 NCBI Description Pisum sativum mRNA for ketol-acid reductoisomerase

Seq. No. 27
 Contig ID 8_6.R1040
 5'-most EST g4304571
 Method BLASTN
 NCBI GI g4210834
 BLAST score 157
 E value 7.0e-83
 Match length 376
 % identity 88
 NCBI Description Pisum sativum mRNA for ketol-acid reductoisomerase

Seq. No. 28
 Contig ID 9_1.R1040
 5'-most EST leu701146904.h1
 Method BLASTX
 NCBI GI g2842490
 BLAST score 791
 E value 1.0e-106
 Match length 337
 % identity 62
 NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No. 29
 Contig ID 9_2.R1040
 5'-most EST LIB3049-020-Q1-E1-E8
 Method BLASTX
 NCBI GI g2842490
 BLAST score 244
 E value 7.0e-27
 Match length 76
 % identity 82
 NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No. 30
 Contig ID 9_3.R1040
 5'-most EST jC-gmst02400068a04d1
 Method BLASTX
 NCBI GI g2842490
 BLAST score 151
 E value 8.0e-10
 Match length 38
 % identity 71
 NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No. 31
 Contig ID 10_1.R1040
 5'-most EST LIB3139-004-P1-N1-H2
 Method BLASTX
 NCBI GI g3243234
 BLAST score 1356
 E value 1.0e-150

Match length 306
 % identity 84
 NCBI Description (AF071477) isoflavone reductase related protein [Pyrus communis]

Seq. No. 32
 Contig ID 11_1.R1040
 5'-most EST uC-gmrominsoy081c11b1
 Method BLASTN
 NCBI GI g166421
 BLAST score 287
 E value 1.0e-160
 Match length 475
 % identity 90
 NCBI Description Medicago sativa ubiquitin carrier protein mRNA, complete cds

Seq. No. 33
 Contig ID 11_2.R1040
 5'-most EST LIB3139-094-P1-N1-A2
 Method BLASTN
 NCBI GI g166421
 BLAST score 282
 E value 1.0e-157
 Match length 630
 % identity 89
 NCBI Description Medicago sativa ubiquitin carrier protein mRNA, complete cds

Seq. No. 34
 Contig ID 11_3.R1040
 5'-most EST wvk700684812.h1
 Method BLASTX
 NCBI GI g136636
 BLAST score 222
 E value 4.0e-36
 Match length 84
 % identity 94
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
 >gi_1076424_pir_S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi_442594_pdb_1AAK Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No. 35
 Contig ID 11_4.R1040
 5'-most EST LIB3106-009-Q1-K1-G1

Seq. No. 36
 Contig ID 11_5.R1040
 5'-most EST LIB3087-001-Q1-K1-E4
 Method BLASTN
 NCBI GI g166421

BLAST score 172
 E value 8.0e-92
 Match length 248
 % identity 92
 NCBI Description Medicago sativa ubiquitin carrier protein mRNA, complete cds

Seq. No. 37
 Contig ID 11_6.R1040
 5'-most EST LIB3092-033-Q1-K1-A7
 Method BLASTN
 NCBI GI g166421
 BLAST score 77
 E value 3.0e-35
 Match length 125
 % identity 90
 NCBI Description Medicago sativa ubiquitin carrier protein mRNA, complete cds

Seq. No. 38
 Contig ID 11_8.R1040
 5'-most EST LIB3051-088-Q1-K1-B12
 Method BLASTN
 NCBI GI g166421
 BLAST score 108
 E value 2.0e-53
 Match length 148
 % identity 93
 NCBI Description Medicago sativa ubiquitin carrier protein mRNA, complete cds

Seq. No. 39
 Contig ID 11_9.R1040
 5'-most EST LIB3106-105-Q1-K1-F5
 Method BLASTN
 NCBI GI g166421
 BLAST score 164
 E value 4.0e-87
 Match length 320
 % identity 88
 NCBI Description Medicago sativa ubiquitin carrier protein mRNA, complete cds

Seq. No. 40
 Contig ID 12_1.R1040
 5'-most EST leu701146018.h1
 Method BLASTX
 NCBI GI g1717950
 BLAST score 1036
 E value 1.0e-113
 Match length 242
 % identity 81
 NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 2 PRECURSOR (RIESKE IRON-SULFUR PROTEIN 2) (RISP2) >gi_530052 (L16810) Rieske iron-sulfur protein [Nicotiana tabacum]

Seq. No. 41

% identity 65
NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No. 47
Contig ID 15_1.R1040
5'-most EST fC-gmle7000742678f1
Method BLASTX
NCBI GI g2618686
BLAST score 989
E value 1.0e-107
Match length 389
% identity 48

NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No. 48
Contig ID 15_2.R1040
5'-most EST CPR6560_700742678_FL
Method BLASTX
NCBI GI g3882018
BLAST score 416
E value 5.0e-66
Match length 324
% identity 47
NCBI Description (Y18377) cytokinin oxidase [Zea mays]

Seq. No. 49
Contig ID 16_1.R1040
5'-most EST uC-gmronoir010b05b1
Method BLASTN
NCBI GI g1663536
BLAST score 219
E value 1.0e-119
Match length 287
% identity 94
NCBI Description Glycine max clone RLG1 disease resistance protein homolog gene, partial cds

Seq. No. 50
Contig ID 16_2.R1040
5'-most EST sat701011581.h1
Method BLASTN
NCBI GI g1663536
BLAST score 346
E value 0.0e+00
Match length 446
% identity 94
NCBI Description Glycine max clone RLG1 disease resistance protein homolog gene, partial cds

Seq. No. 51
Contig ID 17_1.R1040
5'-most EST LIB3051-054-Q1-K2-C3
Method BLASTX
NCBI GI g4262226
BLAST score 277
E value 5.0e-24
Match length 195

% identity 46
NCBI Description (AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No. 52
Contig ID 17_2.R1040
5'-most EST LIB3139-085-P1-N1-A6
Method BLASTX
NCBI GI g4262226
BLAST score 197
E value 5.0e-15
Match length 128
% identity 45

NCBI Description (AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No. 53
Contig ID 17_3.R1040
5'-most EST lus701015877.h1

Seq. No. 54
Contig ID 19_1.R1040
5'-most EST LIB3030-011-Q1-B1-D10
Method BLASTX
NCBI GI g4325041
BLAST score 2609
E value 0.0e+00
Match length 668
% identity 80

NCBI Description (AF117339) FtsH-like protein Pftf precursor [Nicotiana tabacum]

Seq. No. 55
Contig ID 19_2.R1040
5'-most EST jC-gmle01810022f02d1
Method BLASTN
NCBI GI g3808100
BLAST score 80
E value 6.0e-37
Match length 244
% identity 83

NCBI Description Capsicum annuum mRNA for chloroplast protease (CACP) from the AAA atpase family

Seq. No. 56
Contig ID 19_3.R1040
5'-most EST ssr700559811.h1
Method BLASTX
NCBI GI g3808101
BLAST score 392
E value 7.0e-38
Match length 165
% identity 55

NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]

Seq. No. 57
Contig ID 19_4.R1040
5'-most EST jC-gmfl02220072h01a1

5'-most EST CPR3463_700797953_FL
 Method BLASTX
 NCBI GI g3947733
 BLAST score 378
 E value 4.0e-36
 Match length 155
 % identity 54
 NCBI Description (AJ009719) NL25 [Solanum tuberosum]

Seq. No. 64
 Contig ID 24_1.R1040
 5'-most EST jex700908154.h1
 Method BLASTX
 NCBI GI g2088653
 BLAST score 1230
 E value 1.0e-135
 Match length 443
 % identity 54
 NCBI Description (AF002109) Hslpro-1 related protein isolog [Arabidopsis thaliana]

Seq. No. 65
 Contig ID 24_2.R1040
 5'-most EST uC-gmrominsoy256f04b1
 Method BLASTX
 NCBI GI g2088653
 BLAST score 390
 E value 2.0e-37
 Match length 130
 % identity 59
 NCBI Description (AF002109) Hslpro-1 related protein isolog [Arabidopsis thaliana]

Seq. No. 66
 Contig ID 24_3.R1040
 5'-most EST fC-gmle700557849f3
 Method BLASTX
 NCBI GI g2088653
 BLAST score 413
 E value 4.0e-40
 Match length 123
 % identity 65
 NCBI Description (AF002109) Hslpro-1 related protein isolog [Arabidopsis thaliana]

Seq. No. 67
 Contig ID 24_5.R1040
 5'-most EST fua701040369.h1
 Method BLASTX
 NCBI GI g2088653
 BLAST score 352
 E value 3.0e-33
 Match length 134
 % identity 52
 NCBI Description (AF002109) Hslpro-1 related protein isolog [Arabidopsis thaliana]

Seq. No. 68
 Contig ID 25_1.R1040
 5'-most EST CPR3468_700835511_FL
 Method BLASTX
 NCBI GI g3947735
 BLAST score 499
 E value 1.0e-49
 Match length 480
 % identity 41
 NCBI Description (AJ009720) NL27 [Solanum tuberosum]

Seq. No. 69
 Contig ID 26_1.R1040
 5'-most EST fC-gmro700562665z1
 Method BLASTX
 NCBI GI g3947735
 BLAST score 670
 E value 5.0e-70
 Match length 358
 % identity 41
 NCBI Description (AJ009720) NL27 [Solanum tuberosum]

Seq. No. 70
 Contig ID 26_2.R1040
 5'-most EST CPR3475_700870127_FL
 Method BLASTX
 NCBI GI g3860167
 BLAST score 322
 E value 6.0e-29
 Match length 358
 % identity 26
 NCBI Description (AF098964) disease resistance protein RPP1-WsC [Arabidopsis thaliana]

Seq. No. 71
 Contig ID 26_3.R1040
 5'-most EST CPR10175_FL
 Method BLASTX
 NCBI GI g3947735
 BLAST score 442
 E value 3.0e-43
 Match length 360
 % identity 37
 NCBI Description (AJ009720) NL27 [Solanum tuberosum]

Seq. No. 72
 Contig ID 26_4.R1040
 5'-most EST pcp700990320.h1

Seq. No. 73
 Contig ID 26_5.R1040
 5'-most EST LIB3028-048-Q1-B1-A10
 Method BLASTX
 NCBI GI g4204265
 BLAST score 158
 E value 2.0e-10
 Match length 140

% identity	35
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]
Seq. No.	74
Contig ID	26_6.R1040
5'-most EST	LIB3053-011-Q1-N1-A10
Method	BLASTX
NCBI GI	g4388834
BLAST score	333
E value	7.0e-31
Match length	199
% identity	18
NCBI Description	(AC006528) putative disease resistance protein RPP1, 3' partial [Arabidopsis thaliana]
Seq. No.	75
Contig ID	26_11.R1040
5'-most EST	dpv701099972.h1
Seq. No.	76
Contig ID	26_14.R1040
5'-most EST	zsg701118496.h1
Seq. No.	77
Contig ID	27_1.R1040
5'-most EST	CPR3479_700891859_FL
Method	BLASTX
NCBI GI	g1086263
BLAST score	384
E value	2.0e-36
Match length	412
% identity	32
NCBI Description	TMV resistance protein N - tobacco (Nicotiana glutinosa) >gi_558887 (U15605) N [Nicotiana glutinosa]
Seq. No.	78
Contig ID	28_1.R1040
5'-most EST	leu701154138.h1
Method	BLASTX
NCBI GI	g2213598
BLAST score	403
E value	1.0e-38
Match length	342
% identity	21
NCBI Description	(AC000348) T7N9.18 [Arabidopsis thaliana]
Seq. No.	79
Contig ID	30_1.R1040
5'-most EST	gsv701053417.h1
Method	BLASTX
NCBI GI	g2316016
BLAST score	704
E value	3.0e-74
Match length	225
% identity	35
NCBI Description	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No. 80
 Contig ID 30_2.R1040
 5'-most EST LIB3138-032-Q1-N1-B2
 Method BLASTX
 NCBI GI g2316016
 BLAST score 353
 E value 2.0e-33
 Match length 114
 % identity 61
 NCBI Description (U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No. 81
 Contig ID 34_1.R1040
 5'-most EST CPR6213_700991711_FL
 Method BLASTX
 NCBI GI g2088653
 BLAST score 1154
 E value 1.0e-126
 Match length 434
 % identity 53
 NCBI Description (AF002109) Hslpro-1 related protein isolog [Arabidopsis thaliana]

Seq. No. 82
 Contig ID 34_2.R1040
 5'-most EST LIB3049-052-Q1-E1-C5
 Method BLASTX
 NCBI GI g2088653
 BLAST score 586
 E value 1.0e-121
 Match length 435
 % identity 53
 NCBI Description (AF002109) Hslpro-1 related protein isolog [Arabidopsis thaliana]

Seq. No. 83
 Contig ID 37_1.R1040
 5'-most EST CPR6212_700968464_FL
 Method BLASTX
 NCBI GI g4490297
 BLAST score 605
 E value 1.0e-86
 Match length 617
 % identity 36
 NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 84
 Contig ID 37_2.R1040
 5'-most EST uC-gmronoir032h02b1

Seq. No. 85
 Contig ID 37_3.R1040
 5'-most EST uC-gmropic011e09b1

Seq. No. 86
 Contig ID 39_1.R1040
 5'-most EST CPR6214_701001301_FL

Contig ID 45_1.R1040
 5'-most EST zsg701117822.h2
 Method BLASTX
 NCBI GI g3947735
 BLAST score 424
 E value 5.0e-41
 Match length 435
 % identity 40
 NCBI Description (AJ009720) NL27 [Solanum tuberosum]

Seq. No. 92
 Contig ID 45_2.R1040
 5'-most EST LIB3139-050-P1-N1-E6
 Method BLASTX
 NCBI GI g730125
 BLAST score 1929
 E value 0.0e+00
 Match length 488
 % identity 73
 NCBI Description NADPH-CYTOCHROME P450 REDUCTASE >gi_322739_pir_S31502
 NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Madagascar
 periwinkle >gi_18139_emb_CAA49446 (X69791)
 NADPH--ferrihemoprotein reductase [Catharanthus roseus]

Seq. No. 93
 Contig ID 45_3.R1040
 5'-most EST jC-gmro02910024d12a1
 Method BLASTX
 NCBI GI g2580499
 BLAST score 609
 E value 1.0e-112
 Match length 323
 % identity 66
 NCBI Description (U67186) NADPH:ferrihemoprotein oxidoreductase
 [Eschscholzia californica]

Seq. No. 94
 Contig ID 45_4.R1040
 5'-most EST g5058215
 Method BLASTX
 NCBI GI g2580499
 BLAST score 220
 E value 1.0e-17
 Match length 98
 % identity 45
 NCBI Description (U67186) NADPH:ferrihemoprotein oxidoreductase
 [Eschscholzia californica]

Seq. No. 95
 Contig ID 45_5.R1040
 5'-most EST LIB3051-067-Q1-K1-H3
 Method BLASTX
 NCBI GI g480669
 BLAST score 366
 E value 5.0e-35
 Match length 106
 % identity 68

NCBI Description NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Jerusalem artichoke (fragment) >gi_1359894_emb_CAA81210_ (Z26251)
NADPH-ferrihemoprotein reductase [Helianthus tuberosus]

Seq. No. 96
Contig ID 45_6.R1040
5'-most EST LIB3170-037-Q1-K1-D8
Method BLASTX
NCBI GI g730125
BLAST score 312
E value 3.0e-28
Match length 176
% identity 73

NCBI Description NADPH-CYTOCHROME P450 REDUCTASE >gi_322739_pir_S31502
NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Madagascar periwinkle >gi_18139_emb_CAA49446_ (X69791)
NADPH--ferrihemoprotein reductase [Catharanthus roseus]

Seq. No. 97
Contig ID 45_7.R1040
5'-most EST vzy700755269.h1
Method BLASTX
NCBI GI g99737
BLAST score 542
E value 1.0e-55
Match length 150
% identity 67

NCBI Description NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Arabidopsis thaliana >gi_16189_emb_CAA46815_ (X66017)
NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]

Seq. No. 98
Contig ID 46_1.R1040
5'-most EST uC-gmropic067a07b1
Method BLASTX
NCBI GI g322752
BLAST score 1146
E value 0.0e+00
Match length 427
% identity 76

NCBI Description auxin-independent growth promoter - Nicotiana tabacum >gi_559921_emb_CAA56570_ (X80301) axi 1 [Nicotiana tabacum]

Seq. No. 99
Contig ID 48_1.R1040
5'-most EST CPR6563_700945759_FL
Method BLASTX
NCBI GI g2618686
BLAST score 671
E value 3.0e-70
Match length 220
% identity 60

NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No. 100
Contig ID 49_1.R1040
5'-most EST CPR6564_700953259_FL

Method BLASTX
 NCBI GI g4191780
 BLAST score 281
 E value 9.0e-25
 Match length 95
 % identity 54
 NCBI Description (AC005917) putative cytokinin oxidase [Arabidopsis thaliana]

Seq. No. 101
 Contig ID 51_1.R1040
 5'-most EST CPR6639_700684235_FL
 Method BLASTX
 NCBI GI g2258317
 BLAST score 172
 E value 6.0e-12
 Match length 132
 % identity 37
 NCBI Description (AF004879) resistance complex protein I2C-2 [Lycopersicon esculentum]

Seq. No. 102
 Contig ID 52_1.R1040
 5'-most EST CPR6640_700942632_FL
 Method BLASTX
 NCBI GI g3947733
 BLAST score 218
 E value 4.0e-17
 Match length 98
 % identity 47
 NCBI Description (AJ009719) NL25 [Solanum tuberosum]

Seq. No. 103
 Contig ID 54_1.R1040
 5'-most EST zsq701118302.h1
 Method BLASTN
 NCBI GI g310562
 BLAST score 89
 E value 7.0e-42
 Match length 336
 % identity 88
 NCBI Description Glycine max calmodulin (SCaM-5) mRNA, complete cds

Seq. No. 104
 Contig ID 54_2.R1040
 5'-most EST g310562_FL
 Method BLASTN
 NCBI GI g310562
 BLAST score 873
 E value 0.0e+00
 Match length 873
 % identity 100
 NCBI Description Glycine max calmodulin (SCaM-5) mRNA, complete cds

Seq. No. 105
 Contig ID 54_3.R1040
 5'-most EST zzp700831855.h1

Method BLASTN
 NCBI GI g310562
 BLAST score 115
 E value 4.0e-58
 Match length 123
 % identity 98
 NCBI Description Glycine max calmodulin (SCaM-5) mRNA, complete cds

Seq. No. 106
 Contig ID 55_1.R1040
 5'-most EST fC-gmle700560625a1
 Method BLASTX
 NCBI GI g2853078
 BLAST score 393
 E value 7.0e-77
 Match length 594
 % identity 34
 NCBI Description (AL021768) TMV resistance protein N-like [Arabidopsis thaliana]

Seq. No. 107
 Contig ID 55_2.R1040
 5'-most EST fC-gmle700560625i1
 Method BLASTX
 NCBI GI g2853078
 BLAST score 317
 E value 6.0e-29
 Match length 201
 % identity 33
 NCBI Description (AL021768) TMV resistance protein N-like [Arabidopsis thaliana]

Seq. No. 108
 Contig ID 56_1.R1040
 5'-most EST uC-gmrominsoy185f08b1
 Method BLASTX
 NCBI GI g3947735
 BLAST score 638
 E value 4.0e-66
 Match length 402
 % identity 33
 NCBI Description (AJ009720) NL27 [Solanum tuberosum]

Seq. No. 109
 Contig ID 57_1.R1040
 5'-most EST LIB3051-041-Q1-K1-C3
 Method BLASTX
 NCBI GI g3947733
 BLAST score 162
 E value 1.0e-10
 Match length 112
 % identity 34
 NCBI Description (AJ009719) NL25 [Solanum tuberosum]

Seq. No. 110
 Contig ID 58_1.R1040
 5'-most EST CPR6648a_700993771_FL

Method BLASTX
 NCBI GI g4092774
 BLAST score 669
 E value 1.0e-69
 Match length 604
 % identity 31
 NCBI Description (AF105140) disease resistance gene homolog 9N [Brassica napus]

Seq. No. 111
 Contig ID 59_1.R1040
 5'-most EST CPR6649_700999286_FL
 Method BLASTX
 NCBI GI g3947735
 BLAST score 373
 E value 3.0e-35
 Match length 301
 % identity 42
 NCBI Description (AJ009720) NL27 [Solanum tuberosum]

Seq. No. 112
 Contig ID 60_1.R1040
 5'-most EST zhF700962285.h1
 Method BLASTX
 NCBI GI g1652057
 BLAST score 1192
 E value 1.0e-131
 Match length 535
 % identity 51
 NCBI Description (D90902) hypothetical protein [Synechocystis sp.]

Seq. No. 113
 Contig ID 60_2.R1040
 5'-most EST sat701012774.h1

Seq. No. 114
 Contig ID 65_1.R1040
 5'-most EST g5606563
 Method BLASTX
 NCBI GI g3080405
 BLAST score 353
 E value 4.0e-33
 Match length 83
 % identity 77
 NCBI Description (AL022603) Lsd1 like protein [Arabidopsis thaliana]
 >gi_4455269_emb_CAB36805.1_ (AL035527) Lsd1 like protein [Arabidopsis thaliana]

Seq. No. 115
 Contig ID 66_1.R1040
 5'-most EST LIB3106-074-Q1-K1-G6
 Method BLASTX
 NCBI GI g2738248
 BLAST score 3400
 E value 0.0e+00
 Match length 762
 % identity 85

NCBI Description (U97200) cobalamin-independent methionine synthase
[Arabidopsis thaliana]

Seq. No. 116
Contig ID 66_2.R1040
5'-most EST epx701108427.h1
Method BLASTX
NCBI GI g1914683
BLAST score 294
E value 3.0e-26
Match length 74
% identity 77
NCBI Description (Y12013) RAD23, isoform I [Daucus carota]

Seq. No. 117
Contig ID 66_3.R1040
5'-most EST LIB3092-020-Q1-K1-C11
Method BLASTX
NCBI GI g1914683
BLAST score 325
E value 4.0e-30
Match length 109
% identity 61
NCBI Description (Y12013) RAD23, isoform I [Daucus carota]

Seq. No. 118
Contig ID 66_6.R1040
5'-most EST crh700854007.h1
Method BLASTX
NCBI GI g1914683
BLAST score 194
E value 6.0e-15
Match length 52
% identity 75
NCBI Description (Y12013) RAD23, isoform I [Daucus carota]

Seq. No. 119
Contig ID 66_7.R1040
5'-most EST pxt700943841.h1
Method BLASTX
NCBI GI g974782
BLAST score 418
E value 3.0e-46
Match length 111
% identity 86
NCBI Description (Z49150) cobalamine-independent methionine synthase
[Solenostemon scutellarioides]

Seq. No. 120
Contig ID 66_9.R1040
5'-most EST LIB3050-019-Q1-K1-A1
Method BLASTN
NCBI GI g974781
BLAST score 125
E value 8.0e-64
Match length 313
% identity 87

NCBI Description C.blumei kinetoplast met gene for cobalamine-independent methionine synthase

Seq. No. 121
Contig ID 66_16.R1040
5'-most EST wvk700682724.h1
Method BLASTX
NCBI GI g2738248
BLAST score 201
E value 1.0e-31
Match length 82
% identity 90
NCBI Description (U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No. 122
Contig ID 67_1.R1040
5'-most EST zsq701118017.h2
Method BLASTX
NCBI GI g4376158
BLAST score 1940
E value 0.0e+00
Match length 472
% identity 82
NCBI Description (X98873) aspartate kinase [Arabidopsis thaliana]

Seq. No. 123
Contig ID 67_2.R1040
5'-most EST CPR9211_700959057_FL
Method BLASTX
NCBI GI g4376158
BLAST score 1866
E value 0.0e+00
Match length 458
% identity 81
NCBI Description (X98873) aspartate kinase [Arabidopsis thaliana]

Seq. No. 124
Contig ID 67_3.R1040
5'-most EST uC-gmropic064c02b1
Method BLASTN
NCBI GI g2257742
BLAST score 115
E value 1.0e-57
Match length 375
% identity 83
NCBI Description Arabidopsis thaliana lysine-sensitive aspartate kinase mRNA, complete cds

Seq. No. 125
Contig ID 69_1.R1040
5'-most EST CPR9215_701060142_FL
Method BLASTN
NCBI GI g2970446
BLAST score 905
E value 0.0e+00
Match length 1341

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% identity      99
NCBI Description Glycine max aspartokinase-homoserine dehydrogenase
                  (AK-HSDH) mRNA, complete cds

Seq. No.        126
Contig ID       69_2.R1040
5'-most EST     dpv701100440.h1
Method          BLASTX
NCBI GI         g2970447
BLAST score     2096
E value         0.0e+00
Match length    417
% identity      99
NCBI Description (AF049706) aspartokinase-homoserine dehydrogenase [Glycine
                  max]

Seq. No.        127
Contig ID       69_3.R1040
5'-most EST     fC-gmro700865466a2
Method          BLASTN
NCBI GI         g2104674
BLAST score     169
E value         1.0e-89
Match length    477
% identity      84
NCBI Description V.faba mRNA for transcription factor containing bZIP

Seq. No.        128
Contig ID       69_4.R1040
5'-most EST     fC-gmro700798021b2
Method          BLASTN
NCBI GI         g2970446
BLAST score     648
E value         0.0e+00
Match length    656
% identity      100
NCBI Description Glycine max aspartokinase-homoserine dehydrogenase
                  (AK-HSDH) mRNA, complete cds

Seq. No.        129
Contig ID       69_5.R1040
5'-most EST     fC-gmle700557507r2
Method          BLASTN
NCBI GI         g2970446
BLAST score     519
E value         0.0e+00
Match length    535
% identity      99
NCBI Description Glycine max aspartokinase-homoserine dehydrogenase
                  (AK-HSDH) mRNA, complete cds

Seq. No.        130
Contig ID       71_1.R1040
5'-most EST     uxk700672773.h1
Method          BLASTX
NCBI GI         g1762933
BLAST score     485

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E value 2.0e-48
 Match length 186
 % identity 53
 NCBI Description (U66263) tumor-related protein [Nicotiana tabacum]

Seq. No. 131
 Contig ID 72_1.R1040
 5'-most EST CPR9004_701042534_FL
 Method BLASTX
 NCBI GI g2754816
 BLAST score 374
 E value 2.0e-35
 Match length 176
 % identity 43
 NCBI Description (AF021346) non-race specific disease resistance protein [Arabidopsis thaliana]

Seq. No. 132
 Contig ID 74_1.R1040
 5'-most EST LIB3051-114-Q1-K1-H12
 Method BLASTX
 NCBI GI g1742961
 BLAST score 1892
 E value 0.0e+00
 Match length 505
 % identity 73
 NCBI Description (X94756) cystathionine gamma-synthase [Arabidopsis thaliana]

Seq. No. 133
 Contig ID 74_2.R1040
 5'-most EST fC-gmse7000751425d1
 Method BLASTX
 NCBI GI g1791309
 BLAST score 380
 E value 2.0e-36
 Match length 83
 % identity 87
 NCBI Description (U83500) cystathionine gamma-synthase [Arabidopsis thaliana] >gi_2852454_dbj_BAA24699_ (AB010888)
 cystathionine gamma-synthase [Arabidopsis thaliana]

Seq. No. 134
 Contig ID 74_3.R1040
 5'-most EST LIB3051-006-Q1-E1-G10
 Method BLASTX
 NCBI GI g1791309
 BLAST score 424
 E value 9.0e-42
 Match length 146
 % identity 61
 NCBI Description (U83500) cystathionine gamma-synthase [Arabidopsis thaliana] >gi_2852454_dbj_BAA24699_ (AB010888)
 cystathionine gamma-synthase [Arabidopsis thaliana]

Seq. No. 135
 Contig ID 74_10.R1040

5'-most EST eep700867801.h1
 Method BLASTX
 NCBI GI g3202028
 BLAST score 395
 E value 3.0e-38
 Match length 96
 % identity 83
 NCBI Description (AF069317) cystathionine gamma-synthase [Mesembryanthemum crystallinum]

Seq. No. 136
 Contig ID 75_1.R1040
 5'-most EST CPR9221_700567374_FL
 Method BLASTX
 NCBI GI g100728
 BLAST score 1351
 E value 1.0e-149
 Match length 407
 % identity 61
 NCBI Description aspartate transaminase (EC 2.6.1.1) AAT3 precursor - proso millet >gi_1084464_pir_S53304 aspartate aminotransferase - proso millet >gi_20601_emb_CAA45024 (X63430) aspartate aminotransferase [Panicum miliaceum]
 >gi_435459_dbj_BAA04993 (D25323) aspartate aminotransferase [Panicum miliaceum]

Seq. No. 137
 Contig ID 75_2.R1040
 5'-most EST uC-gmropic106a04b1
 Method BLASTX
 NCBI GI g100728
 BLAST score 573
 E value 6.0e-59
 Match length 128
 % identity 77
 NCBI Description aspartate transaminase (EC 2.6.1.1) AAT3 precursor - proso millet >gi_1084464_pir_S53304 aspartate aminotransferase - proso millet >gi_20601_emb_CAA45024 (X63430) aspartate aminotransferase [Panicum miliaceum]
 >gi_435459_dbj_BAA04993 (D25323) aspartate aminotransferase [Panicum miliaceum]

Seq. No. 138
 Contig ID 78_1.R1040
 5'-most EST CPR9214_LIB3039-051-A2_FL
 Method BLASTX
 NCBI GI g2984139
 BLAST score 789
 E value 7.0e-84
 Match length 338
 % identity 48
 NCBI Description (AE000760) aspartate-semialdehyde dehydrogenase [Aquifex aeolicus]

Seq. No. 139
 Contig ID 78_2.R1040
 5'-most EST hrw701060760.h1

Method	BLASTX
NCBI GI	g416901
BLAST score	341
E value	7.0e-32
Match length	111
% identity	59
NCBI Description	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (ASA DEHYDROGENASE) >gi_142828 (L08471) aspartate semialdehyde dehydrogenase [Bacillus subtilis] >gi_2634047_emb_CAB13548 (Z99112) aspartate-semialdehyde dehydrogenase [Bacillus subtilis]
Seq. No.	140
Contig ID	79_1.R1040
5'-most EST	ssr700556460.h1
Method	BLASTX
NCBI GI	g1705463
BLAST score	1460
E value	1.0e-162
Match length	373
% identity	75
NCBI Description	BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi_2129547_pir_S71201 biotin sythase - Arabidopsis thaliana >gi_1045316 (U24147) biotin sythase [Arabidopsis thaliana] >gi_1403662 (U31806) BIO2 protein [Arabidopsis thaliana] >gi_1769457 (L34413) biotin synthase [Arabidopsis thaliana] >gi_2288983 (AC002335) biotin synthase (Bio B) [Arabidopsis thaliana] >gi_1589016_prf_2209438A biotin synthase [Arabidopsis thaliana]
Seq. No.	141
Contig ID	79_2.R1040
5'-most EST	LIB3170-010-Q1-K1-G7
Seq. No.	142
Contig ID	79_3.R1040
5'-most EST	wvk700685486.h1
Seq. No.	143
Contig ID	82_1.R1040
5'-most EST	ssr700555656.h1
Method	BLASTN
NCBI GI	g4098966
BLAST score	335
E value	0.0e+00
Match length	602
% identity	96
NCBI Description	Glycine max putative reistance gene analog genomic sequence
Seq. No.	144
Contig ID	82_2.R1040
5'-most EST	LIB3093-028-Q1-K1-A3
Method	BLASTX
NCBI GI	g1086263
BLAST score	346
E value	4.0e-32
Match length	382
% identity	31

NCBI Description TMV resistance protein N - tobacco (*Nicotiana glutinosa*)
>gi_558887 (U15605) N [*Nicotiana glutinosa*]

Seq. No. 145
Contig ID 83_1.R1040
5'-most EST CPR9217_701001147_FL
Method BLASTX
NCBI GI g1708993
BLAST score 863
E value 7.0e-93
Match length 195
% identity 86
NCBI Description CYSTATHIONINE BETA-LYASE PRECURSOR (CBL)
(BETA-CYSTATHIONASE) (CYSTEINE LYASE)
>gi_2129567_pir_S61429 cystathionine beta-lyase (EC
4.4.1.8) - *Arabidopsis thaliana* >gi_704397 (L40511)
cystathionine beta-lyase [*Arabidopsis thaliana*]

Seq. No. 146
Contig ID 84_1.R1040
5'-most EST uC-gmronoir063g05b1
Method BLASTX
NCBI GI g2129753
BLAST score 1559
E value 0.0e+00
Match length 466
% identity 85
NCBI Description threonine synthase (EC 4.2.99.2) precursor - *Arabidopsis*
thaliana (fragment) >gi_1448917 (L41666) threonine synthase
[*Arabidopsis thaliana*]

Seq. No. 147
Contig ID 85_1.R1040
5'-most EST ssr700556066.h1
Method BLASTX
NCBI GI g4490297
BLAST score 717
E value 3.0e-75
Match length 656
% identity 34
NCBI Description (AL035678) putative protein [*Arabidopsis thaliana*]

Seq. No. 148
Contig ID 85_2.R1040
5'-most EST g5688438
Method BLASTX
NCBI GI g4490297
BLAST score 270
E value 1.0e-23
Match length 129
% identity 41
NCBI Description (AL035678) putative protein [*Arabidopsis thaliana*]

Seq. No. 149
Contig ID 86_1.R1040
5'-most EST epX701108161.h1
Method BLASTX

thaliana]

Seq. No. 154
 Contig ID 88_1.R1040
 5'-most EST CPR10281:2F700737217_FL
 Method BLASTN
 NCBI GI g476215
 BLAST score 912
 E value 0.0e+00
 Match length 1756
 % identity 91
 NCBI Description Glycine max Century 84 p24 oleosin isoform B gene, complete cds

Seq. No. 155
 Contig ID 88_2.R1040
 5'-most EST g5688194
 Method BLASTN
 NCBI GI g944829
 BLAST score 856
 E value 0.0e+00
 Match length 860
 % identity 100
 NCBI Description G.max mRNA for 24 kDa oleosin isoform (clone P24/91)

Seq. No. 156
 Contig ID 88_3.R1040
 5'-most EST CPR10278:2F700678725_FL
 Method BLASTN
 NCBI GI g476213
 BLAST score 907
 E value 0.0e+00
 Match length 1025
 % identity 97
 NCBI Description Glycine max Century 84 p24 oleosin isoform A gene, complete cds

Seq. No. 157
 Contig ID 88_8.R1040
 5'-most EST zpv700759006.h1
 Method BLASTN
 NCBI GI g476213
 BLAST score 172
 E value 4.0e-92
 Match length 276
 % identity 91
 NCBI Description Glycine max Century 84 p24 oleosin isoform A gene, complete cds

Seq. No. 158
 Contig ID 91_1.R1040
 5'-most EST uC-gmflminsoy089b10b1
 Method BLASTX
 NCBI GI g4126401
 BLAST score 1596
 E value 1.0e-178
 Match length 375

% identity 81
NCBI Description (AB011795) flavanone 3-hydroxylase [Citrus sinensis]

Seq. No. 159
Contig ID 92_1.R1040
5'-most EST fC-gmse700669702f4

Seq. No. 160
Contig ID 92_2.R1040
5'-most EST CPR10713_FL
Method BLASTX
NCBI GI g1332411
BLAST score 1410
E value 1.0e-157
Match length 331
% identity 78
NCBI Description (D85102) dihydroflavonol 4-reductase [Rosa hybrida]

Seq. No. 161
Contig ID 92_3.R1040
5'-most EST jC-gmst02400075d12d1
Method BLASTX
NCBI GI g1706377
BLAST score 250
E value 4.0e-21
Match length 79
% identity 66
NCBI Description DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL 4-REDUCTASE) >gi_499018_emb_CAA53578_(X75964) dihydroflavonol reductase [Vitis vinifera]

Seq. No. 162
Contig ID 92_4.R1040
5'-most EST kl1701212272.h1
Method BLASTX
NCBI GI g1888485
BLAST score 657
E value 6.0e-69
Match length 164
% identity 76
NCBI Description (Y11749) dihydroflavonol 4-reductase [Vitis vinifera]

Seq. No. 163
Contig ID 92_5.R1040
5'-most EST jsh701065818.h1
Method BLASTX
NCBI GI g1888485
BLAST score 312
E value 7.0e-29
Match length 71
% identity 83
NCBI Description (Y11749) dihydroflavonol 4-reductase [Vitis vinifera]

Seq. No. 164
Contig ID 93_1.R1040
5'-most EST CPR10721_FL
Method BLASTX

Match length 379
 % identity 90
 NCBI Description (AB013289) Bd 30K [Glycine max]

Seq. No. 169
 Contig ID 95_6.R1040
 5'-most EST txt700733563.h1
 Method BLASTN
 NCBI GI g3097320
 BLAST score 264
 E value 1.0e-147
 Match length 357
 % identity 97
 NCBI Description Glycine max gene for Bd 30K, complete cds

Seq. No. 170
 Contig ID 96_1.R1040
 5'-most EST CPR10171_FL
 Method BLASTN
 NCBI GI g3452139
 BLAST score 124
 E value 2.0e-62
 Match length 312
 % identity 88
 NCBI Description Glycine max mRNA for resistance protein, partial

Seq. No. 171
 Contig ID 98_1.R1040
 5'-most EST kl1701215045.h1
 Method BLASTX
 NCBI GI g1213629
 BLAST score 1711
 E value 0.0e+00
 Match length 480
 % identity 68
 NCBI Description (X95991) pectinesterase [Prunus persica]

Seq. No. 172
 Contig ID 98_2.R1040
 5'-most EST kl1701204315.h2
 Method BLASTX
 NCBI GI g1213629
 BLAST score 220
 E value 7.0e-18
 Match length 91
 % identity 52
 NCBI Description (X95991) pectinesterase [Prunus persica]

Seq. No. 173
 Contig ID 99_1.R1040
 5'-most EST CPR10679:2F701202691H1_FL
 Method BLASTX
 NCBI GI g2832625
 BLAST score 742
 E value 2.0e-78
 Match length 329
 % identity 46

Method BLASTX
 NCBI GI g541849
 BLAST score 740
 E value 2.0e-96
 Match length 253
 % identity 69
 NCBI Description anthranilate synthase (EC 4.1.3.27) beta chain -
 Arabidopsis thaliana >gi_403434 (L22585) anthranilate
 synthase beta subunit [Arabidopsis thaliana]

Seq. No. 179
 Contig ID 106_5.R1040
 5'-most EST LIB3028-047-Q1-B1-C9
 Method BLASTN
 NCBI GI g1173641
 BLAST score 837
 E value 0.0e+00
 Match length 1175
 % identity 96
 NCBI Description Glycine max lipoxygenase (lox7) mRNA, complete cds

Seq. No. 180
 Contig ID 106_6.R1040
 5'-most EST k11701202328.h1
 Method BLASTX
 NCBI GI g1928991
 BLAST score 306
 E value 8.0e-28
 Match length 90
 % identity 73
 NCBI Description (U92815) heat shock protein 70 precursor [Citrullus
 lanatus]

Seq. No. 181
 Contig ID 106_7.R1040
 5'-most EST epx701108350.h1
 Method BLASTX
 NCBI GI g1236949
 BLAST score 964
 E value 0.0e+00
 Match length 858
 % identity 63
 NCBI Description (U50075) lipoxygenase L-5 [Glycine max]

Seq. No. 182
 Contig ID 106_8.R1040
 5'-most EST g1173641_FL
 Method BLASTX
 NCBI GI g1173642
 BLAST score 1190
 E value 0.0e+00
 Match length 854
 % identity 47
 NCBI Description (U36191) lipoxygenase [Glycine max]
 >gi_1588566_prf_2208476A lipoxygenase [Glycine max]

Seq. No. 183

Contig ID 106 9.R1040
 5'-most EST LIB3106-026-Q1-K1-H7
 Method BLASTX
 NCBI GI g585418
 BLAST score 758
 E value 0.0e+00
 Match length 855
 % identity 38
 NCBI Description LIPOXYGENASE-4 (L-4) (VSP94) >gi_2160320_dbj_BAA03101_(D13999) lipxygenase L-4 [Glycine max]

Seq. No. 184
 Contig ID 108 1.R1040
 5'-most EST jC-gmro02910022e06d1
 Method BLASTX
 NCBI GI g115608
 BLAST score 1619
 E value 0.0e+00
 Match length 314
 % identity 98
 NCBI Description PHOSPHOENOLPYRUVATE CARBOXYLASE 1 (PEPCASE)
 >gi_22563_emb_CAA33316 (X15238) phosphoenolpyruvate
 carboxylase (AA 1 - 970) [Zea mays]

Seq. No. 185
 Contig ID 109 1.R1040
 5'-most EST CPR10669:2F701207222H1_FL

Seq. No. 186
 Contig ID 110 1.R1040
 5'-most EST CPR10386_FL
 Method BLASTX
 NCBI GI g2529678
 BLAST score 402
 E value 1.0e-38
 Match length 190
 % identity 31
 NCBI Description (AC002535) unknown protein [Arabidopsis thaliana]

Seq. No. 187
 Contig ID 112 1.R1040
 5'-most EST k11701212463.h1
 Method BLASTX
 NCBI GI g1619602
 BLAST score 602
 E value 4.0e-62
 Match length 215
 % identity 56
 NCBI Description (Y08726) MtN3 [Medicago truncatula]

Seq. No. 188
 Contig ID 112 3.R1040
 5'-most EST k11701205638.h1
 Method BLASTX
 NCBI GI g1619602
 BLAST score 234
 E value 1.0e-19

Match length 96
 % identity 52
 NCBI Description (Y08726) MtN3 [Medicago truncatula]

Seq. No. 189
 Contig ID 113 1.R1040
 5'-most EST 701060596H1.SEQ_FL
 Method BLASTX
 NCBI GI g134151
 BLAST score 218
 E value 2.0e-17
 Match length 109
 % identity 41
 NCBI Description 3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID
 5-ALPHA-REDUCTASE 1) (SR TYPE 1) >gi_1079480_pir_A55274
 3-oxo-5alpha-steroid 4-dehydrogenase (EC 1.3.99.5) - human
 >gi_177767 (M32313) steroid 5-alpha-reductase (EC 1.3.99.5)
 [Homo sapiens] >gi_338476 (M68886) steroid
 5-alpha-reductase [Homo sapiens] >gi_3360435 (AF052126)
 steroid 5-alpha-reductase [Homo sapiens]
 >gi_4507201_ref_NP_001038.1_pSRD5A1
 steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5
 alpha-steroid delta 4-dehydrogenase alpha 1)

Seq. No. 190
 Contig ID 117 1.R1040
 5'-most EST CPR9734_FL
 Method BLASTX
 NCBI GI g3135672
 BLAST score 161
 E value 3.0e-10
 Match length 118
 % identity 39
 NCBI Description (AF064070) putative 1-acyl-sn-glycerol-3-phosphate
 acyltransferase [Burkholderia pseudomallei]

Seq. No. 191
 Contig ID 117 2.R1040
 5'-most EST leu701157888.h1

Seq. No. 192
 Contig ID 118 1.R1040
 5'-most EST 700732879H1.SEQ_FL
 Method BLASTX
 NCBI GI g3873678
 BLAST score 162
 E value 7.0e-11
 Match length 79
 % identity 42
 NCBI Description (Z71178) Similarity with yeast hypothetical protein (Swiss
 prot accession number P40526) [Caenorhabditis elegans]

Seq. No. 193
 Contig ID 119 1.R1040
 5'-most EST asn701132823.h1
 Method BLASTX
 NCBI GI g3738284

Seq. No. 200
 Contig ID 122_1.R1040
 5'-most EST LIB3050-003-Q1-E1-G6
 Method BLASTX
 NCBI GI g2511541
 BLAST score 1505
 E value 1.0e-168
 Match length 392
 % identity 76
 NCBI Description (AF020787) DNA-binding protein GBP16 [Oryza sativa]

Seq. No. 201
 Contig ID 122_2.R1040
 5'-most EST jC-gmle01810085c10d1
 Method BLASTX
 NCBI GI g4539457
 BLAST score 613
 E value 3.0e-63
 Match length 308
 % identity 49
 NCBI Description (AL049500) heat shock transcription factor-like protein [Arabidopsis thaliana]

Seq. No. 202
 Contig ID 122_3.R1040
 5'-most EST fC-gmro700846171a1
 Method BLASTX
 NCBI GI g2511541
 BLAST score 909
 E value 2.0e-98
 Match length 251
 % identity 77
 NCBI Description (AF020787) DNA-binding protein GBP16 [Oryza sativa]

Seq. No. 203
 Contig ID 122_4.R1040
 5'-most EST awf700837002.h1
 Method BLASTX
 NCBI GI g4539457
 BLAST score 586
 E value 3.0e-60
 Match length 255
 % identity 54
 NCBI Description (AL049500) heat shock transcription factor-like protein [Arabidopsis thaliana]

Seq. No. 204
 Contig ID 122_6.R1040
 5'-most EST fC-gmro700864991g1
 Method BLASTX
 NCBI GI g2511541
 BLAST score 331
 E value 2.0e-30
 Match length 77
 % identity 86
 NCBI Description (AF020787) DNA-binding protein GBP16 [Oryza sativa]

% identity 95
 NCBI Description (AL031581) 1-evidence=predicted by content;
 1-method=genefinder;084; 1-method_score=23.36;
 1-evidence_end; 2-evidence=predicted by match;
 2-match_accession=AA141041;
 2-match_description=CK01110.3prime CK Drosophila
 melanogaster

Seq. No. 209
 Contig ID 124_1.R1040
 5'-most EST CPR10667:2F701214015H1_FL
 Method BLASTX
 NCBI GI g535454
 BLAST score 962
 E value 1.0e-104
 Match length 309
 % identity 59
 NCBI Description (U13940) cysteine proteinase [Alnus glutinosa]

Seq. No. 210
 Contig ID 124_2.R1040
 5'-most EST LIB3050-026-Q1-K1-D9
 Method BLASTX
 NCBI GI g535454
 BLAST score 238
 E value 5.0e-20
 Match length 94
 % identity 51
 NCBI Description (U13940) cysteine proteinase [Alnus glutinosa]

Seq. No. 211
 Contig ID 124_3.R1040
 5'-most EST k11701211192.h1
 Method BLASTX
 NCBI GI g2944446
 BLAST score 177
 E value 3.0e-13
 Match length 51
 % identity 71
 NCBI Description (AF050756) cysteine endopeptidase precursor [Ricinus
 communis]

Seq. No. 212
 Contig ID 125_1.R1040
 5'-most EST CPR10665:2F701213140H1_FL
 Method BLASTX
 NCBI GI g3688284
 BLAST score 1204
 E value 1.0e-132
 Match length 371
 % identity 60
 NCBI Description (AJ011567) lanatoside 15'-O-acetylerase [Digitalis
 lanata]

Seq. No. 213
 Contig ID 126_1.R1040
 5'-most EST LIB3051-042-Q1-K1-H5

Method BLASTX
 NCBI GI g1946364
 BLAST score 1416
 E value 1.0e-157
 Match length 420
 % identity 64
 NCBI Description (U93215) lipase isolog [Arabidopsis thaliana]

Seq. No. 214
 Contig ID 127_1.R1040
 5'-most EST CPR6969:2F700980490_FL
 Method BLASTX
 NCBI GI g4165132
 BLAST score 1783
 E value 0.0e+00
 Match length 483
 % identity 69
 NCBI Description (AF098292) endo-beta-1,4-D-glucanase [Lycopersicon
 esculentum]

Seq. No. 215
 Contig ID 127_2.R1040
 5'-most EST LIB3109-002-Q1-K2-H3
 Method BLASTN
 NCBI GI g3170524
 BLAST score 104
 E value 3.0e-51
 Match length 224
 % identity 87
 NCBI Description Fragaria x ananassa cellulase (Cel2) mRNA, complete cds

Seq. No. 216
 Contig ID 130_1.R1040
 5'-most EST k11701211539.h1
 Method BLASTX
 NCBI GI g2367431
 BLAST score 1358
 E value 1.0e-150
 Match length 467
 % identity 56
 NCBI Description (AF000403) putative cytochrome P450 [Lotus japonicus]

Seq. No. 217
 Contig ID 131_1.R1040
 5'-most EST CPR9001:2F700903466_FL
 Method BLASTX
 NCBI GI g3212880
 BLAST score 1185
 E value 1.0e-159
 Match length 455
 % identity 61
 NCBI Description (AC004005) putative Mlo protein [Arabidopsis thaliana]

Seq. No. 218
 Contig ID 131_2.R1040
 5'-most EST pcp700989120.h1
 Method BLASTX

NCBI GI g2765817
 BLAST score 404
 E value 2.0e-39
 Match length 135
 % identity 67
 NCBI Description (Z95352) AtMlo-h1 [Arabidopsis thaliana]
 >gi_3892049_gb_AAC78258.1_AAC78258 (AC002330) AtMlo-h1
 [Arabidopsis thaliana]

Seq. No. 219
 Contig ID 131_4.R1040
 5'-most EST fua701038423.h1
 Method BLASTX
 NCBI GI g2765817
 BLAST score 291
 E value 3.0e-26
 Match length 88
 % identity 62
 NCBI Description (Z95352) AtMlo-h1 [Arabidopsis thaliana]
 >gi_3892049_gb_AAC78258.1_AAC78258 (AC002330) AtMlo-h1
 [Arabidopsis thaliana]

Seq. No. 220
 Contig ID 132_1.R1040
 5'-most EST leu701150403.h1
 Method BLASTX
 NCBI GI g2213598
 BLAST score 389
 E value 5.0e-37
 Match length 312
 % identity 16
 NCBI Description (AC000348) T7N9.18 [Arabidopsis thaliana]

Seq. No. 221
 Contig ID 133_1.R1040
 5'-most EST fC-zmf1700343886_FL
 Method BLASTX
 NCBI GI g4580398
 BLAST score 746
 E value 6.0e-79
 Match length 198
 % identity 71
 NCBI Description (AC007171) putative protein kinase APK1A [Arabidopsis thaliana]

Seq. No. 222
 Contig ID 134_1.R1040
 5'-most EST fC-zmf1700344343_FL
 Method BLASTX
 NCBI GI g3482921
 BLAST score 264
 E value 2.0e-22
 Match length 79
 % identity 62
 NCBI Description (AC003970) Unknown protein [Arabidopsis thaliana]

Seq. No. 223

Contig ID 135_1.R1040
5'-most EST fC-zmfl700352002_FL
Method BLASTX
NCBI GI g585593
BLAST score 220
E value 3.0e-17
Match length 188
% identity 27
NCBI Description NUCLEAR PORE GLYCOPROTEIN P62 (NUCLEOPORIN P62)
>gi_432654_emb_CAA41411_ (X58521) nucleoporin p62 [Homo sapiens]

Seq. No. 224
Contig ID 136_1.R1040
5'-most EST fC-zmle700422033_FL

Seq. No. 225
Contig ID 137_1.R1040
5'-most EST fC-zmfl700351889_FL

Seq. No. 226
Contig ID 138_1.R1040
5'-most EST LIB3093-038-Q1-K1-F11
Method BLASTX
NCBI GI g4126473
BLAST score 876
E value 3.0e-94
Match length 211
% identity 81
NCBI Description (AB014884) adenylyl cyclase associated protein [Gossypium hirsutum]

Seq. No. 227
Contig ID 139_1.R1040
5'-most EST fC-gmst700790741_FL
Method BLASTN
NCBI GI g1785614
BLAST score 49
E value 5.0e-18
Match length 126
% identity 85
NCBI Description Pisum sativum protein kinase homolog PsPK4 mRNA, complete cds

Seq. No. 228
Contig ID 139_2.R1040
5'-most EST uC-gmflminsoy058f07b1

Seq. No. 229
Contig ID 139_3.R1040
5'-most EST LIB3094-030-Q1-K1-D3
Method BLASTN
NCBI GI g1480927
BLAST score 170
E value 2.0e-90
Match length 301
% identity 89

NCBI Description Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene

Seq. No. 230
 Contig ID 139_4.R1040
 5'-most EST LIB3094-072-Q1-K1-A6
 Method BLASTN
 NCBI GI g1480927
 BLAST score 97
 E value 7.0e-47
 Match length 211
 % identity 91

NCBI Description Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene

Seq. No. 231
 Contig ID 139_5.R1040
 5'-most EST jsh701064823.h1
 Method BLASTN
 NCBI GI g1480927
 BLAST score 93
 E value 1.0e-44
 Match length 137
 % identity 92

NCBI Description Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene

Seq. No. 232
 Contig ID 140_1.R1040
 5'-most EST fC-zmfl700344725_FL
 Method BLASTX
 NCBI GI g3786005
 BLAST score 1535
 E value 1.0e-171
 Match length 365
 % identity 80
 NCBI Description (AC005499) putative phosphoethanolamine cytidyltransferase [Arabidopsis thaliana]

Seq. No. 233
 Contig ID 141_1.R1040
 5'-most EST fC-zmfl700352293_FL
 Method BLASTX
 NCBI GI g127112
 BLAST score 450
 E value 4.0e-44
 Match length 175
 % identity 51
 NCBI Description MAK16 PROTEIN >gi_73269_pir_BVBYK6 MAK16 protein - yeast (Saccharomyces cerevisiae) >gi_171880 (J03852) MAK16 protein [Saccharomyces cerevisiae] >gi_595561 (U12980) Mak16p: putative nuclear protein [Saccharomyces cerevisiae]

Seq. No. 234
 Contig ID 142_1.R1040
 5'-most EST fC-gmse700645507_FL
 Method BLASTN

Contig ID 147 1.R1040
 5'-most EST k11701210137.h1
 Method BLASTX
 NCBI GI g4510395
 BLAST score 1198
 E value 1.0e-146
 Match length 394
 % identity 66
 NCBI Description (AC006587) putative beta-galactosidase precursor
 [Arabidopsis thaliana]

Seq. No. 241
 Contig ID 148 1.R1040
 5'-most EST zhf700960184.h1
 Method BLASTX
 NCBI GI g3914394
 BLAST score 2455
 E value 0.0e+00
 Match length 559
 % identity 83
 NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
 (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)
 >gi_2118335_pir_S60473 phosphoglycerate mutase (EC
 5.4.2.1) - common ice plant >gi_602426 (U16021)
 phosphoglyceromutase [Mesembryanthemum crystallinum]

Seq. No. 242
 Contig ID 149 1.R1040
 5'-most EST uaw700661032.h1
 Method BLASTX
 NCBI GI g2244744
 BLAST score 347
 E value 3.0e-32
 Match length 122
 % identity 57
 NCBI Description (Y13676) bZIP DNA-binding protein [Antirrhinum majus]

Seq. No. 243
 Contig ID 149 2.R1040
 5'-most EST LIB3049-016-Q1-E1-B3
 Method BLASTN
 NCBI GI g394735
 BLAST score 36
 E value 1.0e-10
 Match length 52
 % identity 92
 NCBI Description Rice lip19 mRNA for basic/leucine zipper protein

Seq. No. 244
 Contig ID 149 3.R1040
 5'-most EST zzp700836073.h1

Seq. No. 245
 Contig ID 149 4.R1040
 5'-most EST LIB3028-008-Q1-B1-A1

Seq. No. 246

Contig ID 150_1.R1040
 5'-most EST zsg701120848.h1
 Method BLASTX
 NCBI GI g1362002
 BLAST score 990
 E value 1.0e-107
 Match length 242
 % identity 77
 NCBI Description protein kinase 1 - Arabidopsis thaliana >gi_166817 (L05561)
 protein kinase [Arabidopsis thaliana]

Seq. No. 247
 Contig ID 150_2.R1040
 5'-most EST uC-gmropic058h06b1
 Method BLASTX
 NCBI GI g1362002
 BLAST score 256
 E value 9.0e-30
 Match length 130
 % identity 60
 NCBI Description protein kinase 1 - Arabidopsis thaliana >gi_166817 (L05561)
 protein kinase [Arabidopsis thaliana]

Seq. No. 248
 Contig ID 151_1.R1040
 5'-most EST kll701214918.h1
 Method BLASTX
 NCBI GI g2459435
 BLAST score 1494
 E value 1.0e-166
 Match length 452
 % identity 63
 NCBI Description (AC002332) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No. 249
 Contig ID 152_1.R1040
 5'-most EST fC-gmro700562302_FL
 Method BLASTX
 NCBI GI g1888359
 BLAST score 294
 E value 6.0e-33
 Match length 179
 % identity 69
 NCBI Description (Y11689) 3-ketoacyl-acyl carrier protein synthase III
 [Arabidopsis thaliana]

Seq. No. 250
 Contig ID 152_2.R1040
 5'-most EST fC-gmse700854533a1
 Method BLASTX
 NCBI GI g1706757
 BLAST score 1048
 E value 1.0e-114
 Match length 232
 % identity 86
 NCBI Description 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE III A PRECURSOR

(BETA-KETOACYL-ACP SYNTHASE III A) (KAS III A) >gi_1276434
(U15935) beta-ketoacyl-ACP synthase III [Cuphea wrightii]

Seq. No. 251
Contig ID 153_1.R1040
5'-most EST xpa700793632.h1
Method BLASTX
NCBI GI g2346978
BLAST score 344
E value 7.0e-32
Match length 167
% identity 49
NCBI Description (AB006601) ZPT2-14 [Petunia x hybrida]

Seq. No. 252
Contig ID 153_2.R1040
5'-most EST LIB3049-032-Q1-E1-B4
Method BLASTX
NCBI GI g2346976
BLAST score 356
E value 2.0e-33
Match length 152
% identity 54
NCBI Description (AB006600) ZPT2-13 [Petunia x hybrida]

Seq. No. 253
Contig ID 154_1.R1040
5'-most EST awf700836660.h1
Method BLASTX
NCBI GI g2664214
BLAST score 189
E value 2.0e-13
Match length 171
% identity 31
NCBI Description (AJ222646) G2484-1 [Arabidopsis thaliana]

Seq. No. 254
Contig ID 154_2.R1040
5'-most EST LIB3170-039-Q1-J1-H5

Seq. No. 255
Contig ID 155_1.R1040
5'-most EST fC-gmro700566983_FL

Seq. No. 256
Contig ID 156_1.R1040
5'-most EST fC-gmro700567081_FL
Method BLASTX
NCBI GI g1346729
BLAST score 192
E value 4.0e-14
Match length 198
% identity 16
NCBI Description PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA >gi_886024
(U23820) protein kinase Pkwa [Thermomonospora curvata]

Seq. No. 257

Contig ID 157 1.R1040
 5'-most EST g5752858
 Method BLASTX
 NCBI GI g2811029
 BLAST score 385
 E value 6.0e-37
 Match length 107
 % identity 72
 NCBI Description ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT)
 (ACETYLORNITHINE TRANSAMINASE) (AOTA)
 >gi_1944511_emb_CAA69936_ (Y08680) acetylornithine
 aminotransferase [Alnus glutinosa]

Seq. No. 258
 Contig ID 158 1.R1040
 5'-most EST fua701037507.h1
 Method BLASTX
 NCBI GI g1076318
 BLAST score 383
 E value 2.0e-36
 Match length 109
 % identity 41
 NCBI Description dihydrolipoamide S-acetyltransferase (EC 2.3.1.12)
 precursor - Arabidopsis thaliana (fragment)
 >gi_559395_emb_CAA86300_ (Z46230) dihydrolipoamide
 acetyltransferase (E2) subunit of PDC [Arabidopsis
 thaliana]

Seq. No. 259
 Contig ID 158 2.R1040
 5'-most EST zzp700833589.h1
 Method BLASTX
 NCBI GI g2129473
 BLAST score 375
 E value 1.0e-35
 Match length 161
 % identity 47
 NCBI Description arabinogalactan-like protein - loblolly pine >gi_607774
 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No. 260
 Contig ID 158 3.R1040
 5'-most EST fua701041084.h1
 Method BLASTX
 NCBI GI g2129473
 BLAST score 325
 E value 5.0e-30
 Match length 136
 % identity 49
 NCBI Description arabinogalactan-like protein - loblolly pine >gi_607774
 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No. 261
 Contig ID 159 1.R1040
 5'-most EST LIB3049-021-Q1-E1-A2
 Method BLASTX
 NCBI GI g4115914

BLAST score 524
 E value 7.0e-53
 Match length 324
 % identity 38
 NCBI Description (AF118222) contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=297.8, E=1.3e-85, N=1) [Arabidopsis thaliana] >gi_4539410_emb_CAB40043.1 (AL049524) putative Fe(II)/ascorbate oxidase [Arabidopsis thaliana]

Seq. No. 262
 Contig ID 159_2.R1040
 5'-most EST leu701153539.h1

Seq. No. 263
 Contig ID 160_1.R1040
 5'-most EST LIB3028-040-Q1-B1-E7
 Method BLASTX
 NCBI GI g2780955
 BLAST score 238
 E value 3.0e-19
 Match length 214
 % identity 35
 NCBI Description Phosphatidylinositol Transfer Protein Sec14p From Saccharomyces Cerevisiae

Seq. No. 264
 Contig ID 160_2.R1040
 5'-most EST LIB3049-026-Q1-E1-A3

Seq. No. 265
 Contig ID 161_1.R1040
 5'-most EST jC-gmf102220098b09d1
 Method BLASTX
 NCBI GI g1352186
 BLAST score 1271
 E value 1.0e-140
 Match length 473
 % identity 51
 NCBI Description ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE) (CYTOCHROME P450 74) >gi_404866 (U00428) allene oxide synthase [Linum usitatissimum]

Seq. No. 266
 Contig ID 161_2.R1040
 5'-most EST fC-gmse700751003d2
 Method BLASTN
 NCBI GI g18662
 BLAST score 903
 E value 0.0e+00
 Match length 974
 % identity 98
 NCBI Description Glycine max hsp 70 gene

Seq. No. 267
 Contig ID 161_3.R1040
 5'-most EST jC-gmst02400030e01d1

5'-most EST fC-zmst700621904_FL
 Method BLASTX
 NCBI GI g113029
 BLAST score 1716
 E value 0.0e+00
 Match length 452
 % identity 74
 NCBI Description ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
 >gi_68209_pir_WZCNIU isocitrate lyase (EC 4.1.3.1) -
 upland cotton >gi_18486_emb_CAA36381_ (X52136) isocitrate
 lyase (AA 1-576) [Gossypium hirsutum]

Seq. No. 273
 Contig ID 164_1.R1040
 5'-most EST fC-gmle700786490_FL
 Method BLASTX
 NCBI GI g4204849
 BLAST score 948
 E value 1.0e-102
 Match length 223
 % identity 78
 NCBI Description (U55875) protein kinase [Arabidopsis thaliana]

Seq. No. 274
 Contig ID 165_1.R1040
 5'-most EST LIB3109-022-Q1-K1-G3
 Method BLASTX
 NCBI GI g3688123
 BLAST score 2069
 E value 0.0e+00
 Match length 619
 % identity 66
 NCBI Description (AJ006293) granule-bound starch synthase [Antirrhinum
 majus]

Seq. No. 275
 Contig ID 165_5.R1040
 5'-most EST LIB3092-018-Q1-K1-G2

Seq. No. 276
 Contig ID 166_1.R1040
 5'-most EST fC-zmro700835672_FL
 Method BLASTX
 NCBI GI g3450842
 BLAST score 894
 E value 3.0e-96
 Match length 269
 % identity 62
 NCBI Description (AF080436) mitogen activated protein kinase kinase [Oryza
 sativa]

Seq. No. 277
 Contig ID 167_1.R1040
 5'-most EST fC-zmro700835718_FL
 Method BLASTX
 NCBI GI g2829275
 BLAST score 837

E value 1.0e-89
 Match length 236
 % identity 70
 NCBI Description (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana] >gi_3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_ (AL049525) nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana]

Seq. No. 278
 Contig ID 167_2.R1040
 5'-most EST LIB3093-031-Q1-K1-H3
 Method BLASTX
 NCBI GI g2829275
 BLAST score 125
 E value 6.0e-09
 Match length 70
 % identity 60
 NCBI Description (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana] >gi_3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_ (AL049525) nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana]

Seq. No. 279
 Contig ID 168_1.R1040
 5'-most EST fC-zmro700835944_FL
 Method BLASTX
 NCBI GI g3901012
 BLAST score 1162
 E value 1.0e-128
 Match length 274
 % identity 75
 NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]

Seq. No. 280
 Contig ID 168_2.R1040
 5'-most EST uC-gmropic070h06b1
 Method BLASTX
 NCBI GI g3901012
 BLAST score 1197
 E value 1.0e-132
 Match length 278
 % identity 78
 NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]

Seq. No. 281
 Contig ID 168_3.R1040
 5'-most EST fC-gmse700670426g2
 Method BLASTX
 NCBI GI g3901012
 BLAST score 514
 E value 4.0e-52

5'-most EST LIB3055-004-Q1-N1-H3
 Method BLASTX
 NCBI GI g585973
 BLAST score 353
 E value 4.0e-53
 Match length 127
 % identity 89
 NCBI Description FRUCTOKINASE >gi_626018_pir_S39997 fructokinase (EC 2.7.1.4) - potato >gi_297015_emb_CAA78283_ (Z12823) fructokinase [Solanum tuberosum] >gi_1095321_prf_2108342A fructokinase [Solanum tuberosum]

Seq. No. 287
 Contig ID 170_1.R1040
 5'-most EST fC-zmle700426440_FL
 Method BLASTX
 NCBI GI g2736286
 BLAST score 322
 E value 1.0e-51
 Match length 125
 % identity 80
 NCBI Description (AF031079) isopentenyl diphosphate isomerase I [Camptotheca acuminata]

Seq. No. 288
 Contig ID 171_5.R1040
 5'-most EST LIB3106-113-Q1-K1-C5
 Method BLASTN
 NCBI GI g18730
 BLAST score 85
 E value 7.0e-40
 Match length 89
 % identity 99
 NCBI Description Soybean 4.5 - 5S rRNA intergenic region

Seq. No. 289
 Contig ID 171_6.R1040
 5'-most EST wvk700685569.h1
 Method BLASTN
 NCBI GI g18730
 BLAST score 72
 E value 3.0e-32
 Match length 72
 % identity 100
 NCBI Description Soybean 4.5 - 5S rRNA intergenic region

Seq. No. 290
 Contig ID 171_7.R1040
 5'-most EST wrq700791869.h1

Seq. No. 291
 Contig ID 171_8.R1040
 5'-most EST LIB3092-010-Q1-K1-F5
 Method BLASTX
 NCBI GI g1173218
 BLAST score 237
 E value 1.0e-19

% identity 65
 NCBI Description ATAF1 protein - Arabidopsis thaliana (fragment)
 >gi_1345506_emb_CAA52771_ (X74755) ATAF1 [Arabidopsis thaliana]

Seq. No. 309
 Contig ID 171_26.R1040
 5'-most EST LIB3072-021-Q1-E1-C1
 Method BLASTX
 NCBI GI g3551838
 BLAST score 331
 E value 4.0e-49
 Match length 151
 % identity 75
 NCBI Description (AF070967) SKP1-like protein [Nicotiana clevelandii]

Seq. No. 310
 Contig ID 171_27.R1040
 5'-most EST LIB3138-085-P1-N1-A12
 Method BLASTN
 NCBI GI g210811
 BLAST score 163
 E value 4.0e-86
 Match length 704
 % identity 85
 NCBI Description Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No. 311
 Contig ID 171_28.R1040
 5'-most EST awf700838388.h1
 Method BLASTX
 NCBI GI g480618
 BLAST score 423
 E value 6.0e-41
 Match length 233
 % identity 48
 NCBI Description ATAF1 protein - Arabidopsis thaliana (fragment)
 >gi_1345506_emb_CAA52771_ (X74755) ATAF1 [Arabidopsis thaliana]

Seq. No. 312
 Contig ID 171_29.R1040
 5'-most EST LIB3107-010-Q1-K1-B8
 Method BLASTX
 NCBI GI g1350954
 BLAST score 148
 E value 5.0e-23
 Match length 129
 % identity 62
 NCBI Description 40S RIBOSOMAL PROTEIN S15A >gi_422493_pir_S33498 ribosomal protein DS15a - fruit fly (Drosophila melanogaster)
 >gi_311606_emb_CAA79771_ (Z21673) ribosomal protein 15a (40S subunit) [Drosophila melanogaster]

Seq. No. 313
 Contig ID 171_30.R1040


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Method                BLASTN
NCBI GI               g1204128
BLAST score           169
E value               8.0e-90
Match length          325
% identity            88
NCBI Description       M.sativa MMK2 mRNA for protein kinase

Seq. No.              319
Contig ID             173_1.R1040
5'-most EST           fC-gmfl700905635_FL
Method               BLASTX
NCBI GI               g2246376
BLAST score           418
E value              1.0e-40
Match length          164
% identity            65
NCBI Description       (Z86093) b-Zip DNA binding protein [Arabidopsis thaliana]

Seq. No.              320
Contig ID             174_1.R1040
5'-most EST           fC-gmfl700905531_FL
Method               BLASTN
NCBI GI               g2739045
BLAST score           1015
E value              0.0e+00
Match length          1015
% identity            100
NCBI Description       Glycine max polyphosphoinositide binding protein Ssh2p
                      (SSH2) mRNA, complete cds

Seq. No.              321
Contig ID             175_1.R1040
5'-most EST           zhf700957320.h1
Method               BLASTX
NCBI GI               g1352660
BLAST score           219
E value              4.0e-17
Match length          178
% identity            31
NCBI Description       COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR
                      >gi_924850 (U26264) CHOp24 [Cricetulus griseus]

Seq. No.              322
Contig ID             176_1.R1040
5'-most EST           jC-gmro02800028f01a1
Method               BLASTX
NCBI GI               g3024013
BLAST score           761
E value              1.0e-80
Match length          304
% identity            51
NCBI Description       EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT
                      (EIF-2-ALPHA) >gi_2706460_emb_CAA15918.1_ (AL021046)
                      translational initiation factor 2 alpha
                      [Schizosaccharomyces pombe]

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NCBI Description (X99210) myb-related transcription factor [*Lycopersicon
esculentum*]

Seq. No. 328
Contig ID 180 2.R1040
5'-most EST ncj700977108.h1

Seq. No. 329
Contig ID 180 3.R1040
5'-most EST leu701150112.h1
Method BLASTX
NCBI GI g2827545
BLAST score 379
E value 1.0e-36
Match length 69
% identity 94

NCBI Description (AL021635) myb-like protein [*Arabidopsis thaliana*]

Seq. No. 330
Contig ID 181_1.R1040
5'-most EST fC-gmst700890686_FL
Method BLASTX
NCBI GI g3256068
BLAST score 325
E value 1.0e-29
Match length 135
% identity 50

NCBI Description (Y14068) Heat Shock Factor 3 [*Arabidopsis thaliana*]

Seq. No. 331
Contig ID 182 1.R1040
5'-most EST fC-gmro700844279_FL
Method BLASTX
NCBI GI g2687724
BLAST score 1622
E value 0.0e+00
Match length 318
% identity 100

NCBI Description (AJ003245) NADPH:isoflavone reductase [*Glycine max*]

Seq. No. 332
Contig ID 182 2.R1040
5'-most EST fua701040175.h1
Method BLASTN
NCBI GI g2687723
BLAST score 544
E value 0.0e+00
Match length 964
% identity 89

NCBI Description *Glycine max* mRNA for putative NADPH:isoflavone reductase

Seq. No. 333
Contig ID 182 3.R1040
5'-most EST g5057872
Method BLASTN
NCBI GI g2687723
BLAST score 234

Seq. No. 339
 Contig ID 188_1.R1040
 5'-most EST fC-gmst700889529_FL
 Method BLASTX
 NCBI GI g1518540
 BLAST score 780
 E value 3.0e-83
 Match length 180
 % identity 86
 NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No. 340
 Contig ID 188_2.R1040
 5'-most EST zhf700964379.h1
 Method BLASTX
 NCBI GI g1518540
 BLAST score 164
 E value 1.0e-11
 Match length 34
 % identity 97
 NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No. 341
 Contig ID 189_1.R1040
 5'-most EST fC-gmst700888192_FL
 Method BLASTX
 NCBI GI g1827893
 BLAST score 314
 E value 1.0e-28
 Match length 93
 % identity 61
 NCBI Description Maize Nonspecific Lipid Transfer Protein Complexed With
 Palmitate >gi_1827894_pdb_1MZL_ Maize Nonspecific Lipid
 Transfer Protein >gi_2194092_pdb_1AFH_ Lipid Transfer
 Protein From Maize Seedlings, Nmr, 15 Structures

Seq. No. 342
 Contig ID 190_1.R1040
 5'-most EST fC-gmf1700902987_FL
 Method BLASTN
 NCBI GI g2627180
 BLAST score 276
 E value 1.0e-153
 Match length 468
 % identity 90
 NCBI Description Pisum sativum mRNA for cycloartenol synthase, complete cds

Seq. No. 343
 Contig ID 191_1.R1040
 5'-most EST LIB3139-030-P1-N1-A6

Seq. No. 344
 Contig ID 192_1.R1040
 5'-most EST fC-gmro700845184_FL
 Method BLASTX
 NCBI GI g2465010

BLAST score 422
 E value 3.0e-41
 Match length 141
 % identity 63
 NCBI Description (AJ001446) acyl carrier protein [Fragaria vesca]

Seq. No. 345
 Contig ID 192_2.R1040
 5'-most EST fua701038142.h1
 Method BLASTX
 NCBI GI g2465010
 BLAST score 382
 E value 2.0e-36
 Match length 139
 % identity 58
 NCBI Description (AJ001446) acyl carrier protein [Fragaria vesca]

Seq. No. 346
 Contig ID 193_1.R1040
 5'-most EST fC-gmst700790793_FL
 Method BLASTX
 NCBI GI g1708236
 BLAST score 1861
 E value 0.0e+00
 Match length 446
 % identity 77
 NCBI Description HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE)
 (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)
 >gi_2129617_pir_JC4567 hydroxymethylglutaryl-CoA synthase
 (EC 4.1.3.5) - Arabidopsis thaliana
 >gi_1143390_emb_CAA58763_ (X83882)
 hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]
 >gi_1586548_prf_2204245A hydroxy methylglutaryl CoA
 synthase [Arabidopsis thaliana]

Seq. No. 347
 Contig ID 194_1.R1040
 5'-most EST fC-zmfl700337153_FL
 Method BLASTX
 NCBI GI g1155255
 BLAST score 323
 E value 1.0e-29
 Match length 130
 % identity 48
 NCBI Description (U39228) beta-glucosidase [Prunus avium]

Seq. No. 348
 Contig ID 195_1.R1040
 5'-most EST fC-zmfl700354918_FL
 Method BLASTX
 NCBI GI g548493
 BLAST score 916
 E value 7.0e-99
 Match length 289
 % identity 59
 NCBI Description EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
 (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)

>gi_629854_pir_S30067 polygalacturonase - maize
 >gi_288612_emb_CAA47052_ (X66422) polygalacturonase [Zea
 mays]

Seq. No. 349
 Contig ID 196_1.R1040
 5'-most EST fC-zmfl700354921_FL
 Method BLASTN
 NCBI GI g429006
 BLAST score 39
 E value 3.0e-12
 Match length 95
 % identity 85
 NCBI Description Rice mRNA for MCM3 (gene name SS300), partial cds

Seq. No. 350
 Contig ID 197_1.R1040
 5'-most EST fC-zmfl700357449_FL
 Method BLASTX
 NCBI GI g3402722
 BLAST score 1200
 E value 1.0e-132
 Match length 302
 % identity 75
 NCBI Description (AC004261) CPDK-related protein [Arabidopsis thaliana]

Seq. No. 351
 Contig ID 198_1.R1040
 5'-most EST fC-zmfl700379641_FL
 Method BLASTX
 NCBI GI g3342242
 BLAST score 1840
 E value 0.0e+00
 Match length 463
 % identity 72
 NCBI Description (AF030421) cell wall invertase; beta-fructofuranosidase;
 fructosidase [Triticum aestivum]

Seq. No. 352
 Contig ID 199_1.R1040
 5'-most EST fC-zmfl700379870_FL
 Method BLASTX
 NCBI GI g3057120
 BLAST score 1314
 E value 1.0e-145
 Match length 292
 % identity 82
 NCBI Description (AF023159) starch synthase DULL1 [Zea mays]

Seq. No. 353
 Contig ID 200_1.R1040
 5'-most EST fC-zmro700829959_FL
 Method BLASTX
 NCBI GI g4154352
 BLAST score 392
 E value 1.0e-37
 Match length 241

% identity 39
 NCBI Description (AF110333) PrMC3 [Pinus radiata]

Seq. No. 354
 Contig ID 202_1.R1040
 5'-most EST fC-zmro700831955_FL
 Method BLASTX
 NCBI GI g3850630
 BLAST score 700
 E value 1.0e-73
 Match length 199
 % identity 62
 NCBI Description (AJ012581) cytochrome P450 [Cicer arietinum]

Seq. No. 355
 Contig ID 202_2.R1040
 5'-most EST fC-zmro700831544_FL
 Method BLASTX
 NCBI GI g3850630
 BLAST score 234
 E value 1.0e-36
 Match length 119
 % identity 54
 NCBI Description (AJ012581) cytochrome P450 [Cicer arietinum]

Seq. No. 356
 Contig ID 202_3.R1040
 5'-most EST g4396629
 Method BLASTX
 NCBI GI g4200044
 BLAST score 1306
 E value 1.0e-144
 Match length 382
 % identity 63
 NCBI Description (AB022732) cytochrome P450 [Glycyrrhiza echinata]

Seq. No. 357
 Contig ID 203_1.R1040
 5'-most EST fC-zmro700832243_FL
 Method BLASTX
 NCBI GI g3335378
 BLAST score 614
 E value 2.0e-63
 Match length 234
 % identity 54
 NCBI Description (AC003028) Myb-related transcription activator [Arabidopsis thaliana]

Seq. No. 358
 Contig ID 204_1.R1040
 5'-most EST fC-gmle700870704h2
 Method BLASTX
 NCBI GI g2129770
 BLAST score 1151
 E value 1.0e-126
 Match length 291
 % identity 71

NCBI Description xyloglucan endotransglycosylase-related protein XTR-2 -
 Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan
 endotransglycosylase-related protein [Arabidopsis thaliana]
 >gi_2154611_dbj_BAA20290_ (D63510) endoxyloglucan
 transferase related protein [Arabidopsis thaliana]

Seq. No. 359
 Contig ID 204_2.R1040
 5'-most EST fC-gmse7000756651r1
 Method BLASTX
 NCBI GI g2129770
 BLAST score 517
 E value 2.0e-52
 Match length 145
 % identity 66

NCBI Description xyloglucan endotransglycosylase-related protein XTR-2 -
 Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan
 endotransglycosylase-related protein [Arabidopsis thaliana]
 >gi_2154611_dbj_BAA20290_ (D63510) endoxyloglucan
 transferase related protein [Arabidopsis thaliana]

Seq. No. 360
 Contig ID 204_3.R1040
 5'-most EST LIB3051-115-Q1-K1-D8
 Method BLASTX
 NCBI GI g2129770
 BLAST score 415
 E value 1.0e-40
 Match length 98
 % identity 73

NCBI Description xyloglucan endotransglycosylase-related protein XTR-2 -
 Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan
 endotransglycosylase-related protein [Arabidopsis thaliana]
 >gi_2154611_dbj_BAA20290_ (D63510) endoxyloglucan
 transferase related protein [Arabidopsis thaliana]

Seq. No. 361
 Contig ID 204_4.R1040
 5'-most EST LIB3107-038-Q1-K1-C9
 Method BLASTX
 NCBI GI g2129770
 BLAST score 109
 E value 8.0e-13
 Match length 52
 % identity 70

NCBI Description xyloglucan endotransglycosylase-related protein XTR-2 -
 Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan
 endotransglycosylase-related protein [Arabidopsis thaliana]
 >gi_2154611_dbj_BAA20290_ (D63510) endoxyloglucan
 transferase related protein [Arabidopsis thaliana]

Seq. No. 362
 Contig ID 204_5.R1040
 5'-most EST dpv701102314.h1
 Method BLASTX
 NCBI GI g2129770
 BLAST score 177

E value 7.0e-13
 Match length 45
 % identity 71
 NCBI Description xyloglucan endotransglycosylase-related protein XTR-2 -
 Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan
 endotransglycosylase-related protein [Arabidopsis thaliana]
 >gi_2154611_dbj_BAA20290_ (D63510) endoxyloglucan
 transferase related protein [Arabidopsis thaliana]

Seq. No. 363
 Contig ID 205_1.R1040
 5'-most EST fC-zmro700833257_FL
 Method BLASTX
 NCBI GI g2494329
 BLAST score 378
 E value 8.0e-36
 Match length 310
 % identity 34
 NCBI Description GLUCAN 1,3-BETA-GLUCOSIDASE PRECURSOR
 (EXO-1,3-BETA-GLUCANASE) >gi_1150694_emb_CAA86952_ (Z46872)
 exo-1,3-beta-glucanase/1,3-beta-D-glucan glucanohydrolase
 [Yarrowia lipolytica]

Seq. No. 364
 Contig ID 205_2.R1040
 5'-most EST zsg701127354.h1
 Method BLASTX
 NCBI GI g1050956
 BLAST score 295
 E value 4.0e-26
 Match length 157
 % identity 46
 NCBI Description (U26160) 43 kDa secreted glycoprotein precursor
 [Paracoccidioides brasiliensis] >gi_1588394_prf_2208385A
 glycoprotein gp43 [Paracoccidioides brasiliensis]

Seq. No. 365
 Contig ID 206_1.R1040
 5'-most EST fC-zmro700833909_FL
 Method BLASTX
 NCBI GI g3128195
 BLAST score 1524
 E value 1.0e-170
 Match length 361
 % identity 83
 NCBI Description (AC004521) putative phosphoribosyl pyrophosphate synthetase
 [Arabidopsis thaliana] >gi_3341673 (AC003672) putative
 phosphoribosyl pyrophosphate synthetase [Arabidopsis
 thaliana]

Seq. No. 366
 Contig ID 207_1.R1040
 5'-most EST fC-zmro700833923_FL
 Method BLASTX
 NCBI GI g3540200
 BLAST score 237
 E value 2.0e-19

Match length	186
% identity	35
NCBI Description	(AC004260) Similar to TINY [Arabidopsis thaliana]
Seq. No.	367
Contig ID	208_1.R1040
5'-most EST	fC-zmro700834004_FL
Method	BLASTX
NCBI GI	g2979553
BLAST score	511
E value	1.0e-51
Match length	166
% identity	59
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]
Seq. No.	368
Contig ID	210_1.R1040
5'-most EST	fC-gmro700845739_FL
Seq. No.	369
Contig ID	210_3.R1040
5'-most EST	LIB3170-026-Q1-J1-F6
Seq. No.	370
Contig ID	210_4.R1040
5'-most EST	LIB3107-065-Q1-K1-B11
Seq. No.	371
Contig ID	211_1.R1040
5'-most EST	fC-gmro700849012_FL
Method	BLASTX
NCBI GI	g3643607
BLAST score	193
E value	1.0e-14
Match length	45
% identity	78
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.	372
Contig ID	212_1.R1040
5'-most EST	fC-gmst700791347_FL
Method	BLASTX
NCBI GI	g3643601
BLAST score	252
E value	3.0e-21
Match length	96
% identity	54
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]
Seq. No.	373
Contig ID	213_3.R1040
5'-most EST	bth700845603.h1
Method	BLASTN
NCBI GI	g2804153
BLAST score	304
E value	1.0e-170
Match length	693

% identity 88
NCBI Description Lupinus albus mRNA for aquaporin, partial

Seq. No. 374
Contig ID 213_4.R1040
5'-most EST LIB3073-005-Q1-K1-G8
Method BLASTX
NCBI GI g1175012
BLAST score 1285
E value 1.0e-142

Match length 283
% identity 86
NCBI Description PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN B) (TMP-B) >gi_396218_emb_CAA49155_(X69294) transmembrane protein TMP-B [Arabidopsis thaliana]

Seq. No. 375
Contig ID 213_5.R1040
5'-most EST leu701152670.h1
Method BLASTN
NCBI GI g3037046
BLAST score 402
E value 0.0e+00
Match length 656
% identity 91
NCBI Description Phaseolus vulgaris 1-aminocyclopropane-1-carboxylic acid oxidase mRNA, complete cds

Seq. No. 376
Contig ID 213_6.R1040
5'-most EST LIB3040-044-Q1-E1-D4
Method BLASTN
NCBI GI g2385377
BLAST score 162
E value 2.0e-85
Match length 517
% identity 85
NCBI Description Nicotiana tabacum mRNA for aquaporin

Seq. No. 377
Contig ID 213_7.R1040
5'-most EST g1575728_FL
Method BLASTN
NCBI GI g1575728
BLAST score 638
E value 0.0e+00
Match length 790
% identity 95
NCBI Description Glycine max 14-3-3 related protein SGF14C mRNA, complete cds

Seq. No. 378
Contig ID 213_8.R1040
5'-most EST uC-gmropic107f05b1
Method BLASTN
NCBI GI g2149954
BLAST score 221

E value 1.0e-120
 Match length 801
 % identity 88
 NCBI Description Phaseolus vulgaris putative aquaporin-1 (Mip-1) mRNA,
 complete cds

Seq. No. 379
 Contig ID 214_1.R1040
 5'-most EST LIB3170-004-Q1-K1-H9
 Method BLASTX
 NCBI GI g1149595
 BLAST score 1054
 E value 1.0e-115
 Match length 256
 % identity 77
 NCBI Description (Z49860) 1-acyl-sn-glycerol-3-phosphate acyltransferase
 [Brassica napus]

Seq. No. 380
 Contig ID 214_2.R1040
 5'-most EST jC-gmro02910070h01a1
 Method BLASTX
 NCBI GI g1149595
 BLAST score 200
 E value 2.0e-15
 Match length 63
 % identity 60
 NCBI Description (Z49860) 1-acyl-sn-glycerol-3-phosphate acyltransferase
 [Brassica napus]

Seq. No. 381
 Contig ID 215_1.R1040
 5'-most EST g5605705
 Method BLASTX
 NCBI GI g710626
 BLAST score 155
 E value 6.0e-10
 Match length 42
 % identity 57
 NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941
 (AC004625) dehydration-induced protein ERD15 [Arabidopsis
 thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis
 thaliana]

Seq. No. 382
 Contig ID 215_2.R1040
 5'-most EST g4291035
 Method BLASTX
 NCBI GI g710626
 BLAST score 147
 E value 5.0e-09
 Match length 42
 % identity 57
 NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941
 (AC004625) dehydration-induced protein ERD15 [Arabidopsis
 thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis
 thaliana]

5'-most EST rca700997536.h1
 Method BLASTX
 NCBI GI g1653655
 BLAST score 364
 E value 5.0e-34
 Match length 163
 % identity 44
 NCBI Description (D90915) ATP-dependent Clp protease proteolytic subunit [Synechocystis sp.]

Seq. No. 388
 Contig ID 220_1.R1040
 5'-most EST fC-gmro700844894_FL
 Method BLASTX
 NCBI GI g4512651
 BLAST score 616
 E value 7.0e-64
 Match length 222
 % identity 50
 NCBI Description (AC007048) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No. 389
 Contig ID 221_1.R1040
 5'-most EST jC-gmst02400054a06d1
 Method BLASTX
 NCBI GI g349379
 BLAST score 337
 E value 3.0e-31
 Match length 127
 % identity 63
 NCBI Description (L22847) HAHB-1 [Helianthus annuus]

Seq. No. 390
 Contig ID 221_2.R1040
 5'-most EST gsv701054757.h1
 Method BLASTX
 NCBI GI g349379
 BLAST score 295
 E value 2.0e-26
 Match length 129
 % identity 57
 NCBI Description (L22847) HAHB-1 [Helianthus annuus]

Seq. No. 391
 Contig ID 222_1.R1040
 5'-most EST fC-gmro700847730_FL
 Method BLASTX
 NCBI GI g4415914
 BLAST score 367
 E value 1.0e-34
 Match length 198
 % identity 37
 NCBI Description (AC006282) unknown protein [Arabidopsis thaliana]

Seq. No. 392
 Contig ID 223_1.R1040

5'-most EST fC-gmle7000741669a1
 Method BLASTX
 NCBI GI g1169586
 BLAST score 1610
 E value 1.0e-180
 Match length 338
 % identity 89
 NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC
 (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
 (CY-F1) >gi_542079_pir_S41287 fructose-bisphosphatase (EC
 3.1.3.11) - potato >gi_440591_emb_CAA54265_ (X76946)
 fructose-1,6-bisphosphatase [Solanum tuberosum]

Seq. No. 393
 Contig ID 223_2.R1040
 5'-most EST fC-gmle7000741457a1
 Method BLASTX
 NCBI GI g3913640
 BLAST score 591
 E value 4.0e-61
 Match length 120
 % identity 92
 NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC
 (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
 >gi_3041775_dbj_BAA25422_ (AB007193)
 fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No. 394
 Contig ID 223_3.R1040
 5'-most EST ncj700986460.h1
 Method BLASTX
 NCBI GI g3913640
 BLAST score 523
 E value 3.0e-53
 Match length 111
 % identity 86
 NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC
 (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
 >gi_3041775_dbj_BAA25422_ (AB007193)
 fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No. 395
 Contig ID 223_4.R1040
 5'-most EST fC-gmle700873234a1
 Method BLASTX
 NCBI GI g2494416
 BLAST score 434
 E value 2.0e-61
 Match length 127
 % identity 92
 NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC
 (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
 >gi_166956 (M80597) fructose-1,6-bisphosphatase [Beta
 vulgaris] >gi_444324_prf_1906373A cytosolic fructose
 bisphosphatase [Beta vulgaris]

Seq. No. 396

Contig ID	224_1.R1040
5'-most EST	fC-gmro700849195_FL
Method	BLASTX
NCBI GI	g4490335
BLAST score	267
E value	5.0e-23
Match length	153
% identity	44
NCBI Description	(AL035656) receptor kinase-like protein [Arabidopsis thaliana]
Seq. No.	397
Contig ID	224_2.R1040
5'-most EST	fC-gmle700875134r1
Seq. No.	398
Contig ID	225_1.R1040
5'-most EST	LIB3092-012-Q1-K1-A12
Seq. No.	399
Contig ID	226_1.R1040
5'-most EST	fC-gmro700864101_FL
Method	BLASTX
NCBI GI	g2924777
BLAST score	187
E value	8.0e-14
Match length	107
% identity	43
NCBI Description	(AC002334) putative receptor protein kinase [Arabidopsis thaliana]
Seq. No.	400
Contig ID	226_2.R1040
5'-most EST	LIB3139-100-P1-N1-A12
Seq. No.	401
Contig ID	227_1.R1040
5'-most EST	fC-gmro700865543_FL
Method	BLASTX
NCBI GI	g4455129
BLAST score	317
E value	1.0e-28
Match length	120
% identity	52
NCBI Description	(AF127761) ribonucleoprotein ZRNP1 [Homo sapiens]
Seq. No.	402
Contig ID	227_2.R1040
5'-most EST	LIB3106-022-Q1-K1-E1
Method	BLASTX
NCBI GI	g4455129
BLAST score	201
E value	2.0e-16
Match length	80
% identity	61
NCBI Description	(AF127761) ribonucleoprotein ZRNP1 [Homo sapiens]

Seq. No.	403
Contig ID	228_1.R1040
5'-most EST	fC-gmro700868230_FL
Method	BLASTX
NCBI GI	g4544403
BLAST score	720
E value	5.0e-76
Match length	206
% identity	62
NCBI Description	(AC007047) putative glucan endo-1,3-beta-D-glucosidase precursor [Arabidopsis thaliana]
Seq. No.	404
Contig ID	228_2.R1040
5'-most EST	uC-gmrominsoy169b02b1
Method	BLASTX
NCBI GI	g3641838
BLAST score	647
E value	1.0e-132
Match length	329
% identity	74
NCBI Description	(AL023094) putative protein (fragment) [Arabidopsis thaliana]
Seq. No.	405
Contig ID	229_1.R1040
5'-most EST	fC-gmle700743613f1
Method	BLASTN
NCBI GI	g435678
BLAST score	132
E value	9.0e-68
Match length	323
% identity	86
NCBI Description	L.esculentum Mill (cv. Rutgers) mRNA for ribosomal protein S25
Seq. No.	406
Contig ID	229_2.R1040
5'-most EST	gsv701055480.h1
Method	BLASTN
NCBI GI	g435678
BLAST score	120
E value	1.0e-60
Match length	323
% identity	85
NCBI Description	L.esculentum Mill (cv. Rutgers) mRNA for ribosomal protein S25
Seq. No.	407
Contig ID	229_3.R1040
5'-most EST	V4L-01-Q1-B1-E8
Method	BLASTX
NCBI GI	g3249084
BLAST score	1818
E value	0.0e+00
Match length	567
% identity	60

NCBI Description (AC004473) Similar to red-1 (related to thioredoxin) gene
gb_X92750 from *Mus musculus*. ESTs gb_AA712687 and
gb_Z37223 come from this gene [*Arabidopsis thaliana*]

Seq. No. 408
Contig ID 229_4.R1040
5'-most EST cfl700863563.h1
Method BLASTX
NCBI GI g4567232
BLAST score 239
E value 1.0e-30
Match length 83
% identity 85
NCBI Description (AC007119) putative 40S ribosomal protein S25 [*Arabidopsis thaliana*]

Seq. No. 409
Contig ID 230_1.R1040
5'-most EST uC-gmronoir037a08b1
Method BLASTX
NCBI GI gl922964
BLAST score 609
E value 8.0e-63
Match length 171
% identity 73
NCBI Description (AC000106) Similar to *Schizosaccharomyces* CCAAT-binding
factor (gb_U88525). EST gb_T04310 comes from this gene.
[*Arabidopsis thaliana*]

Seq. No. 410
Contig ID 231_1.R1040
5'-most EST fC-gmro700566893r1
Method BLASTX
NCBI GI g4538929
BLAST score 672
E value 4.0e-70
Match length 362
% identity 42
NCBI Description (AL049483) putative nucleic acid binding protein
[*Arabidopsis thaliana*]

Seq. No. 411
Contig ID 231_2.R1040
5'-most EST jC-gmle01810016c05d1
Method BLASTX
NCBI GI g2342727
BLAST score 361
E value 3.0e-34
Match length 90
% identity 70
NCBI Description (AC002341) hypothetical protein [*Arabidopsis thaliana*]

Seq. No. 412
Contig ID 231_3.R1040
5'-most EST fua701043550.h1
Method BLASTX
NCBI GI g4538929

BLAST score 291
 E value 1.0e-25
 Match length 175
 % identity 49
 NCBI Description (AL049483) putative nucleic acid binding protein
 [Arabidopsis thaliana]

Seq. No. 413
 Contig ID 231_4.R1040
 5'-most EST ASG32442DA-02-Q1-E1-F10
 Method BLASTX
 NCBI GI g4538929
 BLAST score 163
 E value 5.0e-11
 Match length 58
 % identity 55
 NCBI Description (AL049483) putative nucleic acid binding protein
 [Arabidopsis thaliana]

Seq. No. 414
 Contig ID 232_1.R1040
 5'-most EST fC-zmro700830348_FL
 Method BLASTX
 NCBI GI g3901012
 BLAST score 1157
 E value 1.0e-127
 Match length 278
 % identity 76
 NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
 sylvatica]

Seq. No. 415
 Contig ID 232_2.R1040
 5'-most EST uC-gmropic018b01b1
 Method BLASTX
 NCBI GI g3901012
 BLAST score 313
 E value 9.0e-29
 Match length 75
 % identity 80
 NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
 sylvatica]

Seq. No. 416
 Contig ID 232_3.R1040
 5'-most EST gsv701049278.h1
 Method BLASTX
 NCBI GI g2129771
 BLAST score 334
 E value 5.0e-31
 Match length 164
 % identity 68
 NCBI Description xyloglucan endotransglycosylase-related protein XTR-6 -
 Arabidopsis thaliana >gi_1244758 (U43488) xyloglucan
 endotransglycosylase-related protein [Arabidopsis thaliana]
 >gi_4539299_emb_CAB39602.1 (AL049480) xyloglucan endo-1,
 4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana]

Seq. No. 417
 Contig ID 232_4.R1040
 5'-most EST zzp700835657.h1
 Method BLASTX
 NCBI GI g3901012
 BLAST score 645
 E value 2.0e-67
 Match length 146
 % identity 79
 NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]

Seq. No. 418
 Contig ID 232_6.R1040
 5'-most EST LIB3139-037-P1-N1-B7
 Method BLASTX
 NCBI GI g3901012
 BLAST score 169
 E value 5.0e-12
 Match length 34
 % identity 82
 NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]

Seq. No. 419
 Contig ID 233_1.R1040
 5'-most EST fC-zmro700832181_FL
 Method BLASTX
 NCBI GI g266685
 BLAST score 969
 E value 1.0e-105
 Match length 439
 % identity 38
 NCBI Description DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE DEHYDROGENASE COMPLEX (E2) (PDC-E2) (70 KD MITOCHONDRIAL AUTOANTIGEN OF PRIMARY BILIARY CIRRHOSIS) (PBC)
 >gi_111580_pir_S21766 dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) - rat

Seq. No. 420
 Contig ID 235_1.R1040
 5'-most EST fC-zmfl700381954_FL
 Method BLASTN
 NCBI GI g22485
 BLAST score 798
 E value 0.0e+00
 Match length 1075
 % identity 98
 NCBI Description Maize mRNA for sucrose synthase (EC 2.4.1.13)

Seq. No. 421
 Contig ID 236_1.R1040
 5'-most EST fC-zmfl700550326_FL
 Method BLASTX
 NCBI GI g4426627
 BLAST score 300

BLAST score 115
 E value 5.0e-58
 Match length 203
 % identity 89
 NCBI Description Glycine max mRNA for squalene synthase, complete cds

Seq. No. 427
 Contig ID 241_2.R1040
 5'-most EST jC-gmle01810087d08d1
 Method BLASTN
 NCBI GI g2463568
 BLAST score 48
 E value 3.0e-18
 Match length 124
 % identity 84
 NCBI Description Glycine max mRNA for squalene synthase, complete cds

Seq. No. 428
 Contig ID 242_1.R1040
 5'-most EST jC-gmro02910002d12a1
 Method BLASTX
 NCBI GI g3805849
 BLAST score 4092
 E value 0.0e+00
 Match length 897
 % identity 86
 NCBI Description (AL031986) cytoplasmatic aconitate hydratase (citrate hydro-lyase)(aconitase)(EC 4.2.1.3) [Arabidopsis thaliana]

Seq. No. 429
 Contig ID 243_1.R1040
 5'-most EST epX701108931.h1
 Method BLASTX
 NCBI GI g2499488
 BLAST score 2683
 E value 0.0e+00
 Match length 610
 % identity 84
 NCBI Description PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849) pyrophosphate-dependent phosphofructokinase alpha subunit [Ricinus communis]

Seq. No. 430
 Contig ID 243_2.R1040
 5'-most EST g5688064
 Method BLASTX
 NCBI GI g3790102
 BLAST score 432
 E value 2.0e-42
 Match length 102
 % identity 80
 NCBI Description (AF095521) pyrophosphate-dependent phosphofructokinase alpha subunit [Citrus X paradisi]

Seq. No. 436
 Contig ID 247_1.R1040
 5'-most EST fC-gmle700553710_FL
 Method BLASTX
 NCBI GI g4337187
 BLAST score 297
 E value 8.0e-27
 Match length 80
 % identity 65
 NCBI Description (AC006403) putative prolylcarboxypeptidase, 5' partial
 [Arabidopsis thaliana]

Seq. No. 437
 Contig ID 247_2.R1040
 5'-most EST LIB3170-041-Q1-K1-F1

Seq. No. 438
 Contig ID 248_1.R1040
 5'-most EST g5509667
 Method BLASTN
 NCBI GI g403328
 BLAST score 59
 E value 3.0e-24
 Match length 95
 % identity 91
 NCBI Description T.repens TrMT1B mRNA for metallothionein-like protein

Seq. No. 439
 Contig ID 248_2.R1040
 5'-most EST g4300393
 Method BLASTN
 NCBI GI g403328
 BLAST score 56
 E value 1.0e-22
 Match length 115
 % identity 91
 NCBI Description T.repens TrMT1B mRNA for metallothionein-like protein

Seq. No. 440
 Contig ID 248_3.R1040
 5'-most EST g4283686
 Method BLASTN
 NCBI GI g403328
 BLAST score 56
 E value 1.0e-22
 Match length 92
 % identity 90
 NCBI Description T.repens TrMT1B mRNA for metallothionein-like protein

Seq. No. 441
 Contig ID 249_1.R1040
 5'-most EST LIB3073-012-Q1-K1-H3
 Method BLASTX
 NCBI GI g4574320
 BLAST score 311
 E value 4.0e-28

E value	4.0e-45
Match length	155
% identity	59
NCBI Description	(AL031018) hypothetical protein [Arabidopsis thaliana]

```
Seq. No.          449
Contig ID         252_3.R1040
5'-most EST      LIB3138-011-Q1-N1-B5
Method            BLASTX
NCBI GI           g3292817
BLAST score       276
E value           2.0e-24
Match length      89
% identity        69
NCBI Description  (AL031018) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.          450
Contig ID         253_1.R1040
5'-most EST      fC-gmse700841225_FL
Method            BLASTX
NCBI GI           g2642430
BLAST score       432
E value           2.0e-42
Match length      157
% identity        62
NCBI Description  (AC002391) putative AP2 domain containing protein
                  [Arabidopsis thaliana]
```

```
Seq. No.          451
Contig ID         254_1.R1040
5'-most EST      LIB3049-015-Q1-E1-C2
Method            BLASTX
NCBI GI           g2894605
BLAST score       267
E value           5.0e-23
Match length      133
% identity        50
NCBI Description  (AL021889) putative protein [Arabidopsis thaliana]
```

```
Seq. No.          452
Contig ID         254_2.R1040
5'-most EST      hrw701059629.h1
Method            BLASTX
NCBI GI           g2894605
BLAST score       301
E value           3.0e-27
Match length      131
% identity        55
NCBI Description   (AL021889) putative protein [Arabidopsis thaliana]
```

```
Seq. No.          453
Contig ID         255_1.R1040
5'-most EST      dpv701100539.h1
Method            BLASTX
NCBI GI           g3335372
BLAST score       1134
E value           1.0e-124
```


NCBI Description (AC003033) putative cellulase [Arabidopsis thaliana]

Seq. No. 459
 Contig ID 257_1.R1040
 5'-most EST jC-gmro02910064g02a1
 Method BLASTX
 NCBI GI g1518540
 BLAST score 2252
 E value 0.0e+00
 Match length 480
 % identity 89
 NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No. 460
 Contig ID 257_2.R1040
 5'-most EST fC-gmfl700899609f1
 Method BLASTX
 NCBI GI g3378650
 BLAST score 862
 E value 9.0e-93
 Match length 239
 % identity 70
 NCBI Description (X97606) abscisic acid activated [Medicago sativa]

Seq. No. 461
 Contig ID 257_3.R1040
 5'-most EST LIB3092-040-Q1-K1-H3

Seq. No. 462
 Contig ID 257_4.R1040
 5'-most EST ssr700556162.h1

Seq. No. 463
 Contig ID 257_5.R1040
 5'-most EST g4314063

Seq. No. 464
 Contig ID 257_6.R1040
 5'-most EST jC-gmfl02220146e08d1
 Method BLASTX
 NCBI GI g3378650
 BLAST score 215
 E value 3.0e-17
 Match length 63
 % identity 59
 NCBI Description (X97606) abscisic acid activated [Medicago sativa]

Seq. No. 465
 Contig ID 257_9.R1040
 5'-most EST jC-gmfl02220114g07a1

Seq. No. 466
 Contig ID 257_10.R1040
 5'-most EST uC-gmflminsoy047d09b1

Seq. No. 467
 Contig ID 257_11.R1040

09684016.101000

% identity	87
NCBI Description	(AB007799) NADH-cytochrome b5 reductase [Arabidopsis thaliana] >gi_4240118_dbj_BAA74838_ (AB007800) NADH-cytochrome b5 reductase [Arabidopsis thaliana]
Seq. No.	473
Contig ID	260_2.R1040
5'-most EST	g4396819
Seq. No.	474
Contig ID	261_1.R1040
5'-most EST	fC-zmro700830907_FL
Method	BLASTX
NCBI GI	g4191788
BLAST score	768
E value	1.0e-81
Match length	191
% identity	76
NCBI Description	(AC005917) putative 1-aminocyclopropane-1-carboxylate oxidase [Arabidopsis thaliana]
Seq. No.	475
Contig ID	262_1.R1040
5'-most EST	LIB3051-090-Q1-K1-G3
Method	BLASTN
NCBI GI	g1336096
BLAST score	581
E value	0.0e+00
Match length	1160
% identity	88
NCBI Description	Pisum sativum pyruvate dehydrogenase Elbeta mRNA, nuclear gene encoding mitochondrial protein, complete cds
Seq. No.	476
Contig ID	262_2.R1040
5'-most EST	uC-gmropic021f10b1
Method	BLASTN
NCBI GI	g1336096
BLAST score	153
E value	2.0e-80
Match length	347
% identity	86
NCBI Description	Pisum sativum pyruvate dehydrogenase Elbeta mRNA, nuclear gene encoding mitochondrial protein, complete cds
Seq. No.	477
Contig ID	262_3.R1040
5'-most EST	LIB3051-081-Q1-K1-E5
Method	BLASTN
NCBI GI	g1336096
BLAST score	133
E value	2.0e-68
Match length	335
% identity	85
NCBI Description	Pisum sativum pyruvate dehydrogenase Elbeta mRNA, nuclear gene encoding mitochondrial protein, complete cds

Seq. No. 478
 Contig ID 262_6.R1040
 5'-most EST gsv701054233.h1
 Method BLASTX
 NCBI GI g1709454
 BLAST score 230
 E value 2.0e-19
 Match length 63
 % identity 78
 NCBI Description PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (PDHE1-B) >gi_1336097 (U56697) pyruvate dehydrogenase Elbeta [Pisum sativum]

Seq. No. 479
 Contig ID 264_1.R1040
 5'-most EST fC-zmro700832582_FL
 Method BLASTX
 NCBI GI g2959732
 BLAST score 353
 E value 3.0e-33
 Match length 71
 % identity 89
 NCBI Description (Y13649) homologous to GATA-binding transcription factors [Arabidopsis thaliana]

Seq. No. 480
 Contig ID 265_1.R1040
 5'-most EST fC-zmro700833374_FL
 Method BLASTX
 NCBI GI g1872521
 BLAST score 303
 E value 4.0e-27
 Match length 113
 % identity 36
 NCBI Description (U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi_1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana]

Seq. No. 481
 Contig ID 267_1.R1040
 5'-most EST LIB3052-002-Q1-B1-G3
 Method BLASTX
 NCBI GI g1942405
 BLAST score 4443
 E value 0.0e+00
 Match length 857
 % identity 98
 NCBI Description Lipoxxygenase-3(Soybean) Non-Heme Fe(II) Metalloprotein . >gi_4388888_pdb_1BYT_Lipoxxygenase-3(Soybean) Complex With 4-Nitrocatechol >gi_1794172 (U50081) lipoxxygenase-3 [Glycine max]

Seq. No. 482
 Contig ID 268_2.R1040
 5'-most EST fC-gmro700568375r1
 Method BLASTX
 NCBI GI g1931639

BLAST score 337
 E value 3.0e-31
 Match length 148
 % identity 53
 NCBI Description (U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No. 483
 Contig ID 268_3.R1040
 5'-most EST LIB3074-031-Q1-K2-E10
 Method BLASTX
 NCBI GI g2832681
 BLAST score 199
 E value 7.0e-29
 Match length 71
 % identity 82
 NCBI Description (AL021712) putative protein [Arabidopsis thaliana]

Seq. No. 484
 Contig ID 268_4.R1040
 5'-most EST awf700841481.h1
 Method BLASTN
 NCBI GI g1885372
 BLAST score 601
 E value 0.0e+00
 Match length 641
 % identity 99
 NCBI Description Glycine max small subunit ribosomal RNA gene, partial sequence, internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence, and large subunit ribosomal RNA gene, partial seq

Seq. No. 485
 Contig ID 268_5.R1040
 5'-most EST asn701138178.h1
 Method BLASTX
 NCBI GI g3157928
 BLAST score 911
 E value 1.0e-155
 Match length 404
 % identity 67
 NCBI Description (AC002131) Similar to fumarylacetoacetate hydrolase, gb_L41670 from Emericella nidulans. [Arabidopsis thaliana]

Seq. No. 486
 Contig ID 268_6.R1040
 5'-most EST LIB3107-080-Q1-K1-D2
 Method BLASTN
 NCBI GI g170019
 BLAST score 599
 E value 0.0e+00
 Match length 1094
 % identity 95
 NCBI Description Soybean maturation protein (MAT1) gene, complete cds

Seq. No. 487
 Contig ID 268_7.R1040
 5'-most EST uxk700672229.h1

BLAST score 594
 E value 2.0e-67
 Match length 197
 % identity 69
 NCBI Description (U73937) PK12 protein kinase [Nicotiana tabacum]

Seq. No. 506
 Contig ID 273_15.R1040
 5'-most EST jex700906210.h1

Seq. No. 507
 Contig ID 273_16.R1040
 5'-most EST LIB3051-106-Q1-K1-E6
 Method BLASTN
 NCBI GI g2760164
 BLAST score 52
 E value 1.0e-19
 Match length 182
 % identity 86
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No. 508
 Contig ID 273_17.R1040
 5'-most EST LIB3170-049-Q1-K1-D12
 Method BLASTX
 NCBI GI g3643249
 BLAST score 545
 E value 1.0e-55
 Match length 124
 % identity 75
 NCBI Description (AF090143) thaumatin-like protein precursor Mdt11 [Malus domestica]

Seq. No. 509
 Contig ID 273_18.R1040
 5'-most EST LIB3170-037-Q1-J1-A8
 Method BLASTN
 NCBI GI g22073
 BLAST score 124
 E value 1.0e-62
 Match length 144
 % identity 97
 NCBI Description Mung bean 25S rRNA - 18S rDNA spacer region

Seq. No. 510
 Contig ID 273_19.R1040
 5'-most EST LIB3028-001-Q1-B1-G12
 Method BLASTN
 NCBI GI g1675195
 BLAST score 99
 E value 6.0e-48
 Match length 316
 % identity 86
 NCBI Description Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA, complete cds

Seq. No. 511
 Contig ID 273_20.R1040
 5'-most EST jsh701065521.h1
 Method BLASTX
 NCBI GI g1916809
 BLAST score 483
 E value 1.0e-48
 Match length 148
 % identity 64
 NCBI Description (U81163) auxin-binding protein [Prunus persica]

Seq. No. 512
 Contig ID 273_21.R1040
 5'-most EST LIB3109-028-Q1-K1-C6
 Method BLASTX
 NCBI GI g1703200
 BLAST score 948
 E value 1.0e-102
 Match length 212
 % identity 82
 NCBI Description PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353) protein kinase [Arabidopsis thaliana] >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2) [Arabidopsis thaliana]

Seq. No. 513
 Contig ID 273_22.R1040
 5'-most EST LIB3109-002-Q1-K3-G12
 Method BLASTX
 NCBI GI g4337027
 BLAST score 1473
 E value 1.0e-178
 Match length 687
 % identity 72
 NCBI Description (AF123254) MFP2 [Arabidopsis thaliana]

Seq. No. 514
 Contig ID 273_23.R1040
 5'-most EST LIB3138-064-Q1-N1-B5
 Method BLASTN
 NCBI GI g2656024
 BLAST score 50
 E value 2.0e-18
 Match length 74
 % identity 92
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6

Seq. No. 515
 Contig ID 273_24.R1040
 5'-most EST leu701145525.h1
 Method BLASTX
 NCBI GI g4193388
 BLAST score 182
 E value 6.0e-20
 Match length 171

% identity 29
NCBI Description (AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No. 516
Contig ID 273_25.R1040
5'-most EST g4313694
Method BLASTX
NCBI GI g4006890
BLAST score 472
E value 2.0e-46
Match length 112
% identity 78
NCBI Description (Z99708) ubiquitin--protein ligase-like protein [Arabidopsis thaliana]

Seq. No. 517
Contig ID 273_26.R1040
5'-most EST LIB3139-062-P1-N1-F8
Method BLASTN
NCBI GI g210811
BLAST score 490
E value 0.0e+00
Match length 1716
% identity 86
NCBI Description Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No. 518
Contig ID 274_1.R1040
5'-most EST fC-gmse700606076_FL
Method BLASTX
NCBI GI g1688233
BLAST score 415
E value 2.0e-40
Match length 191
% identity 57
NCBI Description (U77655) DNA binding protein homolog [Solanum tuberosum]

Seq. No. 519
Contig ID 275_1.R1040
5'-most EST fC-gmst700648235_FL
Method BLASTX
NCBI GI g544134
BLAST score 722
E value 5.0e-76
Match length 353
% identity 47
NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR
>gi_99720_pir_S22863 hypothetical protein - Arabidopsis thaliana
>gi_421844_pir_A46260 RecA functional analog
DRT100 - Arabidopsis thaliana (fragment)

Seq. No. 520
Contig ID 276_1.R1040
5'-most EST fC-gmst700658616_FL
Method BLASTX

NCBI GI g2497540
BLAST score 646
E value 2.0e-67
Match length 183
% identity 69
NCBI Description PYRUVATE KINASE, CHLOROPLAST ISOZYME G

Seq. No. 521
Contig ID 277_1.R1040
5'-most EST LIB3167-027-P1-K1-F8
Method BLASTX
NCBI GI g2144584
BLAST score 522
E value 7.0e-53
Match length 198
% identity 56
NCBI Description trypsin inhibitor A (Kunitz) precursor - soybean
>gi_18770_emb_CAA45777_ (X64447) trypsin inhibitor subtype
A [Glycine max]

Seq. No. 522
Contig ID 278_1.R1040
5'-most EST fC-gmst700650610i2
Method BLASTX
NCBI GI g1362078
BLAST score 1082
E value 1.0e-118
Match length 286
% identity 67
NCBI Description endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1)
- common nasturtium >gi_311835_emb_CAA48324_ (X68254)
cellulase [Tropaeolum majus]

Seq. No. 523
Contig ID 278_2.R1040
5'-most EST LIB3106-099-Q1-K1-C4
Method BLASTX
NCBI GI g1084391
BLAST score 472
E value 6.0e-47
Match length 124
% identity 68.
NCBI Description endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG2)
- common nasturtium (fragment) >gi_311837_emb_CAA48325_
(X68255) cellulase [Tropaeolum majus]

Seq. No. 524
Contig ID 278_3.R1040
5'-most EST seb700650991.h1
Method BLASTX
NCBI GI g1362078
BLAST score 197
E value 2.0e-15
Match length 49
% identity 69
NCBI Description endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1)
- common nasturtium >gi_311835_emb_CAA48324_ (X68254)

cellulase [Tropaeolum majus]

Seq. No. 525
 Contig ID 279_1.R1040
 5'-most EST fC-gmse700645511_FL
 Method BLASTX
 NCBI GI g3820648
 BLAST score 1471
 E value 0.0e+00
 Match length 469
 % identity 67
 NCBI Description (Y12636) allene oxide synthase [Arabidopsis thaliana]

Seq. No. 526
 Contig ID 279_2.R1040
 5'-most EST jC-gmro02910032b07d1
 Method BLASTX
 NCBI GI g1890152
 BLAST score 520
 E value 7.0e-53
 Match length 122
 % identity 77
 NCBI Description (X92510) allene oxide synthase [Arabidopsis thaliana]

Seq. No. 527
 Contig ID 279_3.R1040
 5'-most EST jC-gmro02910032e06a1
 Method BLASTX
 NCBI GI g1352186
 BLAST score 406
 E value 1.0e-39
 Match length 141
 % identity 61
 NCBI Description ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE)
 (CYTOCHROME P450 74) >gi_404866 (U00428) allene oxide
 synthase [Linum usitatissimum]

Seq. No. 528
 Contig ID 279_4.R1040
 5'-most EST LIB3139-066-P1-N1-A9
 Method BLASTX
 NCBI GI g1352186
 BLAST score 234
 E value 2.0e-19
 Match length 89
 % identity 56
 NCBI Description ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE)
 (CYTOCHROME P450 74) >gi_404866 (U00428) allene oxide
 synthase [Linum usitatissimum]

Seq. No. 529
 Contig ID 280_1.R1040
 5'-most EST fC-gmse700657716_FL

Seq. No. 530
 Contig ID 281_1.R1040
 5'-most EST fC-gmse700657751_FL

Method BLASTX
 NCBI GI g4006895
 BLAST score 423
 E value 2.0e-41
 Match length 139
 % identity 55
 NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 531
 Contig ID 282_1.R1040
 5'-most EST fC-gmse700657823_FL
 Method BLASTX
 NCBI GI g3157923
 BLAST score 208
 E value 1.0e-16
 Match length 71
 % identity 63
 NCBI Description (AC002131) F12F1.7 [Arabidopsis thaliana]

Seq. No. 532
 Contig ID 283_1.R1040
 5'-most EST fC-gmse700657837_FL

Seq. No. 533
 Contig ID 284_1.R1040
 5'-most EST fC-gmse700658078_FL

Seq. No. 534
 Contig ID 285_1.R1040
 5'-most EST fC-gmse700658166_FL

Seq. No. 535
 Contig ID 286_1.R1040
 5'-most EST pst700645867.h1
 Method BLASTX
 NCBI GI g4510402
 BLAST score 806
 E value 6.0e-86
 Match length 311
 % identity 58
 NCBI Description (AC006587) putative AP2 domain [Arabidopsis thaliana]

Seq. No. 536
 Contig ID 287_1.R1040
 5'-most EST fC-gmse700660136_FL
 Method BLASTX
 NCBI GI g1531760
 BLAST score 1055
 E value 1.0e-115
 Match length 329
 % identity 62
 NCBI Description (X97075) proline oxidase [Arabidopsis thaliana]

Seq. No. 537
 Contig ID 287_2.R1040
 5'-most EST LIB3170-037-Q1-J1-A5
 Method BLASTX

NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT)
 >gi_99657_pir_S20867 adenine phosphoribosyltransferase (EC
 2.4.2.7) - Arabidopsis thaliana >gi_16164_emb_CAA41497_
 (X58640) adenine phosphoribosyltransferase [Arabidopsis
 thaliana] >gi_433050 (L19637) adenine
 phosphoribosyltransferase [Arabidopsis thaliana]
 >gi_3935182 (AC004557) F17L21.25 [Arabidopsis thaliana]

Seq. No. 543
 Contig ID 292_2.R1040
 5'-most EST g4437087
 Method BLASTX
 NCBI GI g399046
 BLAST score 714
 E value 2.0e-75
 Match length 160
 % identity 86

NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT)
 >gi_99657_pir_S20867 adenine phosphoribosyltransferase (EC
 2.4.2.7) - Arabidopsis thaliana >gi_16164_emb_CAA41497_
 (X58640) adenine phosphoribosyltransferase [Arabidopsis
 thaliana] >gi_433050 (L19637) adenine
 phosphoribosyltransferase [Arabidopsis thaliana]
 >gi_3935182 (AC004557) F17L21.25 [Arabidopsis thaliana]

Seq. No. 544
 Contig ID 292_3.R1040
 5'-most EST g4313406

Seq. No. 545
 Contig ID 293_1.R1040
 5'-most EST LIB3028-030-Q1-B1-A3
 Method BLASTX
 NCBI GI g2143629
 BLAST score 227
 E value 3.0e-18
 Match length 172
 % identity 35

NCBI Description Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) IV
 - rat >gi_986941 (L42810) 'Ca2+/calmodulin-dependent
 protein kinase kinase' [Rattus norvegicus]
 >gi_1583255_prf_2120334A Ca/calmodulin-dependent protein
 kinase kinase [Rattus norvegicus]

Seq. No. 546
 Contig ID 293_2.R1040
 5'-most EST zhf700964957.h1
 Method BLASTX
 NCBI GI g2143629
 BLAST score 445
 E value 1.0e-43
 Match length 254
 % identity 42

NCBI Description Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) IV
 - rat >gi_986941 (L42810) 'Ca2+/calmodulin-dependent
 protein kinase kinase' [Rattus norvegicus]
 >gi_1583255_prf_2120334A Ca/calmodulin-dependent protein

09684016.101000

E value 1.0e-57
Match length 119
% identity 92
NCBI Description 60S RIBOSOMAL PROTEIN L13A >gi_2791948_emb_CAA11283_ (AJ223363) ribosomal protein L13a [Lupinus luteus]

Seq. No. 556
Contig ID 297_1.R1040
5'-most EST fC-gmst700662785_FL
Method BLASTX
NCBI GI g2462749
BLAST score 1006
E value 1.0e-136
Match length 374
% identity 70
NCBI Description (AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]

Seq. No. 557
Contig ID 298_1.R1040
5'-most EST fC-gmst700662976_FL

Seq. No. 558
Contig ID 298_2.R1040
5'-most EST hyd700727184.h1

Seq. No. 559
Contig ID 299_1.R1040
5'-most EST fC-gmst700663110_FL
Method BLASTX
NCBI GI g2388581
BLAST score 1062
E value 1.0e-116
Match length 287
% identity 68
NCBI Description (AC000098) Similar to Zea DWARF3 (gb_U32579). [Arabidopsis thaliana]

Seq. No. 560
Contig ID 300_1.R1040
5'-most EST fC-gmst700667704_FL
Method BLASTX
NCBI GI g169705
BLAST score 1433
E value 1.0e-159
Match length 312
% identity 91
NCBI Description (M64737) ATP:pyruvate phosphotransferase [Ricinus communis]

Seq. No. 561
Contig ID 301_1.R1040
5'-most EST LIB3106-093-Q1-K1-D3
Method BLASTX
NCBI GI g479386
BLAST score 2286
E value 0.0e+00
Match length 441

09684016-101000

% identity 100
NCBI Description Rat mRNA for cytochrome b5

Seq. No. 567
Contig ID 306_1.R1040
5'-most EST fC-gmse700658880_FL
Method BLASTX
NCBI GI g3122333
BLAST score 326
E value 6.0e-30
Match length 175
% identity 43

NCBI Description PUTATIVE 3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT
(ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI)
>gi_2648330 (AE000954) 3-isopropylmalate dehydratase, large
subunit (leuC) [Archaeoglobus fulgidus]

Seq. No. 568
Contig ID 307_1.R1040
5'-most EST LIB3106-087-Q1-K1-G7
Method BLASTX
NCBI GI g3894183
BLAST score 432
E value 3.0e-42
Match length 212
% identity 50
NCBI Description (AC005662) calmodulin-like protein [Arabidopsis thaliana]

Seq. No. 569
Contig ID 308_1.R1040
5'-most EST fC-gmse700659152_FL
Method BLASTX
NCBI GI g2459435
BLAST score 746
E value 4.0e-79
Match length 188
% identity 73
NCBI Description (AC002332) putative serine carboxypeptidase [Arabidopsis
thaliana]

Seq. No. 570
Contig ID 309_1.R1040
5'-most EST hrw701061722.h1
Method BLASTX
NCBI GI g1561774
BLAST score 1806
E value 0.0e+00
Match length 460
% identity 76
NCBI Description (U67426) malate dehydrogenase [Vitis vinifera]

Seq. No. 571
Contig ID 309_2.R1040
5'-most EST LIB3170-085-Q1-J1-B1
Method BLASTX
NCBI GI g3687228
BLAST score 129

E value	0.0e+00
Match length	333
% identity	96
NCBI Description	(AB000097) class III acidic endochitinase [Glycine max]
Seq. No.	581
Contig ID	314_2.R1040
5'-most EST	uC-gmrominsoy253g01b1
Method	BLASTX
NCBI GI	g1345971
BLAST score	2308
E value	0.0e+00
Match length	454
% identity	92
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi_541947_pir_JQ2339 omega-3 fatty acid desaturase (EC 1.14.99.-) GMD - soybean >gi_408792 (L22965) omega-3 fatty acid desaturase [Glycine soja]
Seq. No.	582
Contig ID	314_3.R1040
5'-most EST	trc700562720.h1
Method	BLASTN
NCBI GI	g408791
BLAST score	174
E value	1.0e-92
Match length	465
% identity	93
NCBI Description	Glycine soja chloroplast omega-3 fatty acid desaturase (Fadd) mRNA, complete cds
Seq. No.	583
Contig ID	314_4.R1040
5'-most EST	g5688021
Method	BLASTN
NCBI GI	g408791
BLAST score	457
E value	0.0e+00
Match length	473
% identity	99
NCBI Description	Glycine soja chloroplast omega-3 fatty acid desaturase (Fadd) mRNA, complete cds
Seq. No.	584
Contig ID	314_5.R1040
5'-most EST	LIB3139-060-P1-N1-E3
Method	BLASTN
NCBI GI	g408791
BLAST score	157
E value	8.0e-83
Match length	300
% identity	93
NCBI Description	Glycine soja chloroplast omega-3 fatty acid desaturase (Fadd) mRNA, complete cds
Seq. No.	585
Contig ID	314_9.R1040

Method BLASTN
 NCBI GI g2055229
 BLAST score 205
 E value 1.0e-111
 Match length 718
 % identity 93
 NCBI Description Soybean mRNA for SRC2, complete cds

Seq. No. 591
 Contig ID 317_3.R1040
 5'-most EST fC-gmse7000757201d1
 Method BLASTN
 NCBI GI g2605511
 BLAST score 161
 E value 2.0e-85
 Match length 283
 % identity 89
 NCBI Description Glycine max mRNA for beta subunit of beta conglycinin, complete cds

Seq. No. 592
 Contig ID 317_4.R1040
 5'-most EST LIB3170-033-Q1-K1-B12
 Method BLASTN
 NCBI GI g2605509
 BLAST score 250
 E value 1.0e-138
 Match length 309
 % identity 95
 NCBI Description Glycine max mRNA for alpha subunit of beta conglycinin, complete cds

Seq. No. 593
 Contig ID 317_5.R1040
 5'-most EST g5057596
 Method BLASTN
 NCBI GI g2605511
 BLAST score 1041
 E value 0.0e+00
 Match length 1510
 % identity 95
 NCBI Description Glycine max mRNA for beta subunit of beta conglycinin, complete cds

Seq. No. 594
 Contig ID 317_6.R1040
 5'-most EST vwf700678652.h1
 Method BLASTN
 NCBI GI g736001
 BLAST score 1339
 E value 0.0e+00
 Match length 1782
 % identity 96
 NCBI Description G.soja (SH1) Gy5 mRNA for glycinin

Seq. No. 595
 Contig ID 317_7.R1040

NCBI Description Glycine max mRNA for 6-phosphogluconate dehydrogenase, complete cds

Seq. No. 616
 Contig ID 324_6.R1040
 5'-most EST ep_x701109643.h1
 Method BLASTN
 NCBI GI g2529228
 BLAST score 83
 E value 5.0e-39
 Match length 139
 % identity 90

NCBI Description Glycine max mRNA for 6-phosphogluconate dehydrogenase, complete cds

Seq. No. 617
 Contig ID 324_7.R1040
 5'-most EST kl1701214664.h1
 Method BLASTN
 NCBI GI g2529228
 BLAST score 102
 E value 3.0e-50
 Match length 166
 % identity 90

NCBI Description Glycine max mRNA for 6-phosphogluconate dehydrogenase, complete cds

Seq. No. 618
 Contig ID 325_1.R1040
 5'-most EST fua701043454.h1
 Method BLASTX
 NCBI GI g1705587
 BLAST score 4790
 E value 0.0e+00
 Match length 967
 % identity 95

NCBI Description PHOSPHOENOLPYRUVATE CARBOXYLASE (PEPCASE)
 >gi_474020_dbj_BAA03100_ (D13998) phosphoenolpyruvate carboxylase [Glycine max]

Seq. No. 619
 Contig ID 325_2.R1040
 5'-most EST g218266_FL
 Method BLASTX
 NCBI GI g399182
 BLAST score 4874
 E value 0.0e+00
 Match length 967
 % identity 97

NCBI Description PHOSPHOENOLPYRUVATE CARBOXYLASE, HOUSEKEEPING ISOZYME (PEPCASE) >gi_320128_pir_S28428 phosphoenolpyruvate carboxylase (EC 4.1.1.31) - soybean
 >gi_218267_dbj_BAA01560_ (D10717) phosphoenolpyruvate carboxylase [Glycine max]

Seq. No. 620
 Contig ID 325_3.R1040

Seq. No. 641
 Contig ID 335_2.R1040
 5'-most EST LIB3170-060-Q1-K1-G8
 Method BLASTX
 NCBI GI g3913192
 BLAST score 2659
 E value 0.0e+00
 Match length 509
 % identity 100
 NCBI Description CYTOCHROME P450 93A1 >gi_2129824_pir_S62899 cytochrome P450 (CYP93 A1) - soybean >gi_1232111_dbj_BAA12159_ (D83968) Cytochrome P-450 (CYP93A1) [Glycine max] >gi_1588679_prf_2209281A cytochrome P450 [Glycine max]

Seq. No. 642
 Contig ID 335_3.R1040
 5'-most EST LIB3051-072-Q1-K1-A6
 Method BLASTX
 NCBI GI g3334665
 BLAST score 2452
 E value 0.0e+00
 Match length 503
 % identity 95
 NCBI Description (Y10492) putative cytochrome P450 [Glycine max]

Seq. No. 643
 Contig ID 335_4.R1040
 5'-most EST jC-gmst02400015c10d1

Seq. No. 644
 Contig ID 335_5.R1040
 5'-most EST LIB3051-054-Q1-K2-E2

Seq. No. 645
 Contig ID 335_7.R1040
 5'-most EST g5126796
 Method BLASTN
 NCBI GI g3334664
 BLAST score 221
 E value 1.0e-121
 Match length 221
 % identity 100
 NCBI Description G.max mRNA for putative cytochrome P450, clone CP5

Seq. No. 646
 Contig ID 336_1.R1040
 5'-most EST LIB3139-056-P1-N1-H4
 Method BLASTX
 NCBI GI g1663724
 BLAST score 2054
 E value 0.0e+00
 Match length 542
 % identity 74
 NCBI Description (U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]

Seq. No. 647

Contig ID 336_3.R1040
 5'-most EST gsv701045038.h1
 Method BLASTN
 NCBI GI g18517
 BLAST score 177
 E value 9.0e-95
 Match length 315
 % identity 94
 NCBI Description Glycine max L. Merr mRNA for 4-coumarate:CoA ligase (clone 4CL14)

Seq. No. 648
 Contig ID 337_1.R1040
 5'-most EST uC-gmrominsoy236d07b1
 Method BLASTX
 NCBI GI g3258637
 BLAST score 2115
 E value 0.0e+00
 Match length 537
 % identity 77
 NCBI Description (AF041050) 4-coumarate:CoA ligase [Populus tremuloides]

Seq. No. 649
 Contig ID 338_1.R1040
 5'-most EST jC-gmst02400078b03a1
 Method BLASTX
 NCBI GI g3355486
 BLAST score 1358
 E value 1.0e-150
 Match length 419
 % identity 63
 NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 650
 Contig ID 338_2.R1040
 5'-most EST g4218186_FL
 Method BLASTX
 NCBI GI g4218187
 BLAST score 4397
 E value 0.0e+00
 Match length 854
 % identity 98
 NCBI Description (AJ010165) leghemoglobin activating factor [Glycine max]

Seq. No. 651
 Contig ID 339_1.R1040
 5'-most EST jC-gmro02910013b11a1
 Method BLASTX
 NCBI GI g4468193
 BLAST score 2258
 E value 0.0e+00
 Match length 502
 % identity 90
 NCBI Description (AJ010201) inosine monophosphate dehydrogenase [Glycine max]

Seq. No. 652

Method BLASTN
 NCBI GI g3341442
 BLAST score 219
 E value 1.0e-120
 Match length 386
 % identity 92
 NCBI Description Glycine max mRNA for root nodule acid phosphatase

Seq. No. 658
 Contig ID 342_3.R1040
 5'-most EST jC-gmf102220114h03a1
 Method BLASTN
 NCBI GI g3341442
 BLAST score 187
 E value 1.0e-101
 Match length 301
 % identity 92
 NCBI Description Glycine max mRNA for root nodule acid phosphatase

Seq. No. 659
 Contig ID 343_1.R1040
 5'-most EST LIB3072-047-Q1-K1-D6
 Method BLASTN
 NCBI GI g296442
 BLAST score 621
 E value 0.0e+00
 Match length 703
 % identity 97
 NCBI Description G.max ADR11 mRNA

Seq. No. 660
 Contig ID 343_2.R1040
 5'-most EST LIB3028-010-Q1-B1-C1
 Method BLASTN
 NCBI GI g296442
 BLAST score 376
 E value 0.0e+00
 Match length 721
 % identity 94
 NCBI Description G.max ADR11 mRNA

Seq. No. 661
 Contig ID 343_3.R1040
 5'-most EST LIB3170-024-Q1-K1-B4
 Method BLASTN
 NCBI GI g296442
 BLAST score 101
 E value 3.0e-49
 Match length 288
 % identity 93
 NCBI Description G.max ADR11 mRNA

Seq. No. 662
 Contig ID 344_3.R1040
 5'-most EST g5678078
 Method BLASTN
 NCBI GI g296444

Match length 1123
 % identity 94
 NCBI Description G.max ADR6 mRNA

Seq. No. 668
 Contig ID 346_1.R1040
 5'-most EST bth700848391.h1
 Method BLASTN
 NCBI GI g2687725
 BLAST score 1232
 E value 0.0e+00
 Match length 1357
 % identity 98
 NCBI Description Glycine max mRNA for putative 2-hydroxydihydrodaidzein reductase

Seq. No. 669
 Contig ID 346_3.R1040
 5'-most EST jC-gmro02800032e12d1
 Method BLASTN
 NCBI GI g2687725
 BLAST score 172
 E value 7.0e-92
 Match length 354
 % identity 88
 NCBI Description Glycine max mRNA for putative 2-hydroxydihydrodaidzein reductase

Seq. No. 670
 Contig ID 348_1.R1040
 5'-most EST LIB3093-001-Q1-K1-B4
 Method BLASTX
 NCBI GI g3334449
 BLAST score 1703
 E value 0.0e+00
 Match length 321
 % identity 100
 NCBI Description ALTERNATIVE OXIDASE 1 PRECURSOR >gi_395216_emb_CAA48653_(X68702) alternative oxidase [Glycine max]
 >gi_740229_prf_2004454A respiratory chain terminal oxidase [Glycine max]

Seq. No. 671
 Contig ID 350_1.R1040
 5'-most EST vwf700677744.h1
 Method BLASTN
 NCBI GI g479144
 BLAST score 553
 E value 0.0e+00
 Match length 611
 % identity 97
 NCBI Description G.max mRNA for ATP synthase subunit

Seq. No. 672
 Contig ID 351_1.R1040
 5'-most EST LIB3072-052-Q1-E1-E12
 Method BLASTN

NCBI GI g18540
 BLAST score 432
 E value 0.0e+00
 Match length 481
 % identity 98
 NCBI Description G.max BBI mRNA for proteinase inhibitor

Seq. No. 673
 Contig ID 351 2.R1040
 5'-most EST LIB3029-009-Q1-B1-A6
 Method BLASTN
 NCBI GI g18540
 BLAST score 200
 E value 1.0e-108
 Match length 431
 % identity 95
 NCBI Description G.max BBI mRNA for proteinase inhibitor

Seq. No. 674
 Contig ID 352 1.R1040
 5'-most EST euj700697942.h1
 Method BLASTX
 NCBI GI g434061
 BLAST score 2023
 E value 0.0e+00
 Match length 421
 % identity 91
 NCBI Description (D16107) basic 7S globulin [Glycine max]

Seq. No. 675
 Contig ID 352 2.R1040
 5'-most EST zpv700757208.h1
 Method BLASTN
 NCBI GI g434060
 BLAST score 347
 E value 0.0e+00
 Match length 483
 % identity 95
 NCBI Description Soybean DNA for basic 7S globulin, complete cds

Seq. No. 676
 Contig ID 352 6.R1040
 5'-most EST txt700732264.h1
 Method BLASTN
 NCBI GI g18542
 BLAST score 220
 E value 1.0e-120
 Match length 343
 % identity 98
 NCBI Description Soybean Bg gene for basic 7S globulin

Seq. No. 677
 Contig ID 353 1.R1040
 5'-most EST g3334658_FL
 Method BLASTX
 NCBI GI g3334659
 BLAST score 2330

[Homo sapiens] >gi_4507223_ref_NP_003130.1_pSRPR_ signal
recognition particle receptor ('docking protein')

Seq. No. 697
Contig ID 367_3.R1040
5'-most EST LIB3139-078-P1-N1-A12
Method BLASTX
NCBI GI g134892
BLAST score 184
E value 4.0e-13
Match length 125
% identity 42
NCBI Description SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT
(SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA)
>gi_88607_pir_A29440 signal recognition particle receptor
- human >gi_30866_emb_CAA29608_ (X06272) docking protein
[Homo sapiens] >gi_4507223_ref_NP_003130.1_pSRPR_ signal
recognition particle receptor ('docking protein')

Seq. No. 698
Contig ID 367_4.R1040
5'-most EST rlr700898123.h1
Method BLASTX
NCBI GI g134891
BLAST score 392
E value 8.0e-38
Match length 113
% identity 66
NCBI Description SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT
(SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA)
>gi_89066_pir_A24570 signal recognition particle receptor
precursor - dog >gi_997_emb_CAA26945_ (X03184) signal
recognition particle receptor [Canis sp.]
>gi_224778_prf_1112224A signal recognition particle
receptor [Canis familiaris]

Seq. No. 699
Contig ID 367_5.R1040
5'-most EST LIB3092-036-Q1-K1-F9
Method BLASTN
NCBI GI g18584
BLAST score 316
E value 1.0e-177
Match length 562
% identity 98
NCBI Description G.max ENOD55-1 mRNA

Seq. No. 700
Contig ID 370_1.R1040
5'-most EST LIB3051-027-Q1-K1-D6
Method BLASTN
NCBI GI g2052028
BLAST score 824
E value 0.0e+00
Match length 909
% identity 98
NCBI Description G.max mRNA for glutathione transferase

Seq. No. 701
 Contig ID 370_2.R1040
 5'-most EST jC-gmle01810024d08a1
 Method BLASTN
 NCBI GI g2920665
 BLAST score 779
 E value 0.0e+00
 Match length 858
 % identity 97
 NCBI Description Glycine max 2,4-D inducible glutathione S-transferase (GSTa) mRNA, complete cds

Seq. No. 702
 Contig ID 370_3.R1040
 5'-most EST LIB3051-051-Q1-K1-A5
 Method BLASTN
 NCBI GI g2920665
 BLAST score 329
 E value 0.0e+00
 Match length 341
 % identity 99
 NCBI Description Glycine max 2,4-D inducible glutathione S-transferase (GSTa) mRNA, complete cds

Seq. No. 703
 Contig ID 370_5.R1040
 5'-most EST LIB3051-097-Q1-K1-E8
 Method BLASTN
 NCBI GI g2920665
 BLAST score 252
 E value 1.0e-139
 Match length 284
 % identity 97
 NCBI Description Glycine max 2,4-D inducible glutathione S-transferase (GSTa) mRNA, complete cds

Seq. No. 704
 Contig ID 374_1.R1040
 5'-most EST pxt700943646.h1
 Method BLASTN
 NCBI GI g505584
 BLAST score 915
 E value 0.0e+00
 Match length 931
 % identity 100
 NCBI Description G.max mRNA for Glyoxalase I

Seq. No. 705
 Contig ID 376_1.R1040
 5'-most EST fC-gmst700653759a1
 Method BLASTX
 NCBI GI g121336
 BLAST score 1799
 E value 0.0e+00
 Match length 342
 % identity 98

NCBI Description GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME (GLUTAMATE--AMMONIA LIGASE) >gi_81774_pir_JQ0937 glutamate--ammonia ligase (EC 6.3.1.2), cytosolic - soybean >gi_256143_bbs_113802 (S46513) cytosolic glutamine synthetase, GS [EC 6.3.1.2] [Glycine max=soybeans, var Prize, Peptide, 355 aa] [Glycine max]

Seq. No. 706
 Contig ID 376_2.R1040
 5'-most EST asj700967306.h1
 Method BLASTX
 NCBI GI g3128203
 BLAST score 465
 E value 3.0e-61
 Match length 171
 % identity 73
 NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 707
 Contig ID 376_3.R1040
 5'-most EST LIB3109-056-Q1-K1-D5
 Method BLASTN
 NCBI GI g547507
 BLAST score 1332
 E value 0.0e+00
 Match length 1431
 % identity 99
 NCBI Description G.max mRNA for glutamine synthetase

Seq. No. 708
 Contig ID 376_4.R1040
 5'-most EST g587119_FL
 Method BLASTX
 NCBI GI g587120
 BLAST score 1756
 E value 0.0e+00
 Match length 340
 % identity 96
 NCBI Description (X81460) glutamate--ammonia ligase [Glycine max]

Seq. No. 709
 Contig ID 376_5.R1040
 5'-most EST jC-gmst02400005f10d1
 Method BLASTN
 NCBI GI g256142
 BLAST score 397
 E value 0.0e+00
 Match length 458
 % identity 95
 NCBI Description cytosolic glutamine synthetase [Glycine max=soybeans, var Prize, mRNA, 1450 nt]

Seq. No. 710
 Contig ID 376_6.R1040
 5'-most EST fC-gmst700653759h1
 Method BLASTN
 NCBI GI g256142

BLAST score 453
 E value 0.0e+00
 Match length 707
 % identity 95
 NCBI Description cytosolic glutamine synthetase [Glycine max=soybeans, var Prize, mRNA, 1450 nt]

Seq. No. 711
 Contig ID 376 7.R1040
 5'-most EST pcp700994236.h1

Seq. No. 712
 Contig ID 376 10.R1040
 5'-most EST zhf700959375.h1

Seq. No. 713
 Contig ID 376 11.R1040
 5'-most EST fde700875135.h1
 Method BLASTN
 NCBI GI g312300
 BLAST score 77
 E value 3.0e-35
 Match length 242
 % identity 94
 NCBI Description G.max cDNA for glutamine synthetase (3' region)

Seq. No. 714
 Contig ID 379 1.R1040
 5'-most EST LIB3051-029-Q1-K1-E5
 Method BLASTN
 NCBI GI g18642
 BLAST score 720
 E value 0.0e+00
 Match length 737
 % identity 99
 NCBI Description G.max mRNA from stress-induced gene (H4)

Seq. No. 715
 Contig ID 379 2.R1040
 5'-most EST LIB3051-111-Q1-K1-C1
 Method BLASTN
 NCBI GI g18743
 BLAST score 743
 E value 0.0e+00
 Match length 771
 % identity 99
 NCBI Description G.max mRNA from stress-induced gene (SAM22)

Seq. No. 716
 Contig ID 379 4.R1040
 5'-most EST LIB3051-111-Q1-K1-G5
 Method BLASTN
 NCBI GI g18642
 BLAST score 409
 E value 0.0e+00
 Match length 662
 % identity 93

NCBI Description G.max mRNA from stress-induced gene (H4)

Seq. No. 717
 Contig ID 379 5.R1040
 5'-most EST g4396357
 Method BLASTN
 NCBI GI g18743
 BLAST score 266
 E value 1.0e-148
 Match length 478
 % identity 93

NCBI Description G.max mRNA from stress-induced gene (SAM22)

Seq. No. 718
 Contig ID 379 6.R1040
 5'-most EST zsg701125214.h1
 Method BLASTN
 NCBI GI g18743
 BLAST score 425
 E value 0.0e+00
 Match length 547
 % identity 96

NCBI Description G.max mRNA from stress-induced gene (SAM22)

Seq. No. 719
 Contig ID 379 10.R1040
 5'-most EST LIB3051-048-Q1-K1-C11
 Method BLASTN
 NCBI GI g18743
 BLAST score 337
 E value 0.0e+00
 Match length 431
 % identity 98

NCBI Description G.max mRNA from stress-induced gene (SAM22)

Seq. No. 720
 Contig ID 379 15.R1040
 5'-most EST LIB3051-022-Q1-K1-F2
 Method BLASTN
 NCBI GI g18743
 BLAST score 140
 E value 9.0e-73
 Match length 309
 % identity 93

NCBI Description G.max mRNA from stress-induced gene (SAM22)

Seq. No. 721
 Contig ID 380 1.R1040
 5'-most EST kl1701212864.h1
 Method BLASTN
 NCBI GI g18644
 BLAST score 761
 E value 0.0e+00
 Match length 761
 % identity 100

NCBI Description Soybean mRNA for HMG-1 like protein

Seq. No. 722
 Contig ID 380_2.R1040
 5'-most EST LIB3167-078-P1-K2-H1
 Method BLASTN
 NCBI GI g18644
 BLAST score 148
 E value 2.0e-77
 Match length 172
 % identity 97
 NCBI Description Soybean mRNA for HMG-1 like protein

Seq. No. 723
 Contig ID 380_3.R1040
 5'-most EST jC-gmst02400001g11a1
 Method BLASTN
 NCBI GI g18644
 BLAST score 287
 E value 1.0e-160
 Match length 339
 % identity 96
 NCBI Description Soybean mRNA for HMG-1 like protein

Seq. No. 724
 Contig ID 380_4.R1040
 5'-most EST uC-gmflminsoy069c08b1
 Method BLASTN
 NCBI GI g18644
 BLAST score 148
 E value 2.0e-77
 Match length 311
 % identity 95
 NCBI Description Soybean mRNA for HMG-1 like protein

Seq. No. 725
 Contig ID 381_1.R1040
 5'-most EST kl1701213229.h1
 Method BLASTN
 NCBI GI g18646
 BLAST score 791
 E value 0.0e+00
 Match length 832
 % identity 99
 NCBI Description Soybean mRNA for HMG-Y related protein, variant A

Seq. No. 726
 Contig ID 381_2.R1040
 5'-most EST LIB3039-026-Q1-E1-H1
 Method BLASTN
 NCBI GI g18648
 BLAST score 577
 E value 0.0e+00
 Match length 585
 % identity 100
 NCBI Description Soybean mRNA for HMG-Y related protein, variant B

Seq. No. 727
 Contig ID 383_1.R1040

5'-most EST g662923_FL
 Method BLASTN
 NCBI GI g662923
 BLAST score 504
 E value 0.0e+00
 Match length 654
 % identity 100
 NCBI Description G.max mRNA for heat shock transcription factor

Seq. No. 728
 Contig ID 384_1.R1040
 5'-most EST jC-gmro02910010e01a1
 Method BLASTN
 NCBI GI g662925
 BLAST score 1373
 E value 0.0e+00
 Match length 1373
 % identity 100
 NCBI Description G.max mRNA for heat shock transcription factor

Seq. No. 729
 Contig ID 384_2.R1040
 5'-most EST jC-gmro02910074f07a1
 Method BLASTN
 NCBI GI g662927
 BLAST score 1188
 E value 0.0e+00
 Match length 1188
 % identity 100
 NCBI Description G.max mRNA for heat shock transcription factor

Seq. No. 730
 Contig ID 384_3.R1040
 5'-most EST ncj700982933.h1

Seq. No. 731
 Contig ID 385_1.R1040
 5'-most EST g662931_FL
 Method BLASTX
 NCBI GI g2129832
 BLAST score 1659
 E value 0.0e+00
 Match length 370
 % identity 87
 NCBI Description heat shock transcription factor 5 - soybean
 >gi_671868_emb_CAA87080_ (Z46956) heat shock transcription
 factor 5 [Glycine max]

Seq. No. 732
 Contig ID 385_2.R1040
 5'-most EST g662926_FL
 Method BLASTN
 NCBI GI g662926
 BLAST score 988
 E value 0.0e+00
 Match length 1014
 % identity 100

E value 1.0e-109
 Match length 426
 % identity 91
 NCBI Description Glycine max 14-3-3 related protein SGF14A mRNA, complete cds

Seq. No. 743
 Contig ID 392_1.R1040
 5'-most EST uC-gmropic050e09b1
 Method BLASTN
 NCBI GI g3452090
 BLAST score 390
 E value 0.0e+00
 Match length 398
 % identity 99
 NCBI Description Glycine max mRNA for rudimentary enhancer, partial

Seq. No. 744
 Contig ID 392_2.R1040
 5'-most EST k11701213706.h1
 Method BLASTN
 NCBI GI g3452090
 BLAST score 202
 E value 1.0e-110
 Match length 243
 % identity 96
 NCBI Description Glycine max mRNA for rudimentary enhancer, partial

Seq. No. 745
 Contig ID 393_1.R1040
 5'-most EST LIB3051-007-Q1-E1-D10
 Method BLASTN
 NCBI GI g3452136
 BLAST score 235
 E value 1.0e-129
 Match length 243
 % identity 100
 NCBI Description Glycine max mRNA for glucose-6-phosphate-dehydrogenase, partial

Seq. No. 746
 Contig ID 393_2.R1040
 5'-most EST hrw701063583.h1
 Method BLASTN
 NCBI GI g603218
 BLAST score 392
 E value 0.0e+00
 Match length 752
 % identity 88
 NCBI Description Medicago sativa glucose-6-phosphate dehydrogenase mRNA, complete cds

Seq. No. 747
 Contig ID 395_1.R1040
 5'-most EST rlr700896427.h1
 Method BLASTN
 NCBI GI g3452143

NCBI GI g126398
 BLAST score 4277
 E value 0.0e+00
 Match length 839
 % identity 98
 NCBI Description SEED LIPOXYGENASE-1 (L-1) >gi_2144382_pir_DASYL2
 lipoxygenase (EC 1.13.11.12) 1 - soybean
 >gi_1000060_pdb_2SBL_B Lipoxxygenase-1 (Soybean)
 (E.C.1.13.11.12) >gi_2392632_pdb_1YGE Lipoxxygenase-1
 (Soybean) At 100k >gi_18675_emb_CAA47717 (X67304)
 lipoxygenase [Glycine max] >gi_295118 (J02795)
 lipoxygenase-1 [Glycine max]

Seq. No. 753
 Contig ID 400_1.R1040
 5'-most EST uC-gmrominsoyl25f04b1
 Method BLASTN
 NCBI GI g1262439
 BLAST score 229
 E value 1.0e-125
 Match length 585
 % identity 85
 NCBI Description Glycine max lipoxygenase (vlxC) mRNA, complete cds

Seq. No. 754
 Contig ID 400_2.R1040
 5'-most EST dpv701096996.h1
 Method BLASTX
 NCBI GI g436169
 BLAST score 752
 E value 6.0e-80
 Match length 219
 % identity 64
 NCBI Description (U04526) lipoxygenase [Glycine max]

Seq. No. 755
 Contig ID 400_3.R1040
 5'-most EST dpv701102162.h1
 Method BLASTX
 NCBI GI g3319774
 BLAST score 174
 E value 3.0e-12
 Match length 43
 % identity 72
 NCBI Description (Y16228) TOM7 protein [Solanum tuberosum]

Seq. No. 756
 Contig ID 400_4.R1040
 5'-most EST fC-gmse7000756638a1
 Method BLASTX
 NCBI GI g126409
 BLAST score 1062
 E value 0.0e+00
 Match length 739
 % identity 78
 NCBI Description LIPOXYGENASE 1 >gi_100005_pir_S22153 lipoxygenase (EC
 1.13.11.12) - kidney bean >gi_21017_emb_CAA45088_ (X63525)

lipoxygenase [Phaseolus vulgaris]

Seq. No. 757
 Contig ID 400_5.R1040
 5'-most EST uC-gmflminsoy016g08b1
 Method BLASTX
 NCBI GI g1262440
 BLAST score 1354
 E value 0.0e+00
 Match length 861
 % identity 94
 NCBI Description (U26457) lipoxygenase [Glycine max]

Seq. No. 758
 Contig ID 400_6.R1040
 5'-most EST uC-gmflminsoy011c10b1
 Method BLASTX
 NCBI GI g126411
 BLAST score 1189
 E value 0.0e+00
 Match length 874
 % identity 61
 NCBI Description SEED LIPOXYGENASE >gi_99932_pir_S13381 lipoxygenase (EC 1.13.11.12) - soybean >gi_18746_emb_CAA39604_ (X56139) lipoxygenase [Glycine max]

Seq. No. 759
 Contig ID 400_7.R1040
 5'-most EST uC-gmrominsoy256a03b1
 Method BLASTX
 NCBI GI g126404
 BLAST score 1058
 E value 0.0e+00
 Match length 873
 % identity 49
 NCBI Description SEED LIPOXYGENASE-2 (L-2) >gi_66331_pir_DASYL1 lipoxygenase (EC 1.13.11.12) 2 - soybean >gi_170014 (J03211) lipoxygenase (EC 1.13.11.12) [Glycine max]

Seq. No. 760
 Contig ID 401_1.R1040
 5'-most EST ncj700981157.h1
 Method BLASTX
 NCBI GI g116157
 BLAST score 1901
 E value 0.0e+00
 Match length 455
 % identity 84
 NCBI Description G2/MITOTIC-SPECIFIC CYCLIN S13-6 (B-LIKE CYCLIN) >gi_99895_pir_S16522 cyclin, mitotic - soybean >gi_18682_emb_CAA44632_ (X62820) mitotic cyclin [Glycine max]

Seq. No. 761
 Contig ID 403_1.R1040
 5'-most EST uC-gmropic091h10b1
 Method BLASTN

Match length 1109
 % identity 99
 NCBI Description Glycine max mRNA for pyrroline-5-carboxylate reductase

Seq. No. 772
 Contig ID 418 1.R1040
 5'-most EST LIB3040-022-Q1-E1-A7
 Method BLASTN
 NCBI GI g18725
 BLAST score 783
 E value 0.0e+00
 Match length 874
 % identity 97
 NCBI Description Soybean (G. max) mRNA for proliferating cell nuclear antigen (PCNA), partial

Seq. No. 773
 Contig ID 418 2.R1040
 5'-most EST LIB3040-005-Q1-E1-E6
 Method BLASTN
 NCBI GI g18725
 BLAST score 311
 E value 1.0e-175
 Match length 315
 % identity 100
 NCBI Description Soybean (G. max) mRNA for proliferating cell nuclear antigen (PCNA), partial

Seq. No. 774
 Contig ID 419 1.R1040
 5'-most EST LIB3049-020-Q1-E1-E6
 Method BLASTN
 NCBI GI g3021374
 BLAST score 361
 E value 0.0e+00
 Match length 389
 % identity 98
 NCBI Description Glycine max mRNA for profilin, PRO1

Seq. No. 775
 Contig ID 419 2.R1040
 5'-most EST leu701145541.h1
 Method BLASTN
 NCBI GI g556835
 BLAST score 309
 E value 1.0e-173
 Match length 617
 % identity 89
 NCBI Description P.vulgaris mRNA for profilin

Seq. No. 776
 Contig ID 419 3.R1040
 5'-most EST LIB3040-004-Q1-E1-E1
 Method BLASTX
 NCBI GI g2213610
 BLAST score 245
 E value 1.0e-20

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Seq. No.          783
Contig ID         419 11.R1040
5'-most EST      fua701042750.h1
Method           BLASTN
NCBI GI          g3021374
BLAST score       129
E value          2.0e-66
Match length     137
% identity       99
NCBI Description  Glycine max mRNA for profilin, PRO1
```

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Seq. No.          784
Contig ID         419 14.R1040
5'-most EST      LIB3072-021-Q1-E1-B8
Method            BLASTN
NCBI GI           g3021374
BLAST score       83
E value           9.0e-39
Match length      123
% identity        92
NCBI Description  Glycine max mRNA for profilin, PRO1
```

Seq. No.	785
Contig ID	419_21.R1040
5'-most EST	LIB3050-021-Q1-K1-C3
Method	BLASTN
NCBI GI	g3021374
BLAST score	116
E value	1.0e-58
Match length	140
% identity	96
NCBI Description	Glycine max mRNA for profilin, PRO1

215

Seq. No. 787
 Contig ID 422_1.R1040
 5'-most EST g1321821_FL
 Method BLASTN
 NCBI GI g1321821
 BLAST score 720
 E value 0.0e+00
 Match length 1302
 % identity 99
 NCBI Description G.max mRNA for glycinamide ribonucleotide transformylase

Seq. No. 788
 Contig ID 422_2.R1040
 5'-most EST epx701103931.h1
 Method BLASTN
 NCBI GI g1321821
 BLAST score 169
 E value 4.0e-90
 Match length 306
 % identity 98
 NCBI Description G.max mRNA for glycinamide ribonucleotide transformylase

Seq. No. 789
 Contig ID 423_1.R1040
 5'-most EST sat701005463.h1
 Method BLASTX
 NCBI GI g112837
 BLAST score 1630
 E value 0.0e+00
 Match length 315
 % identity 100
 NCBI Description NAD(P)H DEPENDENT 6'-DEOXYCHALCONE SYNTHASE
 >gi_99953_pir_S14222 reductase - soybean
 >gi_18728_emb_CAA39261_ (X55730) reductase [Glycine max]

Seq. No. 790
 Contig ID 423_2.R1040
 5'-most EST bth700849472.h1
 Method BLASTX
 NCBI GI g112837
 BLAST score 1139
 E value 1.0e-125
 Match length 315
 % identity 66
 NCBI Description NAD(P)H DEPENDENT 6'-DEOXYCHALCONE SYNTHASE
 >gi_99953_pir_S14222 reductase - soybean
 >gi_18728_emb_CAA39261_ (X55730) reductase [Glycine max]

Seq. No. 791
 Contig ID 423_3.R1040
 5'-most EST uC-gmrominsoy046b12b1
 Method BLASTX
 NCBI GI g112837
 BLAST score 447
 E value 1.0e-50
 Match length 147
 % identity 67

5'-most EST fua701037217.h1
 Method BLASTX
 NCBI GI g550452
 BLAST score 3467
 E value 0.0e+00
 Match length 674
 % identity 100
 NCBI Description (U08469) 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]

Seq. No. 838
 Contig ID 448_1.R1040
 5'-most EST LIB3052-013-Q1-N1-A10
 Method BLASTX
 NCBI GI g267076
 BLAST score 1628
 E value 0.0e+00
 Match length 334
 % identity 93
 NCBI Description TUBULIN BETA-3 CHAIN >gi_81953_pir_S20870 tubulin beta-3 chain - garden pea (fragment) >gi_388255_emb_CAA38615_(X54846) beta-tubulin 3 [Pisum sativum]

Seq. No. 839
 Contig ID 448_2.R1040
 5'-most EST ncj700978473.h1
 Method BLASTN
 NCBI GI g1399449
 BLAST score 370
 E value 0.0e+00
 Match length 789
 % identity 90
 NCBI Description Lupinus albus beta-tubulin 2 (TubB2) gene, complete cds

Seq. No. 840
 Contig ID 448_3.R1040
 5'-most EST LIB3049-023-Q1-E1-F11
 Method BLASTX
 NCBI GI g2983997
 BLAST score 348
 E value 1.0e-34
 Match length 159
 % identity 45
 NCBI Description (AE000749) hypothetical protein [Aquifex aeolicus]

Seq. No. 841
 Contig ID 448_4.R1040
 5'-most EST pmv700892602.h1
 Method BLASTN
 NCBI GI g170061
 BLAST score 545
 E value 0.0e+00
 Match length 932
 % identity 94
 NCBI Description Soybean (G.max L.) beta-tubulin (S-beta-2) gene, complete cds

SECRET

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Seq. No.      890
Contig ID     462_3.R1040
5'-most EST   jC-gmro02910024d01d1
Method        BLASTN
NCBI GI       g1217993
BLAST score    118
E value       1.0e-59
Match length   258
% identity     86
NCBI Description Glycine max dynamin-like protein SDL12A mRNA, complete cds
```

```
Seq. No.      891
Contig ID     463 1.R1040
5'-most EST   sat701012537.h1
Method        BLASTN
NCBI GI       g886099
BLAST score    983
E value       0.0e+00
Match length   1196
% identity     96
NCBI Description Glycine max putative water channel protein (Pip1) mRNA,
                  complete cds
```

```
Seq. No.          892
Contig ID         463_2.R1040
5'-most EST      leu701151271.h1
Method            BLASTN
NCBI GI           g886099
BLAST score       220
E value           1.0e-120
Match length      582
% identity        84
NCBI Description  Glycine max putative water channel protein (Pip1) mRNA,
                  complete cds
```

```
Seq. No.      893
Contig ID     463_3.R1040
5'-most EST   LIB3039-019-Q1-E1-A2
Method        BLASTN
NCBI GI       g886099
BLAST score    204
E value       1.0e-111
Match length   312
```


Seq. No. 918
 Contig ID 475_2.R1040
 5'-most EST LIB3049-011-Q1-E1-D2
 Method BLASTX
 NCBI GI g4185509
 BLAST score 614
 E value 1.0e-63
 Match length 139
 % identity 82
 NCBI Description (AF102821) actin depolymerizing factor 3 [Arabidopsis thaliana]

Seq. No. 919
 Contig ID 475_3.R1040
 5'-most EST LIB3051-062-Q1-K1-H3
 Method BLASTX
 NCBI GI g1408471
 BLAST score 620
 E value 2.0e-64
 Match length 139
 % identity 83
 NCBI Description (U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No. 920
 Contig ID 475_4.R1040
 5'-most EST jC-gmst02400038f11a1
 Method BLASTX
 NCBI GI g1408471
 BLAST score 630
 E value 1.0e-65
 Match length 139
 % identity 84
 NCBI Description (U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No. 921
 Contig ID 475_5.R1040
 5'-most EST LIB3087-010-Q1-K1-H12
 Method BLASTX
 NCBI GI g4185511
 BLAST score 410
 E value 4.0e-40
 Match length 90
 % identity 86
 NCBI Description (AF102822) actin depolymerizing factor 4 [Arabidopsis thaliana]

Seq. No. 922
 Contig ID 475_6.R1040
 5'-most EST uC-gmropic057g10b1
 Method BLASTN
 NCBI GI g1399379
 BLAST score 325
 E value 0.0e+00

Match length 459
 % identity 95
 NCBI Description Glycine max S-adenosyl-L-methionine:delta24-sterol-C-methyltransferase mRNA, complete cds

Seq. No. 923
 Contig ID 475 9.R1040
 5'-most EST crh700854308.h1
 Method BLASTN
 NCBI GI g1399379
 BLAST score 184
 E value 5.0e-99
 Match length 200
 % identity 98
 NCBI Description Glycine max S-adenosyl-L-methionine:delta24-sterol-C-methyltransferase mRNA, complete cds

Seq. No. 924
 Contig ID 476 1.R1040
 5'-most EST LIB3051-085-Q1-K1-H9
 Method BLASTN
 NCBI GI g1236950
 BLAST score 620
 E value 0.0e+00
 Match length 717
 % identity 97
 NCBI Description Glycine max nucleoside diphosphate kinase mRNA, complete cds

Seq. No. 925
 Contig ID 476 2.R1040
 5'-most EST LIB3049-042-Q1-E1-A12
 Method BLASTN
 NCBI GI g1236950
 BLAST score 372
 E value 0.0e+00
 Match length 609
 % identity 92
 NCBI Description Glycine max nucleoside diphosphate kinase mRNA, complete cds

Seq. No. 926
 Contig ID 476 3.R1040
 5'-most EST ncj700981096.h1
 Method BLASTN
 NCBI GI g1236950
 BLAST score 184
 E value 3.0e-99
 Match length 271
 % identity 96
 NCBI Description Glycine max nucleoside diphosphate kinase mRNA, complete cds

Seq. No. 927
 Contig ID 476 4.R1040
 5'-most EST jsh701070081.h2
 Method BLASTN

BLAST score 206
 E value 1.0e-112
 Match length 365
 % identity 96
 NCBI Description Glycine max cysteine proteinase inhibitor mRNA, partial cds

Seq. No. 933
 Contig ID 478_6.R1040
 5'-most EST LIB3073-003-Q1-K1-E2
 Method BLASTN
 NCBI GI g1277165
 BLAST score 103
 E value 2.0e-50
 Match length 227
 % identity 92
 NCBI Description Glycine max cysteine proteinase inhibitor mRNA, partial cds

Seq. No. 934
 Contig ID 479_1.R1040
 5'-most EST ncj700988504.h1
 Method BLASTN
 NCBI GI g1277167
 BLAST score 425
 E value 0.0e+00
 Match length 455
 % identity 98
 NCBI Description Glycine max cysteine proteinase inhibitor mRNA, partial cds

Seq. No. 935
 Contig ID 480_2.R1040
 5'-most EST LIB3051-019-Q1-E1-H7
 Method BLASTN
 NCBI GI g310560
 BLAST score 63
 E value 8.0e-27
 Match length 127
 % identity 98
 NCBI Description Soybean ascorbate peroxidase mRNA, complete cds

Seq. No. 936
 Contig ID 480_3.R1040
 5'-most EST jC-gmst02400069e04a1
 Method BLASTX
 NCBI GI g1679794
 BLAST score 415
 E value 3.0e-53
 Match length 372
 % identity 37
 NCBI Description (U77627) Allele: hi2 [Danio rerio]

Seq. No. 937
 Contig ID 480_4.R1040
 5'-most EST LIB3170-046-Q1-J1-G3
 Method BLASTN
 NCBI GI g1336081
 BLAST score 78
 E value 2.0e-35

Seq. No. 958
 Contig ID 489_7.R1040
 5'-most EST uC-gmrominsoy276g11b1
 Method BLASTX
 NCBI GI g2511691
 BLAST score 539
 E value 1.0e-129
 Match length 330
 % identity 74
 NCBI Description (Z99953) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No. 959
 Contig ID 489_8.R1040
 5'-most EST uC-gmropic034b07b1
 Method BLASTN
 NCBI GI g2257597
 BLAST score 436
 E value 0.0e+00
 Match length 684
 % identity 91
 NCBI Description Robinia pseudoacacia mRNA for phosphoglycerate kinase, partial cds

Seq. No. 960
 Contig ID 489_9.R1040
 5'-most EST LIB3138-009-Q1-N1-B11
 Method BLASTN
 NCBI GI g1619904
 BLAST score 827
 E value 0.0e+00
 Match length 1190
 % identity 94
 NCBI Description Glycine max thiol protease isoform A mRNA, partial cds

Seq. No. 961
 Contig ID 491_1.R1040
 5'-most EST LIB3093-002-Q1-K1-E6
 Method BLASTN
 NCBI GI g456713
 BLAST score 1118
 E value 0.0e+00
 Match length 1160
 % identity 100
 NCBI Description Glycine max gene for ubiquitin, complete cds

Seq. No. 962
 Contig ID 491_2.R1040
 5'-most EST LIB3093-036-Q1-K1-E8
 Method BLASTN
 NCBI GI g303900
 BLAST score 680
 E value 0.0e+00
 Match length 755
 % identity 46
 NCBI Description Soybean gene for ubiquitin, complete cds

Seq. No. 963

E value 0.0e+00
 Match length 379
 % identity 99
 NCBI Description CHALCONE SYNTHASE 7 (NARINGENIN-CHALCONE SYNTHASE 7)
 >gi_478407_pir_JQ2250 naringenin-chalcone synthase (EC
 2.3.1.74) - soybean >gi_169937 (M98871) chalcone synthase
 [Glycine max]

Seq. No. 973
 Contig ID 498_2.R1040
 5'-most EST g4300400
 Method BLASTN
 NCBI GI g169936
 BLAST score 860
 E value 0.0e+00
 Match length 999
 % identity 97
 NCBI Description Glycine max chalcone synthase (chs7) gene, complete cds

Seq. No. 974
 Contig ID 498_3.R1040
 5'-most EST uC-gmropic108h09b1
 Method BLASTN
 NCBI GI g218012
 BLAST score 385
 E value 0.0e+00
 Match length 513
 % identity 95
 NCBI Description Pueraria lobata mRNA for chalcone synthase, complete cds

Seq. No. 975
 Contig ID 498_6.R1040
 5'-most EST uC-gmronoir028c02b1
 Method BLASTN
 NCBI GI g169936
 BLAST score 301
 E value 1.0e-169
 Match length 334
 % identity 99
 NCBI Description Glycine max chalcone synthase (chs7) gene, complete cds

Seq. No. 976
 Contig ID 499_1.R1040
 5'-most EST g545762_FL
 Method BLASTN
 NCBI GI g545762
 BLAST score 518
 E value 0.0e+00
 Match length 526
 % identity 100
 NCBI Description Eu4=urease {clone 5E5} [Glycine max=soybeans, cv. Dare,
 mid-maturation embryos, mRNA Partial, 540 nt]

Seq. No. 977
 Contig ID 500_1.R1040
 5'-most EST LIB3170-038-Q1-K1-E6
 Method BLASTX

NCBI GI g3309269
 BLAST score 1810
 E value 0.0e+00
 Match length 501
 % identity 97
 NCBI Description (AF074940) ferric leghemoglobin reductase-2 precursor
 [Glycine max]

Seq. No. 978
 Contig ID 500_3.R1040
 5'-most EST LIB3087-008-Q1-K1-B10
 Method BLASTN
 NCBI GI g546359
 BLAST score 279
 E value 1.0e-155
 Match length 327
 % identity 96
 NCBI Description ferric leghemoglobin reductase [Glycine max=soybeans, Merr,
 nodules, mRNA, 1740 nt]

Seq. No. 979
 Contig ID 504_1.R1040
 5'-most EST uC-gmflminsoy062a07b1
 Method BLASTX
 NCBI GI g1706522
 BLAST score 2613
 E value 0.0e+00
 Match length 521
 % identity 94
 NCBI Description DIHYDROFOLATE REDUCTASE / THYMIDYLATE SYNTHASE (DHFR-TS)
 >gi_1362048_pir_S55683 dihydrofolate reductase-thymidylate
 synthase - soybean >gi_999190_bbs_166832 (S78087)
 dihydrofolate reductase-thymidylate synthase,
 DHFR-TS=bifunctional enzyme {EC 1.5.1.3} [Glycine max,
 seedling, Peptide, 530 aa] [Glycine max]
 >gi_1096144_prf_2111237A dihydrofolate
 reductase-thymidylate synthase [Glycine max]

Seq. No. 980
 Contig ID 504_2.R1040
 5'-most EST fC-gmst700656887r1
 Method BLASTN
 NCBI GI g999189
 BLAST score 146
 E value 3.0e-76
 Match length 166
 % identity 97
 NCBI Description dihydrofolate reductase-thymidylate synthase=bifunctional
 enzyme [Glycine max, seedling, mRNA, 1794 nt]

Seq. No. 981
 Contig ID 504_4.R1040
 5'-most EST fC-gmro7000746445a1
 Method BLASTN
 NCBI GI g999189
 BLAST score 169
 E value 4.0e-90

Match length 257
 % identity 91
 NCBI Description dihydrofolate reductase-thymidylate synthase=bifunctional enzyme [Glycine max, seedling, mRNA, 1794 nt]

Seq. No. 982
 Contig ID 507_1.R1040
 5'-most EST LIB3065-026-Q1-N1-B7
 Method BLASTN
 NCBI GI g498167
 BLAST score 525
 E value 0.0e+00
 Match length 545
 % identity 99
 NCBI Description Soybean mRNA for leginsulin, complete cds

Seq. No. 983
 Contig ID 517_1.R1040
 5'-most EST g218259_FL
 Method BLASTX
 NCBI GI g730164
 BLAST score 2436
 E value 0.0e+00
 Match length 482
 % identity 100
 NCBI Description EARLY NODULIN 70 >gi_486678_pir_S34800 sulfate transport protein homolog (clone GmN70) - soybean
 >gi_218260_dbj_BAA02723 (D13505) early nodulin [Glycine max] >gi_447137_prf_1913422C nodulin [Glycine max]

Seq. No. 984
 Contig ID 518_2.R1040
 5'-most EST LIB3040-044-Q1-E1-C8
 Method BLASTN
 NCBI GI g218261
 BLAST score 121
 E value 2.0e-61
 Match length 229
 % identity 88
 NCBI Description Soybean mRNA for early nodulin

Seq. No. 985
 Contig ID 521_1.R1040
 5'-most EST seb700650013.h1
 Method BLASTX
 NCBI GI g485495
 BLAST score 2326
 E value 0.0e+00
 Match length 463
 % identity 97
 NCBI Description aspartate transaminase (EC 2.6.1.1) AAT5 precursor - soybean >gi_169915 (L09702) aspartate aminotransferase [Glycine max] >gi_300419_bbs_132011 (S60967) aspartate aminotransferase isozyme 5, AAT5 (EC 2.6.1.1) [Glycine max=soybeans, cv. Century, Peptide Chloroplast, 463 aa] [Glycine max]

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Seq. No. 986
 Contig ID 521_2.R1040
 5'-most EST LIB3049-021-Q1-E1-C8
 Method BLASTN
 NCBI GI g300418
 BLAST score 290
 E value 1.0e-162
 Match length 342
 % identity 96
 NCBI Description aspartate aminotransferase isozyme 5 [Glycine max=soybeans, cv. Century, mRNA, 1755 nt]

Seq. No. 987
 Contig ID 521_3.R1040
 5'-most EST gsv701055975.h1
 Method BLASTN
 NCBI GI g169914
 BLAST score 123
 E value 7.0e-63
 Match length 123
 % identity 100
 NCBI Description Glycine max (clone pSAT17) aspartate aminotransferase mRNA, complete cds

Seq. No. 988
 Contig ID 522_1.R1040
 5'-most EST g169918_FL
 Method BLASTN
 NCBI GI g169918
 BLAST score 1735
 E value 0.0e+00
 Match length 1924
 % identity 99
 NCBI Description Soybean auxin-regulated protein (Aux22) mRNA, complete cds

Seq. No. 989
 Contig ID 522_2.R1040
 5'-most EST rlr700901873.h1
 Method BLASTN
 NCBI GI g169918
 BLAST score 144
 E value 3.0e-75
 Match length 316
 % identity 88
 NCBI Description Soybean auxin-regulated protein (Aux22) mRNA, complete cds

Seq. No. 990
 Contig ID 523_1.R1040
 5'-most EST g169920_FL
 Method BLASTN
 NCBI GI g169920
 BLAST score 1780
 E value 0.0e+00
 Match length 1784
 % identity 100
 NCBI Description Soybean auxin-regulated protein (Aux28) mRNA, complete cds

Seq. No. 991
 Contig ID 523_2.R1040
 5'-most EST leu701151952.h1
 Method BLASTN
 NCBI GI g169920
 BLAST score 213
 E value 1.0e-116
 Match length 531
 % identity 87
 NCBI Description Soybean auxin-regulated protein (Aux28) mRNA, complete cds

Seq. No. 992
 Contig ID 523_3.R1040
 5'-most EST jC-gmfl02220103g11d1
 Method BLASTN
 NCBI GI g169920
 BLAST score 103
 E value 1.0e-50
 Match length 285
 % identity 87
 NCBI Description Soybean auxin-regulated protein (Aux28) mRNA, complete cds

Seq. No. 993
 Contig ID 523_4.R1040
 5'-most EST seb700653443.h1
 Method BLASTX
 NCBI GI g114734
 BLAST score 192
 E value 2.0e-14
 Match length 113
 % identity 47
 NCBI Description AUXIN-INDUCED PROTEIN AUX28 >gi_81759_pir_A28993 aux28
 protein - soybean >gi_169921 (J03919) auxin-regulated
 protein (Aux28) [Glycine max]

Seq. No. 994
 Contig ID 524_1.R1040
 5'-most EST zsg701127613.h1
 Method BLASTX
 NCBI GI g1706546
 BLAST score 1791
 E value 0.0e+00
 Match length 347
 % identity 100
 NCBI Description GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR
 ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
 (BETA-1,3-ENDOGLUCANASE) >gi_169923 (M37753)
 beta-1,3-endoglucanase (EC 3.2.1.39) [Glycine max]

Seq. No. 995
 Contig ID 524_2.R1040
 5'-most EST zzp700832021.h1
 Method BLASTX
 NCBI GI g1403675
 BLAST score 760
 E value 7.0e-81
 Match length 192

Match length 331
 % identity 89
 NCBI Description Glycine max calcium dependent protein kinase mRNA

Seq. No. 1001
 Contig ID 531_1.R1040
 5'-most EST jC-gmst02400047f05a1
 Method BLASTX
 NCBI GI g3096935
 BLAST score 195
 E value 8.0e-15
 Match length 102
 % identity 42
 NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 1002
 Contig ID 531_2.R1040
 5'-most EST g5752719
 Method BLASTX
 NCBI GI g1617206
 BLAST score 275
 E value 4.0e-24
 Match length 129
 % identity 48
 NCBI Description (Z72489) CP12 [Pisum sativum]

Seq. No. 1003
 Contig ID 531_3.R1040
 5'-most EST LIB3170-045-Q1-K1-E4
 Method BLASTX
 NCBI GI g3334150
 BLAST score 1870
 E value 0.0e+00
 Match length 421
 % identity 90
 NCBI Description MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR
 (MG-PROTOPORPHYRIN IX CHELATASE) >gi_2129847_pir_JC4312
 chlorophyll magnesium chelatase (EC 4.99.-.-) - soybean
 chloroplast >gi_1732469_dbj_BAA08291_ (D45857) Mg chelatase
 subunit (46 kD) [Glycine max]

Seq. No. 1004
 Contig ID 531_4.R1040
 5'-most EST LIB3028-039-Q1-B2-B2
 Method BLASTN
 NCBI GI g1732468
 BLAST score 82
 E value 5.0e-38
 Match length 86
 % identity 99
 NCBI Description Soybean mRNA for Mg chelatase subunit (46 kD), complete cds

Seq. No. 1005
 Contig ID 531_5.R1040
 5'-most EST g5510205

Seq. No. 1006

Contig ID 531_6.R1040
 5'-most EST LIB3107-014-Q1-K1-D9
 Method BLASTN
 NCBI GI g1732468
 BLAST score 133
 E value 3.0e-68
 Match length 439
 % identity 91
 NCBI Description Soybean mRNA for Mg chelatase subunit (46 kD), complete cds

Seq. No. 1007
 Contig ID 531_7.R1040
 5'-most EST LIB3074-011-Q1-E1-E12
 Method BLASTN
 NCBI GI g1732468
 BLAST score 82
 E value 3.0e-38
 Match length 86
 % identity 99
 NCBI Description Soybean mRNA for Mg chelatase subunit (46 kD), complete cds

Seq. No. 1008
 Contig ID 531_8.R1040
 5'-most EST g5677965
 Method BLASTX
 NCBI GI g1617206
 BLAST score 244
 E value 1.0e-20
 Match length 79
 % identity 57
 NCBI Description (272489) CP12 [Pisum sativum]

Seq. No. 1009
 Contig ID 531_9.R1040
 5'-most EST uC-gmropic110e07b1
 Method BLASTN
 NCBI GI g1732468
 BLAST score 189
 E value 1.0e-102
 Match length 257
 % identity 93
 NCBI Description Soybean mRNA for Mg chelatase subunit (46 kD), complete cds

Seq. No. 1010
 Contig ID 531_10.R1040
 5'-most EST g5752984
 Method BLASTN
 NCBI GI g1732468
 BLAST score 144
 E value 4.0e-75
 Match length 432
 % identity 98
 NCBI Description Soybean mRNA for Mg chelatase subunit (46 kD), complete cds

Seq. No. 1011
 Contig ID 531_14.R1040
 5'-most EST ssr700557049.h1

Method BLASTN
 NCBI GI g1732468
 BLAST score 180
 E value 7.0e-97
 Match length 244
 % identity 93
 NCBI Description Soybean mRNA for Mg chelatase subunit (46 kD), complete cds

Seq. No. 1012
 Contig ID 534_1.R1040
 5'-most EST jC-gmf102220070f11a1
 Method BLASTX
 NCBI GI g1351410
 BLAST score 2477
 E value 0.0e+00
 Match length 495
 % identity 94
 NCBI Description VACUOLAR PROCESSING ENZYME PRECURSOR (VPE)
 >gi_511938_dbj_BAA06030_ (D28876) cysteine proteinase
 [Glycine max]

Seq. No. 1013
 Contig ID 534_2.R1040
 5'-most EST LIB3107-004-Q1-K1-D4
 Method BLASTN
 NCBI GI g511937
 BLAST score 244
 E value 1.0e-135
 Match length 326
 % identity 94
 NCBI Description Soybean mRNA for cysteine proteinase, complete cds

Seq. No. 1014
 Contig ID 534_3.R1040
 5'-most EST uC-gmropic103c05b1
 Method BLASTN
 NCBI GI g511937
 BLAST score 267
 E value 1.0e-148
 Match length 279
 % identity 99
 NCBI Description Soybean mRNA for cysteine proteinase, complete cds

Seq. No. 1015
 Contig ID 535_1.R1040
 5'-most EST seb700653014.h1
 Method BLASTX
 NCBI GI g2494415
 BLAST score 1914
 E value 0.0e+00
 Match length 394
 % identity 94
 NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
 (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
 >gi_515747. (L34841) fructose-1,6-bisphosphatase [Glycine
 max]

Seq. No. 1021
 Contig ID 539_2.R1040
 5'-most EST leu701153112.h1
 Method BLASTN
 NCBI GI g457569
 BLAST score 373
 E value 0.0e+00
 Match length 780
 % identity 88
 NCBI Description Soybean mRNA for endo-xyloglucan transferase, partial cds

Seq. No. 1022
 Contig ID 539_3.R1040
 5'-most EST LIB3028-050-Q1-B1-A12
 Method BLASTX
 NCBI GI g2813966
 BLAST score 234
 E value 6.0e-19
 Match length 200
 % identity 41
 NCBI Description (Z97053) placental protein Diff33 [Homo sapiens]
 >gi_4545219_gb_AAD22448.1_ (AF112227) TDE homolog [Homo sapiens]

Seq. No. 1023
 Contig ID 539_4.R1040
 5'-most EST ncj700981722.h1
 Method BLASTX
 NCBI GI g2813966
 BLAST score 255
 E value 2.0e-21
 Match length 150
 % identity 35
 NCBI Description (Z97053) placental protein Diff33 [Homo sapiens]
 >gi_4545219_gb_AAD22448.1_ (AF112227) TDE homolog [Homo sapiens]

Seq. No. 1024
 Contig ID 539_5.R1040
 5'-most EST leu701144894.h1
 Method BLASTN
 NCBI GI g457572
 BLAST score 631
 E value 0.0e+00
 Match length 905
 % identity 93
 NCBI Description V.angularis mRNA for endo-xyloglucan transferase, complete cds

Seq. No. 1025
 Contig ID 539_6.R1040
 5'-most EST zhf700959501.h1

Seq. No. 1026
 Contig ID 539_8.R1040
 5'-most EST jC-gmst02400018d10d1

Method BLASTN
 NCBI GI g457569
 BLAST score 250
 E value 1.0e-138
 Match length 250
 % identity 100
 NCBI Description Soybean mRNA for endo-xyloglucan transferase, partial cds

Seq. No. 1027
 Contig ID 539_9.R1040
 5'-most EST LIB3028-006-Q1-B1-C3
 Method BLASTN
 NCBI GI g457569
 BLAST score 206
 E value 1.0e-112
 Match length 298
 % identity 93
 NCBI Description Soybean mRNA for endo-xyloglucan transferase, partial cds

Seq. No. 1028
 Contig ID 539_11.R1040
 5'-most EST zzp700832821.h1

Seq. No. 1029
 Contig ID 539_12.R1040
 5'-most EST LIB3028-024-Q1-B1-D8
 Method BLASTN
 NCBI GI g457569
 BLAST score 273
 E value 1.0e-152
 Match length 297
 % identity 98
 NCBI Description Soybean mRNA for endo-xyloglucan transferase, partial cds

Seq. No. 1030
 Contig ID 539_13.R1040
 5'-most EST jC-gmfl02220082h12a1
 Method BLASTN
 NCBI GI g457572
 BLAST score 387
 E value 0.0e+00
 Match length 666
 % identity 91
 NCBI Description V.angularis mRNA for endo-xyloglucan transferase, complete cds

Seq. No. 1031
 Contig ID 540_1.R1040
 5'-most EST pxt700944790.h1
 Method BLASTN
 NCBI GI g169952
 BLAST score 1024
 E value 0.0e+00
 Match length 1044
 % identity 100
 NCBI Description Glycine max ferritin mRNA, complete cds

Seq. No. 1042
 Contig ID 547_1.R1040
 5'-most EST uC-gmropic074d11b1
 Method BLASTX
 NCBI GI g1346192
 BLAST score 2517
 E value 0.0e+00
 Match length 525
 % identity 94
 NCBI Description GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE)
 >gi_169965 (L11632) glutathione reductase [Glycine max]

Seq. No. 1043
 Contig ID 547_2.R1040
 5'-most EST fde700872675.h1
 Method BLASTN
 NCBI GI g169964
 BLAST score 100
 E value 7.0e-49
 Match length 415
 % identity 88
 NCBI Description Soybean glutathione reductase (GR) mRNA, complete cds

Seq. No. 1044
 Contig ID 552_1.R1040
 5'-most EST g438898_FL
 Method BLASTX
 NCBI GI g1709918
 BLAST score 2776
 E value 0.0e+00
 Match length 548
 % identity 98
 NCBI Description AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR (GLUTAMINE
 PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE)
 (GPAT) >gi_438899 (L23833) glutamine.
 phosphoribosylpyrophosphate amidotransferase [Glycine max]

Seq. No. 1045
 Contig ID 552_2.R1040
 5'-most EST g4303654
 Method BLASTX
 NCBI GI g1709918
 BLAST score 1084
 E value 1.0e-118
 Match length 269
 % identity 85
 NCBI Description AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR (GLUTAMINE
 PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE)
 (GPAT) >gi_438899 (L23833) glutamine
 phosphoribosylpyrophosphate amidotransferase [Glycine max]

Seq. No. 1046
 Contig ID 553_1.R1040
 5'-most EST jC-gmro02910062f11a1
 Method BLASTX
 NCBI GI g1346105

BLAST score 1978
 E value 0.0e+00
 Match length 385
 % identity 99
 NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-1 SUBUNIT
 (GP-ALPHA-1) >gi_439617 (L27418) G protein alpha subunit
 [Glycine max]

Seq. No. 1047
 Contig ID 554_1.R1040
 5'-most EST LIB3049-032-Q1-E1-A12
 Method BLASTX
 NCBI GI g1170031
 BLAST score 2323
 E value 0.0e+00
 Match length 466
 % identity 97
 NCBI Description GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA)
 (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)
 >gi_541940_pir_JQ2263 glutamate 1-semialdehyde
 aminotransferase (EC 2.6.1.-) precursor - soybean
 >gi_310567 (L12453) glutamate 1-semialdehyde
 aminotransferase [Glycine max] >gi_747968 (U20260)
 glutamate 1-semialdehyde aminotransferase [Glycine max]

Seq. No. 1048
 Contig ID 554_2.R1040
 5'-most EST LIB3138-061-Q1-N1-G9
 Method BLASTN
 NCBI GI g310566
 BLAST score 300
 E value 1.0e-168
 Match length 419
 % identity 95
 NCBI Description Soybean glutamate 1-semialdehyde aminotransferase mRNA,
 complete cds

Seq. No. 1049
 Contig ID 555_1.R1040
 5'-most EST LIB3055-006-Q1-N1-B8
 Method BLASTN
 NCBI GI g450634
 BLAST score 954
 E value 0.0e+00
 Match length 998
 % identity 99
 NCBI Description Soybean GTP binding protein mRNA, complete cds

Seq. No. 1050
 Contig ID 555_2.R1040
 5'-most EST g1381677_FL
 Method BLASTN
 NCBI GI g1381677
 BLAST score 706
 E value 0.0e+00
 Match length 888
 % identity 95

NCBI Description Glycine max small GTP-binding protein (sra2) mRNA, complete cds

Seq. No. 1051
 Contig ID 555_3.R1040
 5'-most EST uC-gmropic054b10b1
 Method BLASTN
 NCBI GI g303731
 BLAST score 456
 E value 0.0e+00
 Match length 723
 % identity 92

NCBI Description Pea mRNA for GTP-binding protein, complete cds

Seq. No. 1052
 Contig ID 555_4.R1040
 5'-most EST LIB3050-014-Q1-E1-C4
 Method BLASTN
 NCBI GI g1381677
 BLAST score 336
 E value 0.0e+00
 Match length 443
 % identity 97

NCBI Description Glycine max small GTP-binding protein (sra2) mRNA, complete cds

Seq. No. 1053
 Contig ID 556_1.R1040
 5'-most EST LIB3109-016-Q1-K1-B2
 Method BLASTX
 NCBI GI g1170312
 BLAST score 1640
 E value 0.0e+00
 Match length 379
 % identity 82

NCBI Description HOMEBOX PROTEIN SBH1 >gi_629614_pir_S42543 hypothetical protein - soybean >gi_485406 (L13663) SBH1 [Glycine max]

Seq. No. 1054
 Contig ID 556_2.R1040
 5'-most EST g5666882
 Method BLASTN
 NCBI GI g310568
 BLAST score 279
 E value 1.0e-155
 Match length 455
 % identity 91

NCBI Description Glycine max homeobox-containing (Sbh1) mRNA, complete cds

Seq. No. 1055
 Contig ID 557_1.R1040
 5'-most EST g4313302
 Method BLASTN
 NCBI GI g170048
 BLAST score 393
 E value 0.0e+00
 Match length 494

Method BLASTX
 NCBI GI g1362050
 BLAST score 1771
 E value 0.0e+00
 Match length 339
 % identity 100
 NCBI Description protein kinase 1 - soybean >gi_169991 (L01453) protein kinase [Glycine max]

Seq. No. 1072
 Contig ID 564_4.R1040
 5'-most EST hrw701060550.h1
 Method BLASTN
 NCBI GI g310579
 BLAST score 498
 E value 0.0e+00
 Match length 1118
 % identity 95
 NCBI Description Glycine max protein kinase 2 (SPK-2) mRNA, complete cds

Seq. No. 1073
 Contig ID 564_5.R1040
 5'-most EST ssr700560617.h1
 Method BLASTN
 NCBI GI g310579
 BLAST score 230
 E value 1.0e-126
 Match length 242
 % identity 99
 NCBI Description Glycine max protein kinase 2 (SPK-2) mRNA, complete cds

Seq. No. 1074
 Contig ID 564_7.R1040
 5'-most EST LIB3093-053-Q1-K1-G5
 Method BLASTN
 NCBI GI g169990
 BLAST score 154
 E value 5.0e-81
 Match length 229
 % identity 98
 NCBI Description Soybean protein kinase (SPK-1) mRNA, complete cds

Seq. No. 1075
 Contig ID 567_1.R1040
 5'-most EST LIB3051-090-Q1-K1-A2
 Method BLASTN
 NCBI GI g170009
 BLAST score 1494
 E value 0.0e+00
 Match length 1727
 % identity 99
 NCBI Description Soybean late embryogenesis abundant (LEA) protein mRNA, complete cds

Seq. No. 1076
 Contig ID 567_2.R1040
 5'-most EST LIB3029-001-Q1-B1-F8

Seq. No. 1086
 Contig ID 578_1.R1040
 5'-most EST LIB3056-001-Q1-B1-H5
 Method BLASTN
 NCBI GI g347458
 BLAST score 1016
 E value 0.0e+00
 Match length 1048
 % identity 99
 NCBI Description Glycine max brassinosteroid-regulated protein mRNA,
 complete cds

Seq. No. 1087
 Contig ID 578_2.R1040
 5'-most EST fua701043403.h1
 Method BLASTN
 NCBI GI g347458
 BLAST score 361
 E value 0.0e+00
 Match length 712
 % identity 90
 NCBI Description Glycine max brassinosteroid-regulated protein mRNA,
 complete cds

Seq. No. 1088
 Contig ID 578_6.R1040
 5'-most EST LIB3139-015-P1-N1-H4
 Method BLASTN
 NCBI GI g347458
 BLAST score 216
 E value 1.0e-118
 Match length 365
 % identity 94
 NCBI Description Glycine max brassinosteroid-regulated protein mRNA,
 complete cds

Seq. No. 1089
 Contig ID 579_1.R1040
 5'-most EST txt700731909.h1
 Method BLASTX
 NCBI GI g1345976
 BLAST score 2058
 E value 0.0e+00
 Match length 387
 % identity 97
 NCBI Description OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
 ISOZYME 1 >gi_904152 (L43920) microsomal omega-6 desaturase
 [Glycine max]

Seq. No. 1090
 Contig ID 579_2.R1040
 5'-most EST zpv700757037.h1
 Method BLASTN
 NCBI GI g904151
 BLAST score 375
 E value 0.0e+00
 Match length 560

Method	BLASTN
NCBI GI	g1906001
BLAST score	189
E value	1.0e-102
Match length	189
% identity	100
NCBI Description	Glycine max nitrite reductase gene, complete cds

Seq. No.	1098
Contig ID	585_1.R1040
5'-most EST	LIB3049-002-Q1-E1-B9
Method	BLASTN
NCBI GI	g310575
BLAST score	180
E value	3.0e-96
Match length	844
% identity	88
NCBI Description	Glycine max nodulin-26 mRNA, complete cds

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Seq. No.          1100
Contig ID         587_1.R1040
5'-most EST      leu701153015.h1
Method            BLASTN
NCBI GI           g310577
BLAST score       918
E value           0.0e+00
Match length      963
% identity        99
NCBI Description   Glycine max nodulin-26 mRNA, complete cds
```

BLAST score 715
E value 0.0e+00
Match length 867
% identity 98
NCBI Description Glycine max mutant nitrate reductase mRNA, 3' end

Seq. No. 1102
Contig ID 588_2.R1040
5'-most EST LIB3138-056-Q1-N1-G10
Method BLASTX
NCBI GI g730142
BLAST score 657
E value 5.0e-69
Match length 141
% identity 91
NCBI Description NITRATE REDUCTASE 2 (NR-2) >gi_392992 (U01029) nitrate reductase [Phaseolus vulgaris]

Seq. No. 1103
Contig ID 588_3.R1040
5'-most EST smc700749263.h1
Method BLASTN
NCBI GI g392991
BLAST score 124
E value 5.0e-63
Match length 396
% identity 83
NCBI Description Phaseolus vulgaris nitrate reductase (PVNR2) gene, complete cds

Seq. No. 1104
Contig ID 589_1.R1040
5'-most EST LIB3109-035-Q1-K1-B8
Method BLASTX
NCBI GI g1345979
BLAST score 2322
E value 0.0e+00
Match length 424
% identity 99
NCBI Description OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi_459962 (L29215) plastid omega-6 desaturase [Glycine max]

Seq. No. 1105
Contig ID 589_5.R1040
5'-most EST jC-gmle01810089d01a1
Method BLASTN
NCBI GI g459961
BLAST score 259
E value 1.0e-144
Match length 352
% identity 98
NCBI Description Glycine max proplastid omega-6 desaturase mRNA, complete cds

Seq. No. 1106
Contig ID 592_1.R1040

5'-most EST LIB3109-037-Q1-K1-D4
 Method BLASTN
 NCBI GI g170041
 BLAST score 920
 E value 0.0e+00
 Match length 1093
 % identity 97
 NCBI Description Glycine max cv Prize protein kinase mRNA

Seq. No. 1107
 Contig ID 592_2.R1040
 5'-most EST LIB3109-013-Q1-K1-A1
 Method BLASTN
 NCBI GI g170042
 BLAST score 1216
 E value 0.0e+00
 Match length 1216
 % identity 100
 NCBI Description Glycine max cv Prize protein kinase mRNA

Seq. No. 1108
 Contig ID 592_3.R1040
 5'-most EST uaw700665730.h1
 Method BLASTN
 NCBI GI g170041
 BLAST score 255
 E value 1.0e-141
 Match length 259
 % identity 100
 NCBI Description Glycine max cv Prize protein kinase mRNA

Seq. No. 1109
 Contig ID 592_4.R1040
 5'-most EST leu701155312.h1
 Method BLASTN
 NCBI GI g170042
 BLAST score 246
 E value 1.0e-136
 Match length 341
 % identity 96
 NCBI Description Glycine max cv Prize protein kinase mRNA

Seq. No. 1110
 Contig ID 594_1.R1040
 5'-most EST g736338_FL
 Method BLASTX
 NCBI GI g1171965
 BLAST score 4069
 E value 0.0e+00
 Match length 814
 % identity 97
 NCBI Description PHOSPHATIDYLINOSITOL 3-KINASE, ROOT ISOFORM (PI3-KINASE)
 (PTDINS-3-KINASE) (PI3K) (SPI3K-5) >gi_736339 (L27265)
 phosphatidylinositol 3-kinase [Glycine max]

Seq. No. 1111
 Contig ID 596_1.R1040

5'-most EST g515750_FL
 Method BLASTX
 NCBI GI g1172495
 BLAST score 3387
 E value 0.0e+00
 Match length 1106
 % identity 94
 NCBI Description PHYTOCHROME A >gi_515749 (L34842) phytochrome A [Glycine max] >gi_515751 (L34844) phytochrome A [Glycine max]

Seq. No. 1112
 Contig ID 596_2.R1040
 5'-most EST fC-gmse700654835a6
 Method BLASTN
 NCBI GI g515748
 BLAST score 219
 E value 1.0e-120
 Match length 435
 % identity 94
 NCBI Description Soybean chloroplast phytochrome A (phyA) gene, complete cds

Seq. No. 1113
 Contig ID 596_3.R1040
 5'-most EST uC-gmflminsoy012f11b1
 Method BLASTX
 NCBI GI g3953465
 BLAST score 452
 E value 1.0e-44
 Match length 160
 % identity 55
 NCBI Description (AC002328) F20N2.10 [Arabidopsis thaliana]

Seq. No. 1114
 Contig ID 596_4.R1040
 5'-most EST fC-gmst700660709a4
 Method BLASTN
 NCBI GI g515750
 BLAST score 320
 E value 1.0e-180
 Match length 719
 % identity 91
 NCBI Description Soybean phytochrome A (phyA) mRNA, complete cds

Seq. No. 1115
 Contig ID 597_1.R1040
 5'-most EST g170043_FL
 Method BLASTX
 NCBI GI g117519
 BLAST score 2972
 E value 0.0e+00
 Match length 570
 % identity 100
 NCBI Description PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATURASE)
 >gi_99945_pir_A39597 phytoene dehydrogenase (EC 1.3.-.-) -
 soybean >gi_170044 (M64704) phytoene desaturase [Glycine max]

Seq. No. 1121
 Contig ID 600_5.R1040
 5'-most EST uC-gmropic047d08b1
 Method BLASTN
 NCBI GI g170050
 BLAST score 301
 E value 1.0e-169
 Match length 434
 % identity 94
 NCBI Description Soybean pyruvate kinase mRNA, complete cds

Seq. No. 1122
 Contig ID 600_8.R1040
 5'-most EST ncj700975678.h1
 Method BLASTN
 NCBI GI g170050
 BLAST score 147
 E value 5.0e-77
 Match length 233
 % identity 98
 NCBI Description Soybean pyruvate kinase mRNA, complete cds

Seq. No. 1123
 Contig ID 601_1.R1040
 5'-most EST LIB3109-036-Q1-K1-C10
 Method BLASTN
 NCBI GI g414831
 BLAST score 776
 E value 0.0e+00
 Match length 815
 % identity 99
 NCBI Description Glycine max (Rab1p) mRNA, complete cds

Seq. No. 1124
 Contig ID 602_1.R1040
 5'-most EST g414833_FL
 Method BLASTN
 NCBI GI g414833
 BLAST score 1076
 E value 0.0e+00
 Match length 1118
 % identity 100
 NCBI Description Glycine max (Rab7p) mRNA, complete cds

Seq. No. 1125
 Contig ID 602_2.R1040
 5'-most EST fua701039675.h1
 Method BLASTN
 NCBI GI g414833
 BLAST score 195
 E value 1.0e-106
 Match length 227
 % identity 96
 NCBI Description Glycine max (Rab7p) mRNA, complete cds

Seq. No. 1126

Contig ID 603_1.R1040
 5'-most EST awf700838208.h1
 Method BLASTN
 NCBI GI g170051
 BLAST score 851
 E value 0.0e+00
 Match length 884
 % identity 99
 NCBI Description Glycine max RNA polymerase II fifth largest subunit mRNA, complete cds

Seq. No. 1127
 Contig ID 603_2.R1040
 5'-most EST uC-gmropic009g08b1
 Method BLASTN
 NCBI GI g170051
 BLAST score 354
 E value 0.0e+00
 Match length 433
 % identity 96
 NCBI Description Glycine max RNA polymerase II fifth largest subunit mRNA, complete cds

Seq. No. 1128
 Contig ID 604_1.R1040
 5'-most EST LIB3107-038-Q1-K1-E12
 Method BLASTN
 NCBI GI g170053
 BLAST score 545
 E value 0.0e+00
 Match length 682
 % identity 95
 NCBI Description Soybean ribosomal protein S11 mRNA, 3' end

Seq. No. 1129
 Contig ID 604_2.R1040
 5'-most EST LIB3039-047-Q1-E1-E3
 Method BLASTN
 NCBI GI g170053
 BLAST score 224
 E value 1.0e-122
 Match length 416
 % identity 88
 NCBI Description Soybean ribosomal protein S11 mRNA, 3' end

Seq. No. 1130
 Contig ID 604_3.R1040
 5'-most EST LIB3049-056-Q1-E1-F10
 Method BLASTN
 NCBI GI g170053
 BLAST score 432
 E value 0.0e+00
 Match length 579
 % identity 94
 NCBI Description Soybean ribosomal protein S11 mRNA, 3' end

Seq. No. 1131

Contig ID 604 5.R1040
 5'-most EST LIB3039-015-Q1-E1-H4
 Method BLASTN
 NCBI GI g170053
 BLAST score 175
 E value 1.0e-93
 Match length 211
 % identity 96
 NCBI Description Soybean ribosomal protein S11 mRNA, 3' end

Seq. No. 1132
 Contig ID 604 9.R1040
 5'-most EST LIB3040-029-Q1-E1-H5
 Method BLASTN
 NCBI GI g170053
 BLAST score 91
 E value 1.0e-43
 Match length 195
 % identity 87
 NCBI Description Soybean ribosomal protein S11 mRNA, 3' end

Seq. No. 1133
 Contig ID 605 1.R1040
 5'-most EST ssr700553763.h1
 Method BLASTN
 NCBI GI g454178
 BLAST score 1264
 E value 0.0e+00
 Match length 1285
 % identity 99
 NCBI Description Glycine max rubisco-associated protein mRNA, complete cds

Seq. No. 1134
 Contig ID 606 1.R1040
 5'-most EST LIB3040-030-Q1-E1-B7
 Method BLASTX
 NCBI GI g3915032
 BLAST score 1814
 E value 0.0e+00
 Match length 411
 % identity 86
 NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
 (STEAROYL-ACP DESATURASE) >gi_508603 (L34346) stearyl-acyl
 carrier protein desaturase [Glycine max]

Seq. No. 1135
 Contig ID 606 2.R1040
 5'-most EST uC-gmflminsoy028f03b1
 Method BLASTN
 NCBI GI g508602
 BLAST score 268
 E value 1.0e-149
 Match length 348
 % identity 94
 NCBI Description Glycine max stearyl-acyl carrier protein desaturase
 (SACPD) mRNA, complete cds

% identity 92
NCBI Description Soybean calmodulin (SCaM-3) mRNA, complete cds

Seq. No. 1141
Contig ID 609_2.R1040
5'-most EST LIB3072-053-Q1-E1-E12
Method BLASTN
NCBI GI g170069
BLAST score 705
E value 0.0e+00
Match length 738
% identity 99

NCBI Description Soybean calmodulin (SCaM-1) mRNA, complete cds

Seq. No. 1142
Contig ID 609_3.R1040
5'-most EST LIB3106-104-Q1-K1-F4
Method BLASTN
NCBI GI g170073
BLAST score 431
E value 0.0e+00
Match length 435
% identity 100

NCBI Description Soybean calmodulin (SCaM-3) mRNA, complete cds

Seq. No. 1143
Contig ID 609_5.R1040
5'-most EST uC-gmflminsoy118b07b1
Method BLASTN
NCBI GI g170069
BLAST score 265
E value 1.0e-147
Match length 321
% identity 96

NCBI Description Soybean calmodulin (SCaM-1) mRNA, complete cds

Seq. No. 1144
Contig ID 610_1.R1040
5'-most EST LIB3049-024-Q1-E1-H5
Method BLASTN
NCBI GI g170071
BLAST score 668
E value 0.0e+00
Match length 839
% identity 97

NCBI Description Soybean calmodulin (SCaM-2) mRNA, complete cds

Seq. No. 1145
Contig ID 610_2.R1040
5'-most EST k11701205314.h1
Method BLASTN
NCBI GI g4103958
BLAST score 460
E value 0.0e+00
Match length 788
% identity 92

NCBI Description Phaseolus vulgaris calmodulin (CaM) mRNA, PvCaM-2 allele,

09084016 101000

```
Seq. No.          1147
Contig ID         612_3.R1040
5'-most EST      LIB3053-012-Q1-N1-F1
Method            BLASTN
NCBI GI           g170075
BLAST score       105
E value           6.0e-52
Match length      201
% identity        100
NCBI Description   Soybean calmodulin (SCaM-4) mRNA, complete cds
```

```
Seq. No.          1148
Contig ID         613 1.R1040
5'-most EST      g532289_FL
Method           BLASTX
NCBI GI          g2492792
BLAST score      2806
E value          0.0e+00
Match length     549
% identity       100
NCBI Description  LATE NODULIN 56 (N-56) >gi_532290_dbj_BAA07212_ (D38015)
                  soybean late nodulin [Glycine max]
```

```
Seq. No.          1149
Contig ID         614_1.R1040
5'-most EST      LIB3049-004-Q1-E1-G9
Method           BLASTN
NCBI GI          g1161251
BLAST score      852
E value          0.0e+00
Match length     1364
% identity       98
NCBI Description  Glycine max nucleosome assembly protein 1 (SNAP-1) mRNA,
                  complete cds
```

```
Seq. No.          1150
Contig ID         614_2.R1040
5'-most EST      leu701157276.h1
Method            BLASTN
NCBI GI           g1161251
BLAST score       291
E value           1.0e-162
Match length      901
% identity        87
```


5'-most EST	LIB3072-017-Q1-E1-G4
Method	BLASTN
NCBI GI	g2306978
BLAST score	490
E value	0.0e+00
Match length	502
% identity	99
NCBI Description	Glycine max metallothionein-II protein (PGMPM19) mRNA, complete cds
Seq. No.	1167
Contig ID	627_2.R1040
5'-most EST	LIB3072-028-Q1-E1-G2
Method	BLASTN
NCBI GI	g2270991
BLAST score	287
E value	1.0e-160
Match length	386
% identity	100
NCBI Description	Glycine max metallothionein-II protein mRNA, complete cds
Seq. No.	1168
Contig ID	627_3.R1040
5'-most EST	LIB3072-059-Q1-K1-G7
Method	BLASTN
NCBI GI	g2270991
BLAST score	413
E value	0.0e+00
Match length	413
% identity	100
NCBI Description	Glycine max metallothionein-II protein mRNA, complete cds
Seq. No.	1169
Contig ID	628_1.R1040
5'-most EST	uxk700668563.h1
Method	BLASTN
NCBI GI	g2270993
BLAST score	819
E value	0.0e+00
Match length	964
% identity	99
NCBI Description	Glycine max Ca ²⁺ -binding EF hand protein (GmPM13) mRNA, complete cds
Seq. No.	1170
Contig ID	629_1.R1040
5'-most EST	awf700843103.h1
Method	BLASTN
NCBI GI	g4102691
BLAST score	633
E value	0.0e+00
Match length	633
% identity	100
NCBI Description	Glycine max late-embryogenesis abundant protein mRNA, complete cds
Seq. No.	1171

Contig ID	629 2.R1040
5'-most EST	crh700854653.h1
Method	BLASTN
NCBI GI	g4102691
BLAST score	275
E value	1.0e-153
Match length	532
% identity	91
NCBI Description	Glycine max late-embryogenesis abundant protein mRNA, complete cds
Seq. No.	1172
Contig ID	629 3.R1040
5'-most EST	LIB3170-004-Q1-K1-E10
Method	BLASTN
NCBI GI	g4102691
BLAST score	240
E value	1.0e-132
Match length	519
% identity	93
NCBI Description	Glycine max late-embryogenesis abundant protein mRNA, complete cds
Seq. No.	1173
Contig ID	630 1.R1040
5'-most EST	zpv700757378.h1
Method	BLASTN
NCBI GI	g4097895
BLAST score	728
E value	0.0e+00
Match length	728
% identity	100
NCBI Description	Glycine max napin-type 2S albumin 3 mRNA, complete cds
Seq. No.	1174
Contig ID	630 2.R1040
5'-most EST	uC-gmropic066f10b1
Method	BLASTX
NCBI GI	g4063749
BLAST score	239
E value	6.0e-20
Match length	92
% identity	27
NCBI Description	(AC005851) hypothetical protein [Arabidopsis thaliana]
Seq. No.	1175
Contig ID	630 4.R1040
5'-most EST	LIB3073-008-Q1-K1-G3
Method	BLASTN
NCBI GI	g4097895
BLAST score	129
E value	8.0e-66
Match length	241
% identity	98
NCBI Description	Glycine max napin-type 2S albumin 3 mRNA, complete cds
Seq. No.	1176

Contig ID 630 6.R1040
 5'-most EST vwf700678862.h1
 Method BLASTN
 NCBI GI g2305019
 BLAST score 172
 E value 6.0e-92
 Match length 176
 % identity 99
 NCBI Description Glycine max 2S albumin pre-propeptide mRNA, complete cds

Seq. No. 1177
 Contig ID 631 1.R1040
 5'-most EST LIB3051-110-Q1-K1-F5
 Method BLASTX
 NCBI GI g2253384
 BLAST score 2739
 E value 0.0e+00
 Match length 539
 % identity 99
 NCBI Description (AF007100) biotin carboxylase precursor [Glycine max]

Seq. No. 1178
 Contig ID 631 2.R1040
 5'-most EST fua701040021.h1
 Method BLASTX
 NCBI GI g134892
 BLAST score 654
 E value 2.0e-68
 Match length 194
 % identity 68
 NCBI Description SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT
 (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA)
 >gi_88607_pir_A29440 signal recognition particle receptor
 - human >gi_30866_emb_CAA29608_(X06272) docking protein
 [Homo sapiens] >gi_4507223_ref_NP_003130.1_pSRPR signal
 recognition particle receptor ('docking protein')

Seq. No. 1179
 Contig ID 631 3.R1040
 5'-most EST g3219360_FL
 Method BLASTX
 NCBI GI g3219361
 BLAST score 2741
 E value 0.0e+00
 Match length 539
 % identity 99
 NCBI Description (AF068249) biotin carboxylase precursor [Glycine max]

Seq. No. 1180
 Contig ID 631 6.R1040
 5'-most EST LIB3055-001-Q1-B1-F6
 Method BLASTN
 NCBI GI g3219360
 BLAST score 182
 E value 5.0e-98
 Match length 262
 % identity 93

NCBI Description Glycine max biotin carboxylase precursor (accC-3) mRNA,
nuclear gene encoding chloroplast protein, complete cds

Seq. No. 1181
Contig ID 632_1.R1040
5'-most EST uC-gmropic022d10b1
Method BLASTX
NCBI GI g2245683
BLAST score 1680
E value 0.0e+00
Match length 339
% identity 99
NCBI Description (AF007211) peroxidase precursor [Glycine max]

Seq. No. 1182
Contig ID 632_2.R1040
5'-most EST trc700563017.h1
Method BLASTN
NCBI GI g2245682
BLAST score 289
E value 1.0e-161
Match length 341
% identity 96
NCBI Description Glycine max peroxidase precursor (GMIPER1) mRNA, complete
cds

Seq. No. 1183
Contig ID 633_1.R1040
5'-most EST g4102189_FL
Method BLASTN
NCBI GI g4102189
BLAST score 1208
E value 0.0e+00
Match length 1220
% identity 98
NCBI Description Glycine max 35 kDa seed maturation protein (pGmPM18) mRNA,
complete cds

Seq. No. 1184
Contig ID 633_2.R1040
5'-most EST 6HA-02-Q1-B1-G6
Method BLASTN
NCBI GI g4102189
BLAST score 267
E value 1.0e-148
Match length 461
% identity 86
NCBI Description Glycine max 35 kDa seed maturation protein (pGmPM18) mRNA,
complete cds

Seq. No. 1185
Contig ID 635_1.R1040
5'-most EST LIB3167-042-P1-K1-G11
Method BLASTN
NCBI GI g2738559
BLAST score 715
E value 0.0e+00

Match length 730
 % identity 100
 NCBI Description Glycine max ribosomal protein L22 mRNA, nuclear gene
 encoding chloroplast protein, partial cds

Seq. No. 1186
 Contig ID 635_2.R1040
 5'-most EST ep~~x~~701105174.h1
 Method BLASTN
 NCBI GI g2738559
 BLAST score 264
 E value 1.0e-146
 Match length 347
 % identity 94
 NCBI Description Glycine max ribosomal protein L22 mRNA, nuclear gene
 encoding chloroplast protein, partial cds

Seq. No. 1187
 Contig ID 636_1.R1040
 5'-most EST zh~~f~~700952296.h1
 Method BLASTN
 NCBI GI g2388688
 BLAST score 958
 E value 0.0e+00
 Match length 1105
 % identity 97
 NCBI Description Glycine max GH1 protein (GH1) mRNA, partial cds

Seq. No. 1188
 Contig ID 636_2.R1040
 5'-most EST LIB3107-063-Q1-K1-B2
 Method BLASTN
 NCBI GI g2388688
 BLAST score 308
 E value 1.0e-172
 Match length 825
 % identity 90
 NCBI Description Glycine max GH1 protein (GH1) mRNA, partial cds

Seq. No. 1189
 Contig ID 636_3.R1040
 5'-most EST LIB3109-031-Q1-K1-E12
 Method BLASTN
 NCBI GI g2388688
 BLAST score 214
 E value 1.0e-116
 Match length 385
 % identity 89
 NCBI Description Glycine max GH1 protein (GH1) mRNA, partial cds

Seq. No. 1190
 Contig ID 636_4.R1040
 5'-most EST fua701040689.h1
 Method BLASTN
 NCBI GI g2388688
 BLAST score 71
 E value 2.0e-31

Match length	143
% identity	87
NCBI Description	Glycine max GH1 protein (GH1) mRNA, partial cds
Seq. No.	1191
Contig ID	636_6.R1040
5'-most EST	jC-gmro02910006g06d1
Seq. No.	1192
Contig ID	636_9.R1040
5'-most EST	LIB3039-041-Q1-E1-H8
Seq. No.	1193
Contig ID	637_1.R1040
5'-most EST	g2565258_FL
Method	BLASTX
NCBI GI	g2565259
BLAST score	1641
E value	0.0e+00
Match length	329
% identity	100
NCBI Description	(AF019115) putative cadmium-transporting ATPase [Glycine max]
Seq. No.	1194
Contig ID	638_1.R1040
5'-most EST	jC-gmro02910069c06a1
Method	BLASTN
NCBI GI	g3789722
BLAST score	1223
E value	0.0e+00
Match length	1324
% identity	99
NCBI Description	Glycine max peroxidase (PC7) mRNA, complete cds
Seq. No.	1195
Contig ID	639_1.R1040
5'-most EST	jex700903127.h1
Method	BLASTX
NCBI GI	g4432860
BLAST score	1158
E value	0.0e+00
Match length	637
% identity	32
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]
Seq. No.	1196
Contig ID	639_2.R1040
5'-most EST	LIB3028-042-Q1-B1-F1
Method	BLASTX
NCBI GI	g4432860
BLAST score	1160
E value	1.0e-127
Match length	368
% identity	25
NCBI Description	(AC006300) putative glucose-induced repressor protein

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[Arabidopsis thaliana]

Seq. No. 1197
 Contig ID 639_3.R1040
 5'-most EST uC-gmrominsoy026h10b1
 Method BLASTX
 NCBI GI g4432860
 BLAST score 522
 E value 7.0e-53
 Match length 197
 % identity 59
 NCBI Description (AC006300) putative glucose-induced repressor protein
 [Arabidopsis thaliana]

Seq. No. 1198
 Contig ID 639_4.R1040
 5'-most EST jC-gmst02400023g06a1
 Method BLASTX
 NCBI GI g2407790
 BLAST score 174
 E value 2.0e-12
 Match length 87
 % identity 47
 NCBI Description (AF019910) grr1 [Glycine max]

Seq. No. 1199
 Contig ID 639_5.R1040
 5'-most EST LIB3170-046-Q1-K1-G11
 Method BLASTN
 NCBI GI g2407789
 BLAST score 242
 E value 1.0e-134
 Match length 261
 % identity 99
 NCBI Description Glycine max grr1 (grr1) mRNA, complete cds

Seq. No. 1200
 Contig ID 641_1.R1040
 5'-most EST g2895197_FL
 Method BLASTX
 NCBI GI g3913525
 BLAST score 5544
 E value 0.0e+00
 Match length 1088
 % identity 99
 NCBI Description DNA POLYMERASE DELTA CATALYTIC CHAIN >gi_2895198 (AF020193)
 DNA polymerase delta [Glycine max]

Seq. No. 1201
 Contig ID 641_3.R1040
 5'-most EST leu701151641.h1
 Method BLASTN
 NCBI GI g2895197
 BLAST score 140
 E value 5.0e-73
 Match length 156
 % identity 97

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NCBI Description Glycine max DNA polymerase delta (Pol delta) mRNA, complete cds

Seq. No. 1202
Contig ID 642_1.R1040
5'-most EST LIB3170-048-Q1-J1-E7
Method BLASTN
NCBI GI g2444419
BLAST score 1114
E value 0.0e+00
Match length 1141
% identity 99

NCBI Description Glycine max ribosome-associated protein p40 mRNA, complete cds

Seq. No. 1203
Contig ID 642_2.R1040
5'-most EST LIB3170-036-Q1-K2-F2
Method BLASTN
NCBI GI g2815245
BLAST score 94
E value 4.0e-45
Match length 289
% identity 85

NCBI Description C.arietinum mRNA for class I type 2 metallothionein (clone: CanMT-2)

Seq. No. 1204
Contig ID 642_3.R1040
5'-most EST jC-gmst02400076g08a1
Method BLASTN
NCBI GI g2815245
BLAST score 86
E value 2.0e-40
Match length 242
% identity 84

NCBI Description C.arietinum mRNA for class I type 2 metallothionein (clone: CanMT-2)

Seq. No. 1205
Contig ID 642_4.R1040
5'-most EST zhf700957326.h1
Method BLASTN
NCBI GI g2444419
BLAST score 386
E value 0.0e+00
Match length 494
% identity 95

NCBI Description Glycine max ribosome-associated protein p40 mRNA, complete cds

Seq. No. 1206
Contig ID 642_7.R1040
5'-most EST LIB3170-019-Q1-J1-H3
Method BLASTN
NCBI GI g2444419
BLAST score 176

E value 3.0e-94
 Match length 297
 % identity 92
 NCBI Description Glycine max ribosome-associated protein p40 mRNA, complete cds

Seq. No. 1207
 Contig ID 642 8.R1040
 5'-most EST LIB3107-010-Q1-K1-A2

Seq. No. 1208
 Contig ID 642 9.R1040
 5'-most EST gsv701054621.h1

Seq. No. 1209
 Contig ID 643 1.R1040
 5'-most EST wvk700684093.h1
 Method BLASTX
 NCBI GI g2738982
 BLAST score 2518
 E value 0.0e+00
 Match length 514
 % identity 95
 NCBI Description (AF022157) CYP71A10 [Glycine max]

Seq. No. 1210
 Contig ID 644 1.R1040
 5'-most EST g5509129
 Method BLASTX
 NCBI GI g2738996
 BLAST score 2907
 E value 0.0e+00
 Match length 561
 % identity 100
 NCBI Description (AF022457) CYP97B2p [Glycine max]

Seq. No. 1211
 Contig ID 645 1.R1040
 5'-most EST LIB3139-049-P1-N1-H10
 Method BLASTX
 NCBI GI g2738998
 BLAST score 2669
 E value 0.0e+00
 Match length 509
 % identity 99
 NCBI Description (AF022458) CYP98A2p [Glycine max]

Seq. No. 1212
 Contig ID 646 1.R1040
 5'-most EST leu701146357.h1
 Method BLASTX
 NCBI GI g2739000
 BLAST score 2388
 E value 0.0e+00
 Match length 510
 % identity 92
 NCBI Description (AF022459) CYP71D10p [Glycine max]

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Seq. No. 1213
 Contig ID 647_1.R1040
 5'-most EST LIB3049-016-Q1-E1-A5
 Method BLASTX
 NCBI GI g2739002
 BLAST score 2331
 E value 0.0e+00
 Match length 499
 % identity 91
 NCBI Description (AF022460) CYP83D1p [Glycine max]

Seq. No. 1214
 Contig ID 647_2.R1040
 5'-most EST uC-gmronoir004e08b1
 Method BLASTN
 NCBI GI g2739001
 BLAST score 145
 E value 2.0e-75
 Match length 249
 % identity 90
 NCBI Description Glycine max cytochrome P450 monooxygenase CYP83D1p
 (CYP83D1) mRNA, partial cds

Seq. No. 1215
 Contig ID 648_1.R1040
 5'-most EST jC-gmle01810086g05a1
 Method BLASTX
 NCBI GI g2739004
 BLAST score 2805
 E value 0.0e+00
 Match length 532
 % identity 100
 NCBI Description (AF022461) CYP82C1p [Glycine max]

Seq. No. 1216
 Contig ID 649_1.R1040
 5'-most EST txt700733671.h1
 Method BLASTX
 NCBI GI g2739006
 BLAST score 2248
 E value 0.0e+00
 Match length 498
 % identity 89
 NCBI Description (AF022462) CYP93C1p [Glycine max]

Seq. No. 1217
 Contig ID 649_2.R1040
 5'-most EST g5230725_FL
 Method BLASTX
 NCBI GI g2739006
 BLAST score 2152
 E value 0.0e+00
 Match length 518
 % identity 88
 NCBI Description (AF022462) CYP93C1p [Glycine max]

Match length 1426
 % identity 100
 NCBI Description Glycine max polyphosphoinositide binding protein Sshlp
 (SSH1) mRNA, complete cds

Seq. No. 1224
 Contig ID 653_3.R1040
 5'-most EST leu701149472.h1
 Method BLASTN
 NCBI GI g2739043
 BLAST score 128
 E value 8.0e-66
 Match length 153
 % identity 96
 NCBI Description Glycine max polyphosphoinositide binding protein Sshlp
 (SSH1) mRNA, complete cds

Seq. No. 1225
 Contig ID 653_5.R1040
 5'-most EST LIB3028-044-Q1-B1-G1
 Method BLASTN
 NCBI GI g2739043
 BLAST score 139
 E value 2.0e-72
 Match length 209
 % identity 91
 NCBI Description Glycine max polyphosphoinositide binding protein Sshlp
 (SSH1) mRNA, complete cds

Seq. No. 1226
 Contig ID 655_3.R1040
 5'-most EST uC-gmropic059d06b1
 Method BLASTN
 NCBI GI g3169543
 BLAST score 461
 E value 0.0e+00
 Match length 2275
 % identity 84
 NCBI Description Medicago sativa sucrose synthase mRNA, complete cds

Seq. No. 1227
 Contig ID 655_4.R1040
 5'-most EST jC-gmro02910073c10a1
 Method BLASTX
 NCBI GI g3915046
 BLAST score 679
 E value 0.0e+00
 Match length 791
 % identity 80
 NCBI Description SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)
 >gi_3169544 (AF049487) sucrose synthase [Medicago sativa]

Seq. No. 1228
 Contig ID 657_1.R1040
 5'-most EST g2654093_FL
 Method BLASTX
 NCBI GI g2654094

BLAST score 2186
 E value 0.0e+00
 Match length 456
 % identity 93
 NCBI Description (AF034210) aspartate aminotransferase glyoxysomal isozyme
 AAT1 precursor [Glycine max]

Seq. No. 1229
 Contig ID 658 1.R1040
 5'-most EST LIB3049-014-Q1-E1-B12
 Method BLASTN
 NCBI GI g3377793
 BLAST score 929
 E value 0.0e+00
 Match length 965
 % identity 99
 NCBI Description Glycine max proteasome IOTA subunit mRNA, complete cds

Seq. No. 1230
 Contig ID 658 2.R1040
 5'-most EST g4291492
 Method BLASTN
 NCBI GI g3377793
 BLAST score 330
 E value 0.0e+00
 Match length 390
 % identity 96
 NCBI Description Glycine max proteasome IOTA subunit mRNA, complete cds

Seq. No. 1231
 Contig ID 659 1.R1040
 5'-most EST LIB3030-005-Q1-B1-A12
 Method BLASTX
 NCBI GI g231695
 BLAST score 2683
 E value 0.0e+00
 Match length 492
 % identity 100
 NCBI Description CATALASE >gi_66299_pir_CSSY catalase (EC 1.11.1.6) -
 soybean >gi_18560_emb_CAA78056_ (Z12021) catalase [Glycine
 max] >gi_2661015 (AF035252) catalase [Glycine max]
 >gi_2661017 (AF035253) catalase [Glycine max]

Seq. No. 1232
 Contig ID 659 2.R1040
 5'-most EST LIB3051-080-Q1-K1-F12
 Method BLASTN
 NCBI GI g2661014
 BLAST score 121
 E value 1.0e-61
 Match length 167
 % identity 96
 NCBI Description Glycine max catalase (cat1) mRNA, complete cds

Seq. No. 1233
 Contig ID 659 4.R1040
 5'-most EST LIB3107-016-Q1-K1-G1

BLAST score 337
 E value 0.0e+00
 Match length 341
 % identity 100
 NCBI Description Glycine max catalase (cat4) mRNA, complete cds

Seq. No. 1239
 Contig ID 662_8.R1040
 5'-most EST awf700838945.h1
 Method BLASTN
 NCBI GI g2661020
 BLAST score 175
 E value 6.0e-94
 Match length 251
 % identity 97
 NCBI Description Glycine max catalase (cat4) mRNA, complete cds

Seq. No. 1240
 Contig ID 664_1.R1040
 5'-most EST asn701139293.h1
 Method BLASTX
 NCBI GI g3334122
 BLAST score 1767
 E value 0.0e+00
 Match length 350
 % identity 98
 NCBI Description ARGINASE >gi_2661128 (AF035671) arginase [Glycine max]

Seq. No. 1241
 Contig ID 664_2.R1040
 5'-most EST kl1701203871.h1
 Method BLASTX
 NCBI GI g1168493
 BLAST score 1464
 E value 1.0e-163
 Match length 330
 % identity 87
 NCBI Description ARGINASE >gi_602422 (U15019) arginase [Arabidopsis thaliana] >gi_4325373_gb_AAD17369_ (AF128396) Arabidopsis thaliana arginase (SW:P46637) (Pfam: PF00491, Score=419.6, E=3.7e-142 N=1) [Arabidopsis thaliana]

Seq. No. 1242
 Contig ID 665_1.R1040
 5'-most EST zhf700960949.h1
 Method BLASTX
 NCBI GI g4104561
 BLAST score 1689
 E value 0.0e+00
 Match length 370
 % identity 90
 NCBI Description (AF036960) subtilisin-like protease [Glycine max]

Seq. No. 1243
 Contig ID 666_1.R1040
 5'-most EST g5002233_FL
 Method BLASTN

Match length 115
 % identity 89
 NCBI Description Medicago sativa mitochondrial malate dehydrogenase precursor (mmdh) mRNA, nuclear gene encoding mitochondrial protein, complete cds

Seq. No. 1271
 Contig ID 678_4.R1040
 5'-most EST zsg701125938.h1
 Method BLASTN
 NCBI GI g2827079
 BLAST score 44
 E value 1.0e-15
 Match length 96
 % identity 86
 NCBI Description Medicago sativa mitochondrial malate dehydrogenase precursor (mmdh) mRNA, nuclear gene encoding mitochondrial protein, complete cds

Seq. No. 1272
 Contig ID 679_1.R1040
 5'-most EST pxt700942053.h1
 Method BLASTN
 NCBI GI g3193221
 BLAST score 318
 E value 1.0e-179
 Match length 516
 % identity 93
 NCBI Description Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds

Seq. No. 1273
 Contig ID 680_1.R1040
 5'-most EST uC-gmflminsoy067d03b1
 Method BLASTX
 NCBI GI g3399777
 BLAST score 1700
 E value 0.0e+00
 Match length 347
 % identity 97
 NCBI Description (AF069738) symbiotic ammonium transporter; nodulin [Glycine max]

Seq. No. 1274
 Contig ID 682_1.R1040
 5'-most EST zhf700956708.h1
 Method BLASTN
 NCBI GI g3552012
 BLAST score 1260
 E value 0.0e+00
 Match length 1304
 % identity 99
 NCBI Description Glycine max proline-rich protein precursor, mRNA, complete cds

Seq. No. 1275
 Contig ID 682_3.R1040

5'-most EST jC-gmst02400067c05a1
 Method BLASTN
 NCBI GI g3552012
 BLAST score 145
 E value 1.0e-75
 Match length 504
 % identity 88
 NCBI Description Glycine max proline-rich protein precursor, mRNA, complete cds

Seq. No. 1276
 Contig ID 683_1.R1040
 5'-most EST g957422
 Method BLASTX
 NCBI GI g1076511
 BLAST score 2415
 E value 0.0e+00
 Match length 522
 % identity 90
 NCBI Description H⁺-transporting ATPase (EC 3.6.1.35) - kidney bean
 >gi_758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase
 [Phaseolus vulgaris]

Seq. No. 1277
 Contig ID 683_2.R1040
 5'-most EST jC-gmst02400039g11a1
 Method BLASTN
 NCBI GI g3644031
 BLAST score 175
 E value 2.0e-93
 Match length 183
 % identity 99
 NCBI Description Glycine max plasma membrane proton-ATPase mRNA, partial cds

Seq. No. 1278
 Contig ID 683_3.R1040
 5'-most EST LIB3051-064-Q1-K1-G2
 Method BLASTX
 NCBI GI g1076511
 BLAST score 1765
 E value 0.0e+00
 Match length 371
 % identity 94
 NCBI Description H⁺-transporting ATPase (EC 3.6.1.35) - kidney bean
 >gi_758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase
 [Phaseolus vulgaris]

Seq. No. 1279
 Contig ID 683_5.R1040
 5'-most EST jC-gmfl02220060a11d1
 Method BLASTN
 NCBI GI g3644031
 BLAST score 180
 E value 1.0e-96
 Match length 180
 % identity 100
 NCBI Description Glycine max plasma membrane proton-ATPase mRNA, partial cds

Seq. No. 1280
 Contig ID 683_6.R1040
 5'-most EST uC-gmflminsoy037a02b1
 Method BLASTN
 NCBI GI g758249
 BLAST score 200
 E value 1.0e-108
 Match length 396
 % identity 88
 NCBI Description P.vulgaris mRNA for plasma membrane H+ ATPase

Seq. No. 1281
 Contig ID 683_8.R1040
 5'-most EST g5508913
 Method BLASTN
 NCBI GI g758249
 BLAST score 116
 E value 1.0e-58
 Match length 254
 % identity 94
 NCBI Description P.vulgaris mRNA for plasma membrane H+ ATPase

Seq. No. 1282
 Contig ID 684_1.R1040
 5'-most EST uC-gmflminsoy014b09b1
 Method BLASTX
 NCBI GI g2275219
 BLAST score 1852
 E value 0.0e+00
 Match length 418
 % identity 83
 NCBI Description (AC002337) unknown protein [Arabidopsis thaliana]

Seq. No. 1283
 Contig ID 684_2.R1040
 5'-most EST LIB3051-006-Q1-E1-F11
 Method BLASTX
 NCBI GI g2275219
 BLAST score 371
 E value 1.0e-35
 Match length 138
 % identity 61
 NCBI Description (AC002337) unknown protein [Arabidopsis thaliana]

Seq. No. 1284
 Contig ID 685_1.R1040
 5'-most EST rlr700895815.h1
 Method BLASTX
 NCBI GI g123506
 BLAST score 336
 E value 4.0e-31
 Match length 80
 % identity 81
 NCBI Description HYDROPHOBIC SEED PROTEIN (HPS) >gi_99917_pir_A29385
 hydrophobic seed protein - soybean >gi_349888_pdb_1HYP_
 Hydrophobic Protein From Soybean


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Method                BLASTX
NCBI GI               g3269293
BLAST score           472
E value               6.0e-47
Match length          179
% identity             56
NCBI Description      (AL030978) putative protein [Arabidopsis thaliana]

Seq. No.              1297
Contig ID             689_11.R1040
5'-most EST           rlr700900707.h1
Method                BLASTN
NCBI GI               g2687435
BLAST score           449
E value               0.0e+00
Match length          645
% identity             93
NCBI Description      Hamamelis virginiana large subunit 26S ribosomal RNA gene,
partial sequence

Seq. No.              1298
Contig ID             689_12.R1040
5'-most EST           LIB3050-008-Q1-E1-E9
Method                BLASTX
NCBI GI               g2129752
BLAST score           437
E value               5.0e-43
Match length          104
% identity             75
NCBI Description      thioredoxin - Arabidopsis thaliana >gi_992964_emb_CAA84612_
(Z35475) thioredoxin [Arabidopsis thaliana]

Seq. No.              1299
Contig ID             689_13.R1040
5'-most EST           LIB3170-046-Q1-J1-B4
Method                BLASTN
NCBI GI               g2852442
BLAST score           224
E value               1.0e-122
Match length          510
% identity             86
NCBI Description      Salix bakko mRNA for ADP-ribosylation factor, complete cds

Seq. No.              1300
Contig ID             689_14.R1040
5'-most EST           jC-gmro02910071a04a1
Method                BLASTX
NCBI GI               g1708236
BLAST score           1265
E value               0.0e+00
Match length          462
% identity             66
NCBI Description      HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE)
(3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)
>gi_2129617_pir_JC4567 hydroxymethylglutaryl-CoA synthase
(EC 4.1.3.5) - Arabidopsis thaliana
>gi_1143390_emb_CAA58763 (X83882)

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NCBI Description (M33900) 17.9 kDa heat shock protein (hsp17.9) [Pisum sativum]

Seq. No. 1313
 Contig ID 696_1.R1040
 5'-most EST g4559291_FL
 Method BLASTX
 NCBI GI g4559292
 BLAST score 2962
 E value 0.0e+00
 Match length 557
 % identity 100
 NCBI Description (AF124148) trehalase 1 GMTRE1 [Glycine max]

Seq. No. 1314
 Contig ID 698_1.R1040
 5'-most EST LIB3109-042-Q1-K1-D5
 Method BLASTX
 NCBI GI g4567091
 BLAST score 2104
 E value 0.0e+00
 Match length 507
 % identity 96
 NCBI Description (AF128443) SNF-1-like serine/threonine protein kinase [Glycine max]

Seq. No. 1315
 Contig ID 698_2.R1040
 5'-most EST LIB3051-030-Q1-K1-G7
 Method BLASTN
 NCBI GI g4567090
 BLAST score 105
 E value 1.0e-51
 Match length 205
 % identity 91
 NCBI Description Glycine max SNF-1-like serine/threonine protein kinase mRNA, complete cds

Seq. No. 1316
 Contig ID 698_3.R1040
 5'-most EST jex700907708.h1

Seq. No. 1317
 Contig ID 698_4.R1040
 5'-most EST seb700651919.h1
 Method BLASTN
 NCBI GI g4567090
 BLAST score 137
 E value 6.0e-71
 Match length 277
 % identity 87
 NCBI Description Glycine max SNF-1-like serine/threonine protein kinase mRNA, complete cds

Seq. No. 1318
 Contig ID 698_5.R1040
 5'-most EST zsg701128474.h1

E value 2.0e-46
 Match length 158
 % identity 57
 NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
 >gi_4314397_gb_AAD15607_ (AC006232) putative zinc finger
 protein [Arabidopsis thaliana]

Seq. No. 1338
 Contig ID 717_7.R1040
 5'-most EST rca701002512.h1
 Method BLASTN
 NCBI GI g1438878
 BLAST score 303
 E value 1.0e-170
 Match length 360
 % identity 100
 NCBI Description Glycine max choline kinase GmCK1p mRNA, complete cds

Seq. No. 1339
 Contig ID 717_8.R1040
 5'-most EST g5606823
 Method BLASTX
 NCBI GI g3860274
 BLAST score 216
 E value 3.0e-17
 Match length 54
 % identity 74
 NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
 >gi_4314397_gb_AAD15607_ (AC006232) putative zinc finger
 protein [Arabidopsis thaliana]

Seq. No. 1340
 Contig ID 717_9.R1040
 5'-most EST epx701105723.h1
 Method BLASTN
 NCBI GI g1438878
 BLAST score 430
 E value 0.0e+00
 Match length 448
 % identity 99
 NCBI Description Glycine max choline kinase GmCK1p mRNA, complete cds

Seq. No. 1341
 Contig ID 717_10.R1040
 5'-most EST g5057990
 Method BLASTX
 NCBI GI g3860274
 BLAST score 410
 E value 7.0e-40
 Match length 147
 % identity 54
 NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
 >gi_4314397_gb_AAD15607_ (AC006232) putative zinc finger
 protein [Arabidopsis thaliana]

Seq. No. 1342
 Contig ID 717_11.R1040


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Method                      BLASTX
NCBI GI                     g1518540
BLAST score                 2422
E value                     0.0e+00
Match length                480
% identity                  97
NCBI Description            (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.                    1353
Contig ID                   726_2.R1040
5'-most EST                 jC-gmst02400027a06d1
Method                      BLASTN
NCBI GI                     g1518539
BLAST score                 109
E value                     3.0e-54
Match length                197
% identity                  89
NCBI Description            Glycine max UDP-glucose dehydrogenase mRNA, complete cds

Seq. No.                    1354
Contig ID                   726_6.R1040
5'-most EST                 jsh701069261.h1
Method                      BLASTX
NCBI GI                     g1518540
BLAST score                 329
E value                     5.0e-47
Match length                142
% identity                  75
NCBI Description            (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.                    1355
Contig ID                   727_2.R1040
5'-most EST                 taw700655529.h1
Method                      BLASTN
NCBI GI                     g1778371
BLAST score                 158
E value                     1.0e-83
Match length                220
% identity                  99
NCBI Description            Glycine max asparagine synthetase 1 (AS1) mRNA, complete
                                cds

Seq. No.                    1356
Contig ID                   727_3.R1040
5'-most EST                 fC-gmfl700906171a1
Method                      BLASTN
NCBI GI                     g1778371
BLAST score                 366
E value                     0.0e+00
Match length                927
% identity                  97
NCBI Description            Glycine max asparagine synthetase 1 (AS1) mRNA, complete
                                cds

Seq. No.                    1357
Contig ID                   727_4.R1040
5'-most EST                 crh700855008.h1

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Method BLASTX
 NCBI GI g3789911
 BLAST score 143
 E value 6.0e-27
 Match length 192
 % identity 43
 NCBI Description (AF081802) developmental protein DG1118 [Dictyostelium discoideum]

Seq. No. 1358
 Contig ID 727_5.R1040
 5'-most EST uC-gmropic067d04b1
 Method BLASTX
 NCBI GI g1778372
 BLAST score 1198
 E value 0.0e+00
 Match length 573
 % identity 55
 NCBI Description (U77679) asparagine synthetase 1 [Glycine max]

Seq. No. 1359
 Contig ID 727_6.R1040
 5'-most EST LIB3139-049-P1-N1-G6
 Method BLASTX
 NCBI GI g1778370
 BLAST score 804
 E value 0.0e+00
 Match length 579
 % identity 42
 NCBI Description (U77678) asparagine synthetase 2 [Glycine max]

Seq. No. 1360
 Contig ID 728_1.R1040
 5'-most EST leu701144891.h1
 Method BLASTN
 NCBI GI g1381675
 BLAST score 739
 E value 0.0e+00
 Match length 747
 % identity 100
 NCBI Description Glycine max small GTP-binding protein (sral) mRNA, partial cds

Seq. No. 1361
 Contig ID 728_2.R1040
 5'-most EST jC-gmfl02220078d07a1
 Method BLASTX
 NCBI GI g4262154
 BLAST score 257
 E value 1.0e-21
 Match length 179
 % identity 41
 NCBI Description (AC005275) putative protein phosphatase regulatory subunit [Arabidopsis thaliana]

Seq. No. 1362
 Contig ID 728_3.R1040

% identity	98
NCBI Description	Glycine max farnesylated protein GMFP4 mRNA, partial cds
Seq. No.	1368
Contig ID	733_4.R1040
5'-most EST	LIB3170-083-Q1-K1-D10
Seq. No.	1369
Contig ID	733_5.R1040
5'-most EST	zpv700761634.h1
Method	BLASTX
NCBI GI	g3157949
BLAST score	337
E value	9.0e-34
Match length	89
% identity	87
NCBI Description	(AC002131) Similar to glucan endo-1,3-beta-D-glucosidase precursor gb_Z28697 from <i>Nicotiana tabacum</i> . ESTs gb_Z18185 and gb_AA605362 come from this gene. [<i>Arabidopsis thaliana</i>]
Seq. No.	1370
Contig ID	733_6.R1040
5'-most EST	jC-gmle01810001b03a1
Seq. No.	1371
Contig ID	733_7.R1040
5'-most EST	uC-gmrominsoy283e09b1
Method	BLASTX
NCBI GI	g4467159
BLAST score	145
E value	4.0e-09
Match length	47
% identity	55
NCBI Description	(AL035540) hypothetical protein [<i>Arabidopsis thaliana</i>]
Seq. No.	1372
Contig ID	733_8.R1040
5'-most EST	uxk700671427.h1
Method	BLASTX
NCBI GI	g3157934
BLAST score	509
E value	6.0e-65
Match length	180
% identity	71
NCBI Description	(AC002131) Similar to hypothetical protein F09E5.8 gb_U37429 from <i>C. elegans</i> . ESTs gb_T42019 and gb_N97000 come from this gene. [<i>Arabidopsis thaliana</i>]
Seq. No.	1373
Contig ID	733_9.R1040
5'-most EST	asn701136839.h1
Method	BLASTN
NCBI GI	g18729
BLAST score	58
E value	8.0e-24
Match length	62
% identity	98

NCBI Description Soybean (Glycine max) 18S ribosomal RNA

Seq. No. 1374
 Contig ID 733_10.R1040
 5'-most EST gsv701055023.h1
 Method BLASTN
 NCBI GI g455949
 BLAST score 85
 E value 6.0e-40
 Match length 89
 % identity 99
 NCBI Description 18S rRNA {3' region} [Glycine max=soybeans, var. Pella 86, leaves, rRNA Partial, 111 nt]

Seq. No. 1375
 Contig ID 733_11.R1040
 5'-most EST jsh701069821.h1

Seq. No. 1376
 Contig ID 733_12.R1040
 5'-most EST uxk700672545.h1
 Method BLASTX
 NCBI GI g4539303
 BLAST score 153
 E value 1.0e-20
 Match length 132
 % identity 47
 NCBI Description (AL049480) putative protein [Arabidopsis thaliana]

Seq. No. 1377
 Contig ID 733_13.R1040
 5'-most EST LIB3106-099-Q1-K1-G12
 Method BLASTN
 NCBI GI g4115533
 BLAST score 63
 E value 1.0e-26
 Match length 161
 % identity 88
 NCBI Description Vigna mungo UFGlyT mRNA for UDP-glucose:flavonoid glycosyltransferase, complete cds

Seq. No. 1378
 Contig ID 733_14.R1040
 5'-most EST LIB3092-040-Q1-K1-D2
 Method BLASTN
 NCBI GI g2330648
 BLAST score 549
 E value 0.0e+00
 Match length 1076
 % identity 88
 NCBI Description Pisum sativum mRNA for topoisomerase I

Seq. No. 1379
 Contig ID 733_15.R1040
 5'-most EST leu701145478.h1
 Method BLASTN
 NCBI GI g455949

leaves, rRNA Partial, 111 nt]

Seq. No. 1385
 Contig ID 733_21.R1040
 5'-most EST leu701154457.h1
 Method BLASTX
 NCBI GI g1168548
 BLAST score 329
 E value 3.0e-30
 Match length 110
 % identity 59
 NCBI Description HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-7 (HD-ZIP PROTEIN ATHB-7) >gi_629527_pir_S47137 homeotic protein Athb-7 - Arabidopsis thaliana >gi_499164_emb_CAA47425_ (X67032) orf [Arabidopsis thaliana]

Seq. No. 1386
 Contig ID 733_22.R1040
 5'-most EST LIB3170-066-Q1-J1-H1

Seq. No. 1387
 Contig ID 733_23.R1040
 5'-most EST zhf700960789.h1
 Method BLASTX
 NCBI GI g2959358
 BLAST score 351
 E value 4.0e-62
 Match length 128
 % identity 91
 NCBI Description (X96758) clathrin coat assembly protein AP17 [Zea mays]

Seq. No. 1388
 Contig ID 733_24.R1040
 5'-most EST zvj700605287.h2
 Method BLASTX
 NCBI GI g2642448
 BLAST score 438
 E value 8.0e-43
 Match length 251
 % identity 29
 NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana] >gi_3169187 (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No. 1389
 Contig ID 733_25.R1040
 5'-most EST kmv700738553.h1
 Method BLASTX
 NCBI GI g4530591
 BLAST score 720
 E value 1.0e-95
 Match length 242
 % identity 71
 NCBI Description (AF132475) heme oxygenase 1 [Arabidopsis thaliana] >gi_4530593_gb_AAD22108.1_ (AF132476) heme oxygenase 1 [Arabidopsis thaliana]

Seq. No. 1390
 Contig ID 733_26.R1040
 5'-most EST LIB3072-019-Q1-E1-F5
 Method BLASTN
 NCBI GI g343344
 BLAST score 298
 E value 1.0e-167
 Match length 628
 % identity 96
 NCBI Description Soybean chloroplast 16S rRNA (3' end), 18S rRNA (5' end), Ile-tRNA, and Ala-tRNA genes

Seq. No. 1391
 Contig ID 733_27.R1040
 5'-most EST LIB3051-043-Q1-K1-B7
 Method BLASTN
 NCBI GI g166769
 BLAST score 182
 E value 1.0e-97
 Match length 577
 % identity 84
 NCBI Description A.thaliana heat shock protein 83 mRNA, complete cds

Seq. No. 1392
 Contig ID 733_28.R1040
 5'-most EST LIB3107-079-Q1-K1-F4
 Method BLASTN
 NCBI GI g4097570
 BLAST score 626
 E value 0.0e+00
 Match length 982
 % identity 97
 NCBI Description Glycine max farnesylated protein GMFP5 mRNA, partial cds

Seq. No. 1393
 Contig ID 733_29.R1040
 5'-most EST asn701140463.h1
 Method BLASTN
 NCBI GI g388206
 BLAST score 57
 E value 3.0e-23
 Match length 177
 % identity 84
 NCBI Description Lycopersicon esculentum ubiquitin carrier protein (Ubc) mRNA, complete cds. >gi_2086269_gb_I38279_I38279 Sequence 109 from patent US

Seq. No. 1394
 Contig ID 733_30.R1040
 5'-most EST gsv701053339.h1
 Method BLASTN
 NCBI GI g4097570
 BLAST score 225
 E value 1.0e-123
 Match length 787
 % identity 91
 NCBI Description Glycine max farnesylated protein GMFP5 mRNA, partial cds

carteri] >gi_404089 (L24546) alpha-2 tubulin [Volvox carteri]

Seq. No. 1404
Contig ID 734_1.R1040
5'-most EST LIB3170-037-Q1-K1-H4
Method BLASTX
NCBI GI g4467145
BLAST score 657
E value 7.0e-69
Match length 154
% identity 81
NCBI Description (AL035540) farnesylated protein (ATFP6) [Arabidopsis thaliana]

Seq. No. 1405
Contig ID 734_2.R1040
5'-most EST awf700836821.h1
Method BLASTN
NCBI GI g4097572
BLAST score 567
E value 0.0e+00
Match length 583
% identity 99
NCBI Description Glycine max farnesylated protein GMFP7 mRNA, partial cds

Seq. No. 1406
Contig ID 734_3.R1040
5'-most EST LIB3051-084-Q1-K1-A8
Method BLASTN
NCBI GI g4097572
BLAST score 67
E value 3.0e-29
Match length 178
% identity 88
NCBI Description Glycine max farnesylated protein GMFP7 mRNA, partial cds

Seq. No. 1407
Contig ID 735_1.R1040
5'-most EST awf700837424.h1
Method BLASTN
NCBI GI g1732555
BLAST score 570
E value 0.0e+00
Match length 610
% identity 98
NCBI Description Glycine max desiccation protective protein LEA5 (Lea5) mRNA, complete cds

Seq. No. 1408
Contig ID 737_1.R1040
5'-most EST uC-gmflminsoy047e10b1
Method BLASTN
NCBI GI g1763062
BLAST score 955
E value 0.0e+00
Match length 981

Contig ID 744_2.R1040
 5'-most EST uC-gmropic014a06b1
 Method BLASTX
 NCBI GI g3650037
 BLAST score 1336
 E value 1.0e-180
 Match length 398
 % identity 80
 NCBI Description (AC005396) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No. 1425
 Contig ID 744_3.R1040
 5'-most EST rlr700902458.h1
 Method BLASTN
 NCBI GI g1778822
 BLAST score 377
 E value 0.0e+00
 Match length 449
 % identity 96
 NCBI Description Glycine max early light-induced protein (ELIP) mRNA, complete cds

Seq. No. 1426
 Contig ID 744_4.R1040
 5'-most EST LIB3138-081-P1-N1-C3
 Method BLASTN
 NCBI GI g1778822
 BLAST score 230
 E value 1.0e-126
 Match length 340
 % identity 92
 NCBI Description Glycine max early light-induced protein (ELIP) mRNA, complete cds

Seq. No. 1427
 Contig ID 745_1.R1040
 5'-most EST uC-gmflminsoy054b09b1
 Method BLASTN
 NCBI GI g2769671
 BLAST score 1289
 E value 0.0e+00
 Match length 1297
 % identity 100
 NCBI Description Glycine max alternative oxidase (Aox2) mRNA, nuclear gene encoding mitochondrial protein, complete cds

Seq. No. 1428
 Contig ID 746_1.R1040
 5'-most EST g1946337_FL
 Method BLASTN
 NCBI GI g1946337
 BLAST score 1206
 E value 0.0e+00
 Match length 1220
 % identity 93
 NCBI Description Glycine max alternative oxidase (Aox3) mRNA, nuclear gene

encoding mitochondrial protein, complete cds

Seq. No. 1429
 Contig ID 746_2.R1040
 5'-most EST wrg700788036.h1
 Method BLASTN
 NCBI GI g1946337
 BLAST score 164
 E value 5.0e-87
 Match length 253
 % identity 84
 NCBI Description Glycine max alternative oxidase (Aox3) mRNA, nuclear gene
 encoding mitochondrial protein, complete cds

Seq. No. 1430
 Contig ID 748_1.R1040
 5'-most EST LIB3170-071-Q1-K1-B9
 Method BLASTN
 NCBI GI g18737
 BLAST score 543
 E value 0.0e+00
 Match length 890
 % identity 14
 NCBI Description Glycine max RPRP3 gene for repetitive proline-rich protein

Seq. No. 1431
 Contig ID 748_2.R1040
 5'-most EST uC-gmrominsoy088g05b1
 Method BLASTX
 NCBI GI g4263704
 BLAST score 744
 E value 9.0e-79
 Match length 246
 % identity 61
 NCBI Description (AC006223) putative sugar starvation-induced protein
 [Arabidopsis thaliana]

Seq. No. 1432
 Contig ID 748_3.R1040
 5'-most EST g4289852
 Method BLASTX
 NCBI GI g4263704
 BLAST score 205
 E value 1.0e-15
 Match length 79
 % identity 54
 NCBI Description (AC006223) putative sugar starvation-induced protein
 [Arabidopsis thaliana]

Seq. No. 1433
 Contig ID 748_4.R1040
 5'-most EST jC-gmst02400023b02a1
 Method BLASTX
 NCBI GI g4263704
 BLAST score 501
 E value 2.0e-50
 Match length 167

% identity	61
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana].
Seq. No.	1434
Contig ID	748_5.R1040
5'-most EST	uC-gmropic019e04b1
Method	BLASTX
NCBI GI	g4263704
BLAST score	495
E value	8.0e-50
Match length	187
% identity	56.
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]
Seq. No.	1435
Contig ID	748_6.R1040
5'-most EST	g4405568
Method	BLASTX
NCBI GI	g4263704
BLAST score	194
E value	2.0e-28
Match length	128
% identity	59
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]
Seq. No.	1436
Contig ID	748_11.R1040
5'-most EST	LIB3139-064-P1-N1-C7
Method	BLASTN
NCBI GI	g255407
BLAST score	244
E value	1.0e-134
Match length	706
% identity	16
NCBI Description	repetitive proline-rich protein {cDNA clone 1A10-2} [Glycine max=soybeans, axes germinated for 31 hours, mRNA, 943 nt]
Seq. No.	1437
Contig ID	748_13.R1040
5'-most EST	k11701202974.h1
Method	BLASTN
NCBI GI	g170048
BLAST score	281
E value	1.0e-157
Match length	400
% identity	9
NCBI Description	Glycine max SbPRP1 gene encoding a proline-rich protein, complete cds
Seq. No.	1438
Contig ID	748_16.R1040
5'-most EST	LIB3051-011-Q1-E1-F1
Method	BLASTN

NCBI GI	g170065
BLAST score	350
E value	0.0e+00
Match length	825
% identity	26
NCBI Description	Soybean (G.max) proline-rich cell wall protein (SbPRP2) gene, complete cds
Seq. No.	1439
Contig ID	751_1.R1040
5'-most EST	LIB3139-075-P1-N1-D6
Method	BLASTN
NCBI GI	g1196896
BLAST score	1168
E value	0.0e+00
Match length	1243
% identity	99
NCBI Description	Glycine max acidic ribosomal protein P0 mRNA, complete cds
Seq. No.	1440
Contig ID	751_2.R1040
5'-most EST	uC-gmropic0001e04b1
Method	BLASTN
NCBI GI	g1196896
BLAST score	491
E value	0.0e+00
Match length	848
% identity	92
NCBI Description	Glycine max acidic ribosomal protein P0 mRNA, complete cds
Seq. No.	1441
Contig ID	751_3.R1040
5'-most EST	kl1701212451.h1
Method	BLASTN
NCBI GI	g1196896
BLAST score	227
E value	1.0e-124
Match length	358
% identity	95
NCBI Description	Glycine max acidic ribosomal protein P0 mRNA, complete cds
Seq. No.	1442
Contig ID	753_1.R1040
5'-most EST	ncj700987283.h1
Method	BLASTX
NCBI GI	g1346501
BLAST score	1517
E value	0.0e+00
Match length	352
% identity	95
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
Seq. No.	1443
Contig ID	754_1.R1040
5'-most EST	g310569_FL
Method	BLASTN
NCBI GI	g310569

BLAST score	932
E value	0.0e+00
Match length	1004
% identity	98
NCBI Description	Glycine max seed maturation protein (GmPM3) mRNA, complete cds

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Seq. No.          1444
Contig ID         755_1.R1040
5'-most EST      LIB3049-009-Q1-E1-F10
Method            BLASTX
NCBI GI           g1170878
BLAST score       2971
E value           0.0e+00
Match length      563
% identity        100
NCBI Description  MALATE SYNTHASE, GLYOXYSOMAL (MS) >gi_170026 (L01629)
                  malate synthase [Glycine max]
```

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Seq. No.      1445
Contig ID     755_2.R1040
5'-most EST   fC-gmst700653114f4
Method        BLASTX
NCBI GI       g2708743
BLAST score    180
E value       8.0e-13
Match length   184
% identity     28
NCBI Description (AC003952) putative Tal-1-like reverse transcriptase
                [Arabidopsis thaliana]
```

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Seq. No.          1446
Contig ID         755_3.R1040
5'-most EST      fC-gmst700653647r1
Method            BLASTX
NCBI GI           g4262236
BLAST score       229
E value           2.0e-18
Match length      238
% identity        30
NCBI Description  (AC006200) putative ribose 5-phosphate isomerase
                  [Arabidopsis thaliana]
```

```
Seq. No.          1447
Contig ID         755_4.R1040
5'-most EST      jC-gmst02400054a05a1
Method            BLASTN
NCBI GI           g170025
BLAST score       165
E value           1.0e-87
Match length      257
% identity        91
NCBI Description   Soybean malate synthase (MS) mRNA, 3' end
```

Seq. No.	1448
Contig ID	755_5.R1040
5'-most EST	zpv700758222.h1

Method BLASTN
 NCBI GI g170025
 BLAST score 88
 E value 7.0e-42
 Match length 136
 % identity 91
 NCBI Description Soybean malate synthase (MS) mRNA, 3' end

Seq. No. 1449
 Contig ID 755_6.R1040
 5'-most EST uC-gmflminsoy010h05b1
 Method BLASTN
 NCBI GI g170025
 BLAST score 254
 E value 1.0e-141
 Match length 410
 % identity 91
 NCBI Description Soybean malate synthase (MS) mRNA, 3' end

Seq. No. 1450
 Contig ID 755_8.R1040
 5'-most EST LIB3170-065-Q1-K1-E5
 Method BLASTN
 NCBI GI g170025
 BLAST score 185
 E value 2.0e-99
 Match length 188
 % identity 99
 NCBI Description Soybean malate synthase (MS) mRNA, 3' end

Seq. No. 1451
 Contig ID 755_9.R1040
 5'-most EST txt700736239.h1
 Method BLASTN
 NCBI GI g170025
 BLAST score 407
 E value 0.0e+00
 Match length 575
 % identity 93
 NCBI Description Soybean malate synthase (MS) mRNA, 3' end

Seq. No. 1452
 Contig ID 755_10.R1040
 5'-most EST jC-gmst02400008b12d1
 Method BLASTN
 NCBI GI g170025
 BLAST score 75
 E value 5.0e-34
 Match length 107
 % identity 93
 NCBI Description Soybean malate synthase (MS) mRNA, 3' end

Seq. No. 1453
 Contig ID 756_1.R1040
 5'-most EST jsh701070153.h1
 Method BLASTX
 NCBI GI g1362051

E value 1.0e-180
Match length 532
% identity 98
NCBI Description Glycine max NADP-dependent isocitrate dehydrogenase (IDH1) mRNA, complete cds

Seq. No. 1471
Contig ID 765_3.R1040
5'-most EST k11701213049.h1
Method BLASTN
NCBI GI g3747088
BLAST score 91
E value 1.0e-43
Match length 123
% identity 93
NCBI Description Glycine max NADP-dependent isocitrate dehydrogenase (IDH1) mRNA, complete cds

Seq. No. 1472
Contig ID 769_1.R1040
5'-most EST LIB3109-016-Q1-K1-F8
Method BLASTX
NCBI GI g3128220
BLAST score 1167
E value 1.0e-128
Match length 253
% identity 89
NCBI Description (AC004077) putative urease accessory protein [Arabidopsis thaliana] >gi_3337375 (AC004481) putative urease accessory protein [Arabidopsis thaliana]

Seq. No. 1473
Contig ID 770_1.R1040
5'-most EST sat701011252.h1
Method BLASTX
NCBI GI g2462753
BLAST score 1390
E value 1.0e-154
Match length 407
% identity 62
NCBI Description (AC002292) putative polygalacturonase [Arabidopsis thaliana]

Seq. No. 1474
Contig ID 773_1.R1040
5'-most EST LIB3139-032-P1-N1-A4
Method BLASTX
NCBI GI g4559342
BLAST score 3226
E value 0.0e+00
Match length 701
% identity 85
NCBI Description (AC007087) putative copper methylamine oxidase [Arabidopsis thaliana]

Seq. No. 1475
Contig ID 774_1.R1040

Seq. No. 1490
 Contig ID 787_2.R1040
 5'-most EST LIB3028-056-Q1-B1-A5

Seq. No. 1491
 Contig ID 787_3.R1040
 5'-most EST uC-gmrominsoy200e09b1
 Method BLASTX
 NCBI GI g4455208
 BLAST score 280
 E value 1.0e-24
 Match length 81
 % identity 70
 NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 1492
 Contig ID 787_4.R1040
 5'-most EST uC-gmropic041f08b1
 Method BLASTN
 NCBI GI g436789
 BLAST score 49
 E value 4.0e-18
 Match length 108
 % identity 86
 NCBI Description Tobacco RNA-binding glycine-rich protein (RGP-1a) mRNA

Seq. No. 1493
 Contig ID 787_5.R1040
 5'-most EST LIB3051-083-Q1-K1-D8
 Method BLASTN
 NCBI GI g2267568
 BLAST score 56
 E value 3.0e-22
 Match length 266
 % identity 83
 NCBI Description Pelargonium x hortorum glycine-rich RNA binding protein 2 (GRP2) precursor mRNA, complete cds

Seq. No. 1494
 Contig ID 787_6.R1040
 5'-most EST LIB3106-033-Q1-K1-E8
 Method BLASTX
 NCBI GI g4455208
 BLAST score 155
 E value 7.0e-10
 Match length 101
 % identity 32
 NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 1495
 Contig ID 787_7.R1040
 5'-most EST vwf700678078.h1
 Method BLASTX
 NCBI GI g544424
 BLAST score 163
 E value 7.0e-14
 Match length 84

5'-most EST LIB3106-034-Q1-K1-F2
 Method BLASTX
 NCBI GI g117290
 BLAST score 1660
 E value 0.0e+00
 Match length 392
 % identity 84
 NCBI Description CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT) (P36) (E30) >gi_100071_pir_S23774 triose phosphate/3-phosphoglycerate/phosphate translocator precursor - garden pea >gi_20691_emb_CAA38451_ (X54639) chloroplast import receptor p36 [Pisum sativum] >gi_20853_emb_CAA48210_ (X68077) phosphate translocator [Pisum sativum] >gi_228551_prf_1805409A phosphate translocator [Pisum sativum]

Seq. No. 1501
 Contig ID 788_5.R1040
 5'-most EST asn701136914.h1
 Method BLASTX
 NCBI GI g1363487
 BLAST score 326
 E value 3.0e-30
 Match length 96
 % identity 71
 NCBI Description IAA7 protein - Arabidopsis thaliana >gi_972917 (U18409) IAA7 [Arabidopsis thaliana]

Seq. No. 1502
 Contig ID 790_1.R1040
 5'-most EST LIB3073-002-Q1-K1-F3
 Method BLASTX
 NCBI GI g1717975
 BLAST score 279
 E value 1.0e-24
 Match length 98
 % identity 49
 NCBI Description 14.5 KD TRANSLATIONAL INHIBITOR PROTEIN (P14.5) (UK114 ANTIGEN HOMOLOG) >gi_1177435_emb_CAA64670_ (X95384) 14.5 kDa translational inhibitor protein, p14.5 [Homo sapiens]

Seq. No. 1503
 Contig ID 791_1.R1040
 5'-most EST k11701208271.h1
 Method BLASTX
 NCBI GI g3176673
 BLAST score 210
 E value 2.0e-16
 Match length 76
 % identity 54
 NCBI Description (AC003671) Similar to serine/threonine kinase gb_Y12531 from Brassica oleracea. [Arabidopsis thaliana]

Seq. No. 1504
 Contig ID 791_5.R1040
 5'-most EST LIB3170-028-Q1-K1-B10

Seq. No. 1505
 Contig ID 793_1.R1040
 5'-most EST uxk700667991.h1
 Method BLASTX
 NCBI GI g687844
 BLAST score 283
 E value 5.0e-25
 Match length 172
 % identity 5
 NCBI Description (U21320) contains TPR domain-like repeats [Caenorhabditis elegans]

Seq. No. 1506
 Contig ID 793_2.R1040
 5'-most EST LIB3049-001-Q1-E1-C7

Seq. No. 1507
 Contig ID 794_1.R1040
 5'-most EST LIB3106-104-Q1-K1-G8
 Method BLASTX
 NCBI GI g3859570
 BLAST score 322
 E value 9.0e-30
 Match length 132
 % identity 54
 NCBI Description (AF098753) unknown [Oryza sativa]

Seq. No. 1508
 Contig ID 799_1.R1040
 5'-most EST ssr700556237.h1

Seq. No. 1509
 Contig ID 800_1.R1040
 5'-most EST 2DA-01-Q1-B1-A9

Seq. No. 1510
 Contig ID 801_1.R1040
 5'-most EST kmv700738580.h1
 Method BLASTX
 NCBI GI g4006868
 BLAST score 201
 E value 3.0e-15
 Match length 144
 % identity 38
 NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 1511
 Contig ID 802_1.R1040
 5'-most EST g5677474
 Method BLASTX
 NCBI GI g4193388
 BLAST score 507
 E value 1.0e-51
 Match length 127
 % identity 80
 NCBI Description (AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No. 1512
 Contig ID 803_1.R1040
 5'-most EST LIB3107-017-Q1-K1-E1
 Method BLASTX
 NCBI GI g2623199
 BLAST score 787
 E value 3.0e-84
 Match length 151
 % identity 99
 NCBI Description (AF030290) protein phosphatase X isoform 2 [Arabidopsis thaliana]

Seq. No. 1513
 Contig ID 803_3.R1040
 5'-most EST pxt700946264.h1
 Method BLASTX
 NCBI GI g2623199
 BLAST score 273
 E value 2.0e-24
 Match length 56
 % identity 95
 NCBI Description (AF030290) protein phosphatase X isoform 2 [Arabidopsis thaliana]

Seq. No. 1514
 Contig ID 805_1.R1040
 5'-most EST jC-gmle01810062a02a1
 Method BLASTN
 NCBI GI g3128138
 BLAST score 59
 E value 3.0e-24
 Match length 478
 % identity 86
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFO20, complete sequence [Arabidopsis thaliana]

Seq. No. 1515
 Contig ID 808_1.R1040
 5'-most EST LIB3093-005-Q1-K1-A11
 Method BLASTX
 NCBI GI g1723562
 BLAST score 105
 E value 5.0e-12
 Match length 102
 % identity 42
 NCBI Description PROBABLE EUKARYOTIC INITIATION FACTOR C17C9.03
 >gi_1314155_emb_CAA97349_ (Z73099) probable initiation factor [Schizosaccharomyces pombe]

Seq. No. 1516
 Contig ID 808_2.R1040
 5'-most EST 2DA-01-Q1-B1-B6
 Method BLASTX
 NCBI GI g2895097
 BLAST score 294
 E value 2.0e-26

09684016 " 101000

Match length 128
% identity 47
NCBI Description (AF012072) eIF4GII [Homo sapiens]
>gi_4503541_ref_NP_003751.1_pEIF4G3_ UNKNOWN

Seq. No. 1517
Contig ID 809_1.R1040
5'-most EST pcp700990419.h1

Seq. No. 1518
Contig ID 810_1.R1040
5'-most EST 2DA-01-Q1-B1-B8
Method BLASTX
NCBI GI g3426039
BLAST score 324
E value 6.0e-30
Match length 129
% identity 51
NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 1519
Contig ID 811_1.R1040
5'-most EST 2DA-01-Q1-B1-B9
Method BLASTX
NCBI GI g231551
BLAST score 158
E value 2.0e-10
Match length 124
% identity 3
NCBI Description ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN,
NONERYTHROID)

Seq. No. 1520
Contig ID 811_2.R1040
5'-most EST uC-gmrominsoy124b05b1

Seq. No. 1521
Contig ID 813_1.R1040
5'-most EST LIB3051-065-Q1-K1-D1
Method BLASTX
NCBI GI g416873
BLAST score 260
E value 2.0e-22
Match length 96
% identity 53
NCBI Description 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (HIBADH)
>gi_111295_pir_A32867 3-hydroxyisobutyrate dehydrogenase
(EC 1.1.1.31) precursor - rat (fragment) >gi_556389
(J04628) 3-hydroxyisobutyrate dehydrogenase [Rattus
norvegicus]

Seq. No. 1522
Contig ID 815_1.R1040
5'-most EST epX701105596.h1
Method BLASTX
NCBI GI g2832300
BLAST score 477

E value 9.0e-48
 Match length 118
 % identity 75
 NCBI Description (AF044285) adenosine-5'-phosphosulfate-kinase [Catharanthus roseus]

Seq. No. 1523
 Contig ID 817_1.R1040
 5'-most EST LIB3040-014-Q1-E1-F1
 Method BLASTX
 NCBI GI g4467098
 BLAST score 192
 E value 1.0e-14
 Match length 58
 % identity 60
 NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 1524
 Contig ID 818_1.R1040
 5'-most EST gsv701046553.h1
 Method BLASTX
 NCBI GI g3881497
 BLAST score 176
 E value 6.0e-12
 Match length 318
 % identity 24
 NCBI Description (Z35604) cDNA EST EMBL:Z14593 comes from this gene; cDNA EST EMBL:T01764 comes from this gene; cDNA EST EMBL:D37668 comes from this gene; cDNA EST EMBL:D73892 comes from this gene; cDNA EST EMBL:D71243 comes from this gene; cDN

Seq. No. 1525
 Contig ID 818_2.R1040
 5'-most EST uC-gmrominsoy300b04b1

Seq. No. 1526
 Contig ID 819_5.R1040
 5'-most EST leu701155872.h1

Seq. No. 1527
 Contig ID 819_6.R1040
 5'-most EST g4396041
 Method BLASTX
 NCBI GI g2129577
 BLAST score 270
 E value 1.0e-23
 Match length 64
 % identity 80
 NCBI Description DnaJ homolog protein - Arabidopsis thaliana >gi_727357 (U22340) DnaJ homolog [Arabidopsis thaliana]

Seq. No. 1528
 Contig ID 819_7.R1040
 5'-most EST jC-gmle01810022f03a1
 Method BLASTX
 NCBI GI g4263704
 BLAST score 288

E value 8.0e-26
Match length 102
% identity 54
NCBI Description (AC006223) putative sugar starvation-induced protein
[Arabidopsis thaliana]

Seq. No. 1529
Contig ID 819_8.R1040
5'-most EST jC-gmfl02220088h01a1
Method BLASTX
NCBI GI g4263704
BLAST score 416
E value 3.0e-40
Match length 257
% identity 39
NCBI Description (AC006223) putative sugar starvation-induced protein
[Arabidopsis thaliana]

Seq. No. 1530
Contig ID 819_9.R1040
5'-most EST hrw701060405.h1
Method BLASTX
NCBI GI g4263704
BLAST score 336
E value 8.0e-40
Match length 252
% identity 40
NCBI Description (AC006223) putative sugar starvation-induced protein
[Arabidopsis thaliana]

Seq. No. 1531
Contig ID 819_10.R1040
5'-most EST uC-gmropic067e03b1
Method BLASTX
NCBI GI g1213460
BLAST score 568
E value 4.0e-58
Match length 247
% identity 46
NCBI Description (U03374) C subunit of V-ATPase [Amblyomma americanum]

Seq. No. 1532
Contig ID 819_11.R1040
5'-most EST LIB3107-070-Q1-K1-A6
Method BLASTX
NCBI GI g461944
BLAST score 712
E value 1.0e-132
Match length 419
% identity 54
NCBI Description DNAJ PROTEIN HOMOLOG (DNAJ-1) >gi_18260_emb_CAA47925_
(X67695) cs DnaJ-1 [Cucumis sativus]

Seq. No. 1533
Contig ID 819_12.R1040
5'-most EST LIB3139-030-P1-N1-F3
Method BLASTN

5'-most EST LIB3107-071-Q1-K1-H2
 Method BLASTN
 NCBI GI g12212
 BLAST score 141
 E value 2.0e-73
 Match length 185
 % identity 94
 NCBI Description S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2

Seq. No. 1559
 Contig ID 835_10.R1040
 5'-most EST LIB3138-042-Q1-N1-H5
 Method BLASTN
 NCBI GI g11748
 BLAST score 289
 E value 1.0e-161
 Match length 397
 % identity 95
 NCBI Description Nicotiana debneyi chloroplast DNA for tRNA-Ile and ribosomal protein L2

Seq. No. 1560
 Contig ID 835_13.R1040
 5'-most EST jC-gmle01810032d10d1
 Method BLASTX
 NCBI GI g133939
 BLAST score 314
 E value 9.0e-29
 Match length 80
 % identity 72
 NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70865_pir_R3NT3 ribosomal protein S3 - common tobacco chloroplast >gi_11865_emb_CAA77381_(Z00044) ribosomal protein S3 [Nicotiana tabacum] >gi_225235_prf_1211235BT ribosomal protein S3 [Nicotiana tabacum]

Seq. No. 1561
 Contig ID 836_1.R1040
 5'-most EST hyd700730304.h1

Seq. No. 1562
 Contig ID 837_1.R1040
 5'-most EST uC-gmropic018e03b1
 Method BLASTX
 NCBI GI g2244898
 BLAST score 186
 E value 2.0e-13
 Match length 96
 % identity 44
 NCBI Description (Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]

Seq. No. 1563
 Contig ID 837_3.R1040
 5'-most EST zzp700831795.h1

Seq. No. 1564
 Contig ID 838_1.R1040
 5'-most EST ssr700561089.h1
 Method BLASTN
 NCBI GI g12139
 BLAST score 639
 E value 0.0e+00
 Match length 3513
 % identity 90
 NCBI Description Pea plastid genes rps2, atpI, atpH, atpF, atpA, trnR and trnG coding for ribosomal protein S2, one CF(1) and three CF(0) subunits of ATP synthase and tRNA-Arg and tRNA-Gly

Seq. No. 1565
 Contig ID 838_2.R1040
 5'-most EST fC-gmle700553639a4
 Method BLASTN
 NCBI GI g12139
 BLAST score 145
 E value 1.0e-75
 Match length 414
 % identity 91
 NCBI Description Pea plastid genes rps2, atpI, atpH, atpF, atpA, trnR and trnG coding for ribosomal protein S2, one CF(1) and three CF(0) subunits of ATP synthase and tRNA-Arg and tRNA-Gly

Seq. No. 1566
 Contig ID 838_4.R1040
 5'-most EST zsg701130050.h1
 Method BLASTN
 NCBI GI g12249
 BLAST score 38
 E value 5.0e-12
 Match length 54
 % identity 93
 NCBI Description Spinach plastid genes atpI-H-F for ATP synthase CF(0) subunits IV, III and I

Seq. No. 1567
 Contig ID 838_11.R1040
 5'-most EST jC-gmle01810075f04a1
 Method BLASTN
 NCBI GI g12144
 BLAST score 41
 E value 1.0e-13
 Match length 82
 % identity 94
 NCBI Description Pea chloroplast genes for F(0)-ATP synthase subunits a and c (partial)

Seq. No. 1568
 Contig ID 841_1.R1040
 5'-most EST 2DA-01-Q1-B1-E4
 Method BLASTX
 NCBI GI g2853087
 BLAST score 199
 E value 3.0e-15

Match length 122
 % identity 26
 NCBI Description (AL021768) putative protein [Arabidopsis thaliana]

Seq. No. 1569
 Contig ID 842_1.R1040
 5'-most EST wvk700685058.h1
 Method BLASTX
 NCBI GI g3212854
 BLAST score 410
 E value 2.0e-39
 Match length 297
 % identity 35
 NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 1570
 Contig ID 842_2.R1040
 5'-most EST LIB3107-004-Q1-K1-C2
 Method BLASTX
 NCBI GI g3212854
 BLAST score 149
 E value 2.0e-09
 Match length 57
 % identity 49
 NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 1571
 Contig ID 842_3.R1040
 5'-most EST zzp700835324.h1

Seq. No. 1572
 Contig ID 843_1.R1040
 5'-most EST 2DA-01-Q1-B1-E6
 Method BLASTX
 NCBI GI g3641870
 BLAST score 218
 E value 1.0e-17
 Match length 136
 % identity 41
 NCBI Description (AJ011013) hypothetical protein [Cicer arietinum]

Seq. No. 1573
 Contig ID 844_1.R1040
 5'-most EST uC-gmrominsoy083e10b1
 Method BLASTX
 NCBI GI g2598579
 BLAST score 1461
 E value 1.0e-162
 Match length 364
 % identity 74
 NCBI Description (Y15295) L-ascorbate oxidase [Medicago truncatula]

Seq. No. 1574
 Contig ID 844_2.R1040
 5'-most EST hyd700725411.h1
 Method BLASTN
 NCBI GI g2598578

BLAST score 238
 E value 1.0e-131
 Match length 690
 % identity 84
 NCBI Description Medicago truncatula mRNA for L-ascorbate oxidase

Seq. No. 1575
 Contig ID 844_4.R1040
 5'-most EST g4287777
 Method BLASTX
 NCBI GI g2598579
 BLAST score 161
 E value 3.0e-11
 Match length 49
 % identity 67
 NCBI Description (Y15295) L-ascorbate oxidase [Medicago truncatula]

Seq. No. 1576
 Contig ID 846_1.R1040
 5'-most EST jex700908385.h1
 Method BLASTX
 NCBI GI g2462762
 BLAST score 961
 E value 1.0e-104
 Match length 338
 % identity 58
 NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 1577
 Contig ID 846_2.R1040
 5'-most EST LIB3109-009-Q1-K1-E2
 Method BLASTX
 NCBI GI g2462762
 BLAST score 371
 E value 3.0e-35
 Match length 141
 % identity 57
 NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 1578
 Contig ID 846_4.R1040
 5'-most EST LIB3170-068-Q1-J1-D4

Seq. No. 1579
 Contig ID 846_9.R1040
 5'-most EST gsv701053511.h1
 Method BLASTX
 NCBI GI g2462762
 BLAST score 113
 E value 7.0e-14
 Match length 78
 % identity 55
 NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 1580
 Contig ID 848 1.R1040
 5'-most EST LIB3106-033-Q1-K1-C2
 Method BLASTN
 NCBI GI g4220631
 BLAST score 97
 E value 7.0e-47
 Match length 225
 % identity 86
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
 K5J14, complete sequence [Arabidopsis thaliana]

Seq. No. 1581
 Contig ID 848 2.R1040
 5'-most EST LIB3056-010-Q1-N1-D9
 Method BLASTN
 NCBI GI g4220631
 BLAST score 93
 E value 1.0e-44
 Match length 225
 % identity 85
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
 K5J14, complete sequence [Arabidopsis thaliana]

Seq. No. 1582
 Contig ID 848 3.R1040
 5'-most EST LIB3049-025-Q1-E1-G4
 Method BLASTN
 NCBI GI g4220631
 BLAST score 89
 E value 2.0e-42
 Match length 225
 % identity 85
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
 K5J14, complete sequence [Arabidopsis thaliana]

Seq. No. 1583
 Contig ID 848 6.R1040
 5'-most EST pmv700888989.h1
 Method BLASTN
 NCBI GI g4220631
 BLAST score 65
 E value 3.0e-28
 Match length 181
 % identity 85
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
 K5J14, complete sequence [Arabidopsis thaliana]

Seq. No. 1584
 Contig ID 849 1.R1040
 5'-most EST 2DA-01-Q1-B1-F11
 Method BLASTX
 NCBI GI g3461848
 BLAST score 179
 E value 8.0e-13
 Match length 102
 % identity 49

09634016-101000

NCBI Description (AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No. 1585
Contig ID 850_1.R1040
5'-most EST uC-gmropic026d05b1
Method BLASTX
NCBI GI g3688162
BLAST score 654
E value 3.0e-68
Match length 168
% identity 79
NCBI Description (AJ009672) centrin [Arabidopsis thaliana]

Seq. No. 1586
Contig ID 850_2.R1040
5'-most EST ssr700555006.h1
Method BLASTX
NCBI GI g3386622
BLAST score 227
E value 2.0e-18
Match length 129
% identity 65
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 1587
Contig ID 850_3.R1040
5'-most EST 2DA-01-Q1-B1-F12
Method BLASTX
NCBI GI g3688162
BLAST score 491
E value 2.0e-49
Match length 135
% identity 52
NCBI Description (AJ009672) centrin [Arabidopsis thaliana]

Seq. No. 1588
Contig ID 852_1.R1040
5'-most EST LIB3138-005-Q1-N1-F7
Method BLASTX
NCBI GI g2315451
BLAST score 259
E value 8.0e-22
Match length 142
% identity 30
NCBI Description (AF016448) No definition line found [Caenorhabditis elegans]

Seq. No. 1589
Contig ID 853_1.R1040
5'-most EST 2DA-01-Q1-B1-F4

Seq. No. 1590
Contig ID 854_1.R1040
5'-most EST LIB3092-017-Q1-K1-D4
Method BLASTX
NCBI GI g2708532
BLAST score 1184

E value	1.0e-130
Match length	344
% identity	67
NCBI Description	(AF029351) putative RNA binding protein [Nicotiana tabacum]
Seq. No.	1591
Contig ID	854_2.R1040
5'-most EST	g4397165
Seq. No.	1592
Contig ID	855_1.R1040
5'-most EST	LIB3109-030-Q1-K1-B11
Seq. No.	1593
Contig ID	856_1.R1040
5'-most EST	uC-gmflminsoy040a11b1
Seq. No.	1594
Contig ID	857_1.R1040
5'-most EST	bth700845764.h1
Seq. No.	1595
Contig ID	858_1.R1040
5'-most EST	uC-gmropic078g11b1
Method	BLASTX
NCBI GI	g629692
BLAST score	1174
E value	1.0e-129
Match length	533
% identity	48
NCBI Description	hypothetical protein - common tobacco >gi_506471_emb_CAA56189_ (X79794) unnamed protein product [Nicotiana tabacum]
Seq. No.	1596
Contig ID	858_2.R1040
5'-most EST	zhf700955944.h1
Method	BLASTX
NCBI GI	g629692
BLAST score	846
E value	5.0e-91
Match length	184
% identity	88
NCBI Description	hypothetical protein - common tobacco >gi_506471_emb_CAA56189_ (X79794) unnamed protein product [Nicotiana tabacum]
Seq. No.	1597
Contig ID	861_1.R1040
5'-most EST	dpv701100030.h2
Method	BLASTX
NCBI GI	g1737492
BLAST score	1936
E value	0.0e+00
Match length	624
% identity	49
NCBI Description	(U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No. 1598
 Contig ID 861_2.R1040
 5'-most EST LIB3051-006-Q1-E1-A7

Seq. No. 1599
 Contig ID 861_4.R1040
 5'-most EST uC-gmronoir007h06b1
 Method BLASTX
 NCBI GI g1171978
 BLAST score 156
 E value 2.0e-10
 Match length 48
 % identity 67
 NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi_304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No. 1600
 Contig ID 863_1.R1040
 5'-most EST 2DA-02-Q1-B1-D6
 Method BLASTX
 NCBI GI g1279224
 BLAST score 400
 E value 2.0e-38
 Match length 216
 % identity 31
 NCBI Description (X97454) specific tissue protein 1 [Cicer arietinum]

Seq. No. 1601
 Contig ID 863_2.R1040
 5'-most EST LIB3107-034-Q1-K1-B5
 Method BLASTX
 NCBI GI g3393062
 BLAST score 627
 E value 4.0e-65
 Match length 208
 % identity 57
 NCBI Description (Y17386) putative In2.1 protein [Triticum aestivum]

Seq. No. 1602
 Contig ID 863_4.R1040
 5'-most EST uC-gmropic070d05b1
 Method BLASTX
 NCBI GI g1279224
 BLAST score 324
 E value 7.0e-30
 Match length 186
 % identity 32
 NCBI Description (X97454) specific tissue protein 1 [Cicer arietinum]

Seq. No. 1603
 Contig ID 864_1.R1040
 5'-most EST g5752500
 Method BLASTX
 NCBI GI g3328240

BLAST score	966
E value	1.0e-105
Match length	289
% identity	66
NCBI Description	(AF064775) early nodule-specific protein [Medicago truncatula]
Seq. No.	1604
Contig ID	865_1.R1040
5'-most EST	zhf700952383.h1
Method	BLASTX
NCBI GI	g4210330
BLAST score	2927
E value	0.0e+00
Match length	643
% identity	83
NCBI Description	(AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]
Seq. No.	1605
Contig ID	865_3.R1040
5'-most EST	zzp700832947.h1
Seq. No.	1606
Contig ID	866_1.R1040
5'-most EST	2DA-01-Q1-B1-G6
Seq. No.	1607
Contig ID	868_1.R1040
5'-most EST	2DA-01-Q1-B1-G8
Method	BLASTX
NCBI GI	g1402878
BLAST score	711
E value	4.0e-75
Match length	185
% identity	72
NCBI Description	(X98130) unknown [Arabidopsis thaliana]
Seq. No.	1608
Contig ID	869_1.R1040
5'-most EST	LIB3170-064-Q1-K1-A3
Seq. No.	1609
Contig ID	869_2.R1040
5'-most EST	bth700845877.h1
Method	BLASTX
NCBI GI	g3879119
BLAST score	345
E value	4.0e-32
Match length	168
% identity	48
NCBI Description	(Z70310) similar to Glutathione S-transferases. [Caenorhabditis elegans]
Seq. No.	1610
Contig ID	871_1.R1040
5'-most EST	2DA-01-Q1-B1-H10

NCBI GI g4510383
 BLAST score 188
 E value 4.0e-14
 Match length 63
 % identity 62
 NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 1618
 Contig ID 874 1.R1040
 5'-most EST pxt700945347.h1
 Method BLASTX
 NCBI GI g4539292
 BLAST score 465
 E value 4.0e-46
 Match length 96
 % identity 89
 NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No. 1619
 Contig ID 878 1.R1040
 5'-most EST vwf700677625.h1
 Method BLASTX
 NCBI GI g2980806
 BLAST score 338
 E value 8.0e-42
 Match length 207
 % identity 35
 NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 1620
 Contig ID 878 3.R1040
 5'-most EST sat701013749.h1

Seq. No. 1621
 Contig ID 878 4.R1040
 5'-most EST xpa700792783.h1

Seq. No. 1622
 Contig ID 880 1.R1040
 5'-most EST 2DA-01-Q1-B1-H9

Seq. No. 1623
 Contig ID 881 1.R1040
 5'-most EST zsg701120314.h1
 Method BLASTX
 NCBI GI g4454032
 BLAST score 712
 E value 5.0e-75
 Match length 243
 % identity 60
 NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 1624
 Contig ID 883 1.R1040
 5'-most EST asj700967313.h1
 Method BLASTX

09034016 103000

Seq. No.	1626
Contig ID	885_1.R1040
5'-most EST	wvk700682626.h2

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Seq. No.          1628
Contig ID         886_2.R1040
5'-most EST      LIB3106-111-Q1-K1-G4
Method           BLASTX
NCBI GI           g1172584
BLAST score       509
E value          2.0e-51
Match length      207
% identity        49
NCBI Description  POLYPHENOL OXIDASE PRECURSOR (PPO) (CATECHOL OXIDASE)
                  >gi_1076478_pir_S52984 catechol oxidase (EC 1.10.3.1)
                  precursor - apple tree >gi_507280 (L29450) polyphenol
                  oxidase [Malus domestica]
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Seq. No.          1629
Contig ID         887_1.R1040
5'-most EST      taw700660372.h1
Method            BLASTX
NCBI GI           g728827
BLAST score       612
E value           4.0e-63
Match length      322
% identity        40
NCBI Description  ALLANTOINASE PRECURSOR >gi_458126 (U03471) allantoinase
                  [Rana catesbeiana]
```


E value 2.0e-22
 Match length 60
 % identity 77
 NCBI Description (AC006403) putative protein kinase [Arabidopsis thaliana]

Seq. No. 1637
 Contig ID 893_1.R1040
 5'-most EST LIB3039-043-Q1-E1-C8
 Method BLASTN
 NCBI GI g1902893
 BLAST score 231
 E value 1.0e-126
 Match length 603
 % identity 85
 NCBI Description Solanum melongena mRNA for QM family protein, complete cds

Seq. No. 1638
 Contig ID 893_2.R1040
 5'-most EST wvk700686407.h1
 Method BLASTX
 NCBI GI g1169494
 BLAST score 1343
 E value 0.0e+00
 Match length 479
 % identity 87
 NCBI Description ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
 >gi_2119915_pir_S60659 EF-Tu protein precursor - soybean
 >gi_949873_emb_CAA61444_ (X89058) EF-Tu protein [Glycine max]

Seq. No. 1639
 Contig ID 893_3.R1040
 5'-most EST LIB3106-106-Q1-K1-A5
 Method BLASTN
 NCBI GI g18775
 BLAST score 652
 E value 0.0e+00
 Match length 986
 % identity 93
 NCBI Description G.max tufA gene for chloroplast translation elongation factor EF-Tu

Seq. No. 1640
 Contig ID 893_4.R1040
 5'-most EST LIB3170-014-Q1-K1-F12
 Method BLASTX
 NCBI GI g2500354
 BLAST score 619
 E value 1.0e-111
 Match length 224
 % identity 91
 NCBI Description 60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_ (AB001891) QM family protein [Solanum melongena]

Seq. No. 1641
 Contig ID 893_5.R1040
 5'-most EST hrw701059127.h1

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Method BLASTX
 NCBI GI g121631
 BLAST score 308
 E value 3.0e-28
 Match length 74
 % identity 77
 NCBI Description GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR
 >gi_72323_pir_KNNT2S glycine-rich protein 2 - wood tobacco
 >gi_19743_emb_CAA42622_ (X60007) nsGRP-2 [Nicotiana sylvestris]

Seq. No. 1642
 Contig ID 893_6.R1040
 5'-most EST fde700870636.h1
 Method BLASTN
 NCBI GI g18775
 BLAST score 218
 E value 1.0e-119
 Match length 420
 % identity 97
 NCBI Description G.max tufA gene for chloroplast translation elongation factor EF-Tu

Seq. No. 1643
 Contig ID 893_7.R1040
 5'-most EST LIB3039-016-Q1-E1-H9
 Method BLASTX
 NCBI GI g2500354
 BLAST score 550
 E value 2.0e-56
 Match length 109
 % identity 94
 NCBI Description 60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_ (AB001891) QM family protein [Solanum melongena]

Seq. No. 1644
 Contig ID 893_8.R1040
 5'-most EST LIB3028-019-Q1-B1-F4

Seq. No. 1645
 Contig ID 893_9.R1040
 5'-most EST LIB3106-013-Q1-K1-F4
 Method BLASTX
 NCBI GI g2500354
 BLAST score 213
 E value 4.0e-17
 Match length 46
 % identity 85
 NCBI Description 60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_ (AB001891) QM family protein [Solanum melongena]

Seq. No. 1646
 Contig ID 893_12.R1040
 5'-most EST LIB3106-037-Q1-K1-D3
 Method BLASTX
 NCBI GI g2500354
 BLAST score 635

E value 2.0e-66
 Match length 126
 % identity 93
 NCBI Description 60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_ (AB001891) QM family protein [Solanum melongena]

Seq. No. 1647
 Contig ID 893 19.R1040
 5'-most EST dpv701103675.h1
 Method BLASTX
 NCBI GI g2500354
 BLAST score 348
 E value 3.0e-33
 Match length 63
 % identity 98
 NCBI Description 60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_ (AB001891) QM family protein [Solanum melongena]

Seq. No. 1648
 Contig ID 893 21.R1040
 5'-most EST rlr700902438.h1
 Method BLASTX
 NCBI GI g2500354
 BLAST score 245
 E value 3.0e-21
 Match length 48
 % identity 90
 NCBI Description 60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_ (AB001891) QM family protein [Solanum melongena]

Seq. No. 1649
 Contig ID 894 1.R1040
 5'-most EST LIB3040-038-Q1-E1-G5
 Method BLASTX
 NCBI GI g3868758
 BLAST score 844
 E value 1.0e-90
 Match length 212
 % identity 74
 NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 1650
 Contig ID 895 2.R1040
 5'-most EST uC-gmropic019f08b1

Seq. No. 1651
 Contig ID 896 1.R1040
 5'-most EST k11701210028.h1

Seq. No. 1652
 Contig ID 898 2.R1040
 5'-most EST LIB3039-021-Q1-E1-H5
 Method BLASTX
 NCBI GI g2191136
 BLAST score 985
 E value 1.0e-134
 Match length 446

Seq. No. 1658
 Contig ID 900_3.R1040
 5'-most EST uxk700672265.h1
 Method BLASTN
 NCBI GI g473216
 BLAST score 118
 E value 1.0e-59
 Match length 354
 % identity 83
 NCBI Description P.sativum (little marvel) HSC71.0 mRNA

Seq. No. 1659
 Contig ID 900_4.R1040
 5'-most EST uC-gmrominsoy170b02b1
 Method BLASTX
 NCBI GI g1076746
 BLAST score 1030
 E value 0.0e+00
 Match length 502
 % identity 86
 NCBI Description heat shock protein 70 - rice (fragment)
 >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
 [Oryza sativa]

Seq. No. 1660
 Contig ID 900_5.R1040
 5'-most EST jC-gmst02400010c01a1
 Method BLASTX
 NCBI GI g629641
 BLAST score 1143
 E value 0.0e+00
 Match length 440
 % identity 87
 NCBI Description PsHSC71.0 protein - garden pea >gi_1076530_pir_S53500
 HSC71.0 protein - garden pea >gi_473217_emb_CAA83548_
 (Z32537) PsHSC71.0 [Pisum sativum]

Seq. No. 1661
 Contig ID 900_6.R1040
 5'-most EST wvk700683741.h1
 Method BLASTX
 NCBI GI g629641
 BLAST score 1158
 E value 0.0e+00
 Match length 433
 % identity 84
 NCBI Description PsHSC71.0 protein - garden pea >gi_1076530_pir_S53500
 HSC71.0 protein - garden pea >gi_473217_emb_CAA83548_
 (Z32537) PsHSC71.0 [Pisum sativum]

Seq. No. 1662
 Contig ID 900_7.R1040
 5'-most EST leu701146433.h1
 Method BLASTN
 NCBI GI g473216
 BLAST score 447
 E value 0.0e+00

Match length 1860
 % identity 87
 NCBI Description P.sativum (little marvel) HSC71.0 mRNA

Seq. No. 1663
 Contig ID 901_1.R1040
 5'-most EST uC-gmronoir033b09b1
 Method BLASTX
 NCBI GI g2702277
 BLAST score 397
 E value 2.0e-38
 Match length 109
 % identity 71

NCBI Description (AC003033) putative cyclin g-associated kinase [Arabidopsis thaliana] >gi_2914689 (AC003974) putative cyclin g-associated kinase [Arabidopsis thaliana]

Seq. No. 1664
 Contig ID 901_3.R1040
 5'-most EST fua701040662.h1

Seq. No. 1665
 Contig ID 902_1.R1040
 5'-most EST 2DA-02-Q1-B1-C1

Seq. No. 1666
 Contig ID 905_1.R1040
 5'-most EST 2DA-02-Q1-B1-C12

Seq. No. 1667
 Contig ID 906_1.R1040
 5'-most EST 2DA-02-Q1-B1-C2

Seq. No. 1668
 Contig ID 908_1.R1040
 5'-most EST uC-gmrominsoy040a12b1
 Method BLASTX
 NCBI GI g2979555
 BLAST score 340
 E value 8.0e-32
 Match length 150
 % identity 49
 NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]

Seq. No. 1669
 Contig ID 912_1.R1040
 5'-most EST txt700736440.h1
 Method BLASTX
 NCBI GI g1350983
 BLAST score 1082
 E value 1.0e-118
 Match length 234
 % identity 87
 NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)

Seq. No. 1670
 Contig ID 912_5.R1040

5'-most EST LIB3050-020-Q1-K1-C7
 Method BLASTX
 NCBI GI g1856971
 BLAST score 272
 E value 4.0e-24
 Match length 57
 % identity 88
 NCBI Description (D26058). This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No. 1671
 Contig ID 913 1.R1040
 5'-most EST seb700653717.h1
 Method BLASTX
 NCBI GI g3834307
 BLAST score 739
 E value 3.0e-78
 Match length 226
 % identity 68
 NCBI Description (AC005679) Strong similarity to gene T10I14.120 gi_2832679 putative protein from Arabidopsis thaliana BAC gb_AL021712. ESTs gb_N65887 and gb_N65627 come from this gene. [Arabidopsis thaliana]

Seq. No. 1672
 Contig ID 913 2.R1040
 5'-most EST zzp700835039.h1
 Method BLASTX
 NCBI GI g3834307
 BLAST score 941
 E value 1.0e-102
 Match length 223
 % identity 78
 NCBI Description (AC005679) Strong similarity to gene T10I14.120 gi_2832679 putative protein from Arabidopsis thaliana BAC gb_AL021712. ESTs gb_N65887 and gb_N65627 come from this gene. [Arabidopsis thaliana]

Seq. No. 1673
 Contig ID 913 3.R1040
 5'-most EST LIB3106-099-Q1-K1-D3
 Method BLASTX
 NCBI GI g3834307
 BLAST score 326
 E value 3.0e-30
 Match length 79
 % identity 78
 NCBI Description (AC005679) Strong similarity to gene T10I14.120 gi_2832679 putative protein from Arabidopsis thaliana BAC gb_AL021712. ESTs gb_N65887 and gb_N65627 come from this gene. [Arabidopsis thaliana]

Seq. No. 1674
 Contig ID 913 4.R1040
 5'-most EST zsg701118614.h1
 Method BLASTN

NCBI GI	g3766106
BLAST score	58
E value	1.0e-23
Match length	158
% identity	84
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	1675
Contig ID	913_5.R1040
5'-most EST	leu701147327.h1
Method	BLASTX
NCBI GI	g3834307
BLAST score	253
E value	5.0e-22
Match length	52
% identity	92
NCBI Description	(AC005679) Strong similarity to gene T10I14.120 gi_2832679 putative protein from Arabidopsis thaliana BAC gb_AL021712. ESTs gb_N65887 and gb_N65627 come from this gene. [Arabidopsis thaliana]
Seq. No.	1676
Contig ID	914_1.R1040
5'-most EST	dpv701102672.h1
Method	BLASTX
NCBI GI	g2213592
BLAST score	822
E value	9.0e-88
Match length	287
% identity	37
NCBI Description	(AC000348) T7N9.12 [Arabidopsis thaliana]
Seq. No.	1677
Contig ID	914_2.R1040
5'-most EST	sat701015380.h1
Method	BLASTX
NCBI GI	g2213592
BLAST score	829
E value	1.0e-88
Match length	298
% identity	35
NCBI Description	(AC000348) T7N9.12 [Arabidopsis thaliana]
Seq. No.	1678
Contig ID	914_3.R1040
5'-most EST	LIB3092-053-Q1-K1-B11
Method	BLASTX
NCBI GI	g2213592
BLAST score	291
E value	3.0e-26
Match length	85
% identity	32
NCBI Description	(AC000348) T7N9.12 [Arabidopsis thaliana]
Seq. No.	1679
Contig ID	915_1.R1040

5'-most EST fde700871332.h1
 Method BLASTX
 NCBI GI g3600047
 BLAST score 476
 E value 1.0e-47
 Match length 160
 % identity 61
 NCBI Description (AF080120) similar to elongation factor EF-Ts [Arabidopsis thaliana]

Seq. No. 1680
 Contig ID 917_1.R1040
 5'-most EST zsg701119187.h1
 Method BLASTX
 NCBI GI g1871577
 BLAST score 732
 E value 2.0e-77
 Match length 168
 % identity 82
 NCBI Description (Y11553) putative 21kD protein precursor [Medicago sativa]

Seq. No. 1681
 Contig ID 917_2.R1040
 5'-most EST uC-gmrominsoy256c09b1
 Method BLASTX
 NCBI GI g1871577
 BLAST score 656
 E value 1.0e-68
 Match length 194
 % identity 68
 NCBI Description (Y11553) putative 21kD protein precursor [Medicago sativa]

Seq. No. 1682
 Contig ID 917_3.R1040
 5'-most EST LIB3139-102-P1-N1-G2
 Method BLASTX
 NCBI GI g1871577
 BLAST score 580
 E value 8.0e-64
 Match length 181
 % identity 69
 NCBI Description (Y11553) putative 21kD protein precursor [Medicago sativa]

Seq. No. 1683
 Contig ID 919_1.R1040
 5'-most EST leu701151275.h1
 Method BLASTX
 NCBI GI g3914136
 BLAST score 306
 E value 1.0e-27
 Match length 116
 % identity 54
 NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
 >gi_2632171_emb_CAA05771_ (AJ002958) lipid transfer protein
 [Cicer arietinum]

Seq. No. 1684

Contig ID 919 3.R1040
 5'-most EST LIB3040-061-Q1-E11-F5
 Method BLASTX
 NCBI GI g3914136
 BLAST score 127
 E value 1.0e-12
 Match length 92
 % identity 43
 NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
 >gi_2632171_emb_CAA05771_ (AJ002958) lipid transfer protein
 [Cicer arietinum]

Seq. No. 1685
 Contig ID 920 1.R1040
 5'-most EST sat701013038.h1
 Method BLASTX
 NCBI GI g548770
 BLAST score 1759
 E value 0.0e+00
 Match length 385
 % identity 83
 NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir_S38359 ribosomal
 protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
 ribosomal protein L3 [Oryza sativa]

Seq. No. 1686
 Contig ID 920 2.R1040
 5'-most EST zsg701120409.h1
 Method BLASTX
 NCBI GI g132944
 BLAST score 296
 E value 9.0e-27
 Match length 61
 % identity 89
 NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_81658_pir_JQ0772 ribosomal
 protein L3 (ARP2) - Arabidopsis thaliana >gi_806279
 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No. 1687
 Contig ID 920 3.R1040
 5'-most EST seb700649013.h1
 Method BLASTN
 NCBI GI g2315210
 BLAST score 113
 E value 2.0e-56
 Match length 325
 % identity 84
 NCBI Description Lycopersicon esculentum mRNA for proteasome, alpha subunit

Seq. No. 1688
 Contig ID 922 1.R1040
 5'-most EST jC-gmst02400058e10a1
 Method BLASTN
 NCBI GI g2924734
 BLAST score 112
 E value 8.0e-56
 Match length 371

% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXE10, complete sequence [Arabidopsis thaliana]
Seq. No.	1689
Contig ID	922_2.R1040
5'-most EST	crh700852414.h1
Method	BLASTX
NCBI GI	g728880
BLAST score	183
E value	2.0e-13
Match length	55
% identity	62
NCBI Description	N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG >gi_517485_emb_CAA54691_ (X77588) ARD1 N-acetyl transferase homologue [Homo sapiens] >gi_1302661 (U52112) ARD1 N-acetyl transferase related protein [Homo sapiens]
Seq. No.	1690
Contig ID	923_1.R1040
5'-most EST	rlr700899522.h1
Method	BLASTX
NCBI GI	g2494113
BLAST score	778
E value	6.0e-83
Match length	192
% identity	75
NCBI Description	(AC002376) Strong similarity to Musa pectate lyase (gb_X92943). ESTs gb_AA042458, gb_ATTS4502, gb_N38552 come from this gene. [Arabidopsis thaliana]
Seq. No.	1691
Contig ID	924_2.R1040
5'-most EST	kll701207620.h1
Seq. No.	1692
Contig ID	925_1.R1040
5'-most EST	LIB3051-106-Q1-K1-C8
Method	BLASTX
NCBI GI	g136057
BLAST score	980
E value	1.0e-106
Match length	253
% identity	74
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_99499_pir_A32187 (S)-tetrahydroberberine oxidase - Coptis japonica >gi_556171 (J04121) triosephosphate isomerase [Coptis japonica]
Seq. No.	1693
Contig ID	925_2.R1040
5'-most EST	LIB3109-003-Q1-K1-C9
Method	BLASTX
NCBI GI	g1351279
BLAST score	359
E value	2.0e-44
Match length	113

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Contig ID 931 2.R1040
5'-most EST eep700868348.h1
Method BLASTX
NCBI GI g4200044
BLAST score 471
E value 4.0e-47
Match length 165
% identity 55
NCBI Description (AB022732) cytochrome P450 [Glycyrrhiza echinata]

Seq. No. 1704
Contig ID 931 4.R1040
5'-most EST rlr700900741.h1
Method BLASTX
NCBI GI g4559358
BLAST score 205
E value 6.0e-16
Match length 72
% identity 53
NCBI Description (AC006585) putative steroid binding protein [Arabidopsis thaliana]

Seq. No. 1705
Contig ID 932 1.R1040
5'-most EST jC-gmro02910036a06d1
Method BLASTX
NCBI GI g629602
BLAST score 3123
E value 0.0e+00
Match length 750
% identity 77
NCBI Description probable imbibition protein - wild cabbage
>gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No. 1706
Contig ID 932 2.R1040
5'-most EST g5606124
Method BLASTX
NCBI GI g629602
BLAST score 587
E value 3.0e-60
Match length 142
% identity 76
NCBI Description probable imbibition protein - wild cabbage
>gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No. 1707
Contig ID 932 3.R1040
5'-most EST LIB3170-050-Q1-K1-D8

Seq. No. 1708
Contig ID 933 1.R1040
5'-most EST 2DA-02-Q1-B1-E9
Method BLASTX
NCBI GI g3367569

BLAST score 175
 E value 4.0e-12
 Match length 173
 % identity 31
 NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

Seq. No. 1709
 Contig ID 934_1.R1040
 5'-most EST leu701144440.h1
 Method BLASTX
 NCBI GI g2832617
 BLAST score 256
 E value 4.0e-22
 Match length 71
 % identity 66
 NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 1710
 Contig ID 936_1.R1040
 5'-most EST hrw701057246.h1

Seq. No. 1711
 Contig ID 938_1.R1040
 5'-most EST 2DA-02-Q1-B1-F2
 Method BLASTX
 NCBI GI g3077640
 BLAST score 304
 E value 9.0e-28
 Match length 116
 % identity 55
 NCBI Description (AJ223151) O-methyltransferase [Prunus dulcis]

Seq. No. 1712
 Contig ID 941_1.R1040
 5'-most EST LIB3170-085-Q1-K1-G6
 Method BLASTX
 NCBI GI g2447107
 BLAST score 328
 E value 3.0e-30
 Match length 172
 % identity 42
 NCBI Description (U42580) A638R [Paramecium bursaria Chlorella virus 1]

Seq. No. 1713
 Contig ID 942_1.R1040
 5'-most EST 2DA-02-Q1-B1-F6

Seq. No. 1714
 Contig ID 942_2.R1040
 5'-most EST rlr700899163.h1

Seq. No. 1715
 Contig ID 943_1.R1040
 5'-most EST LIB3039-005-Q1-E1-G3
 Method BLASTX
 NCBI GI g125722
 BLAST score 365

5'-most EST g5126873
 Method BLASTX
 NCBI GI g4426565
 BLAST score 145
 E value 7.0e-09
 Match length 66
 % identity 39
 NCBI Description (AF031483) unknown [Rattus norvegicus]

Seq. No. 1721
 Contig ID 947_4.R1040
 5'-most EST LIB3093-014-Q1-K1-B9
 Method BLASTX
 NCBI GI g4426565
 BLAST score 175
 E value 8.0e-12
 Match length 238
 % identity 34
 NCBI Description (AF031483) unknown [Rattus norvegicus]

Seq. No. 1722
 Contig ID 947_5.R1040
 5'-most EST LIB3074-003-Q1-K1-B7
 Method BLASTX
 NCBI GI g126085
 BLAST score 242
 E value 5.0e-26
 Match length 236
 % identity 28
 NCBI Description SEED LECTIN SUBUNITS I AND II PRECURSOR
 >gi_81750_pir_A29572 lectin precursor - horse gram
 >gi_167564 (J02721) lectin subunit I precursor [Dolichos
 biflorus]

Seq. No. 1723
 Contig ID 947_6.R1040
 5'-most EST ncj700986678.h1
 Method BLASTX
 NCBI GI g3851636
 BLAST score 255
 E value 9.0e-22
 Match length 58
 % identity 83
 NCBI Description (AF098519) unknown [Avicennia marina] >gi_4128206
 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No. 1724
 Contig ID 948_1.R1040
 5'-most EST jC-gmst02400054d09a1

Seq. No. 1725
 Contig ID 948_2.R1040
 5'-most EST asn701132457.h1

Seq. No. 1726
 Contig ID 950_1.R1040
 5'-most EST LIB3050-005-Q1-K1-C10

Method BLASTX
 NCBI GI g4325282
 BLAST score 584
 E value 7.0e-60
 Match length 158
 % identity 70
 NCBI Description (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
 >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
 [Arabidopsis thaliana]

Seq. No. 1727
 Contig ID 950_2.R1040
 5'-most EST jC-gmle01810020d08a1
 Method BLASTX
 NCBI GI g4218535
 BLAST score 591
 E value 7.0e-61
 Match length 167
 % identity 63
 NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]

Seq. No. 1728
 Contig ID 950_3.R1040
 5'-most EST zzp700834856.h1
 Method BLASTX
 NCBI GI g2058282
 BLAST score 716
 E value 2.0e-75
 Match length 177
 % identity 78
 NCBI Description (X97377) atranbpla [Arabidopsis thaliana]

Seq. No. 1729
 Contig ID 950_4.R1040
 5'-most EST leu701152450.h1

Seq. No. 1730
 Contig ID 950_5.R1040
 5'-most EST LIB3030-006-Q1-B1-A1
 Method BLASTX
 NCBI GI g4218535
 BLAST score 525
 E value 3.0e-53
 Match length 144
 % identity 65
 NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]

Seq. No. 1731
 Contig ID 950_6.R1040
 5'-most EST pcp700992258.h1
 Method BLASTX
 NCBI GI g2443890
 BLAST score 221
 E value 1.0e-17
 Match length 66
 % identity 68
 NCBI Description (AC002294) similar to NAM (gp_X92205_1321924) and CUC2

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(gp_AB002560_1944132) proteins [Arabidopsis thaliana]

Seq. No.	1732
Contig ID	950_9.R1040
5'-most EST	LIB3092-043-Q1-K1-E1
Method	BLASTX
NCBI GI	g4218535
BLAST score	374
E value	6.0e-36
Match length	93
% identity	70
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]
Seq. No.	1733
Contig ID	950_10.R1040
5'-most EST	jC-gmst02400071g08d1
Seq. No.	1734
Contig ID	950_11.R1040
5'-most EST	uC-gmflminsoy049c06b1
Seq. No.	1735
Contig ID	950_12.R1040
5'-most EST	LIB3074-028-Q1-K1-C3
Seq. No.	1736
Contig ID	950_14.R1040
5'-most EST	zsq701127580.h1
Seq. No.	1737
Contig ID	950_15.R1040
5'-most EST	LIB3039-012-Q1-E1-H3
Method	BLASTX
NCBI GI	g1732511
BLAST score	511
E value	6.0e-52
Match length	121
% identity	79
NCBI Description	(U62742) Ran binding protein 1 homolog [Arabidopsis thaliana]
Seq. No.	1738
Contig ID	950_16.R1040
5'-most EST	LIB3073-009-Q1-K1-C4
Seq. No.	1739
Contig ID	950_19.R1040
5'-most EST	LIB3106-112-Q1-K1-A7
Method	BLASTN
NCBI GI	g1336081
BLAST score	45
E value	4.0e-16
Match length	77
% identity	90
NCBI Description	Glycine max var. Century ascorbate peroxidase 2 (APx2) mRNA, complete cds

Seq. No. 1740
Contig ID 950_24.R1040
5'-most EST LIB3106-061-Q1-K1-G2

Seq. No. 1741
Contig ID 950_25.R1040
5'-most EST hyd700726095.h1

Seq. No. 1742
Contig ID 951_1.R1040
5'-most EST LIB3039-026-Q1-E1-H3
Method BLASTX
NCBI GI g1173209
BLAST score 681
E value 1.0e-71
Match length 140
% identity 94
NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal protein S16 protein - upland cotton
>gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit [Gossypium hirsutum]

Seq. No. 1743
Contig ID 951_2.R1040
5'-most EST dpv701100901.h1
Method BLASTX
NCBI GI g1173209
BLAST score 683
E value 8.0e-72
Match length 140
% identity 95
NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal protein S16 protein - upland cotton
>gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit [Gossypium hirsutum]

Seq. No. 1744
Contig ID 951_3.R1040
5'-most EST jC-gmst02400009b06a1
Method BLASTX
NCBI GI g1173209
BLAST score 592
E value 2.0e-61
Match length 125
% identity 93
NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal protein S16 protein - upland cotton
>gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit [Gossypium hirsutum]

Seq. No. 1745
Contig ID 954_1.R1040
5'-most EST sat701007156.h1
Method BLASTX
NCBI GI g1486472
BLAST score 963
E value 1.0e-107

Match length	240
% identity	84
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]
Seq. No.	1746
Contig ID	954_2.R1040
5'-most EST	gsv701045595.h1
Seq. No.	1747
Contig ID	954_3.R1040
5'-most EST	LIB3107-070-Q1-K1-G12
Method	BLASTX
NCBI GI	g1486472
BLAST score	625
E value	4.0e-65
Match length	135
% identity	90
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]
Seq. No.	1748
Contig ID	954_4.R1040
5'-most EST	uC-gmropic109e10b1
Method	BLASTX
NCBI GI	g2244847
BLAST score	1400
E value	1.0e-155
Match length	529
% identity	56
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]
Seq. No.	1749
Contig ID	954_5.R1040
5'-most EST	LIB3109-052-Q1-K1-D9
Seq. No.	1750
Contig ID	954_6.R1040
5'-most EST	jC-gmle01810016e03a1
Seq. No.	1751
Contig ID	955_1.R1040
5'-most EST	LIB3065-024-Q1-N1-B5
Seq. No.	1752
Contig ID	956_1.R1040
5'-most EST	LIB3138-047-Q1-N1-D3
Method	BLASTX
NCBI GI	g3513736
BLAST score	311
E value	2.0e-28
Match length	141
% identity	49
NCBI Description	(AF080118) No definition line found [Arabidopsis thaliana] >gi_4539367_emb_CAB40061.1_ (AL049525) putative protein [Arabidopsis thaliana]

Match length	122
% identity	85
NCBI Description	Arabidopsis thaliana casein kinase II beta subunit CKB1 mRNA, complete cds
Seq. No.	1768
Contig ID	967_1.R1040
5'-most EST	g5677191
Seq. No.	1769
Contig ID	968_1.R1040
5'-most EST	jC-gmst02400015g09d1
Seq. No.	1770
Contig ID	970_1.R1040
5'-most EST	jC-gmle01810044a05d1
Method	BLASTX
NCBI GI	g4006868
BLAST score	382
E value	9.0e-37
Match length	110
% identity	65
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]
Seq. No.	1771
Contig ID	974_1.R1040
5'-most EST	hyd700727370.h1
Seq. No.	1772
Contig ID	975_1.R1040
5'-most EST	jC-gmro02910008f01a1
Method	BLASTX
NCBI GI	g687844
BLAST score	982
E value	1.0e-106
Match length	629
% identity	19
NCBI Description	(U21320) contains TPR domain-like repeats [Caenorhabditis elegans]
Seq. No.	1773
Contig ID	975_2.R1040
5'-most EST	LIB3106-034-Q1-K1-D4
Seq. No.	1774
Contig ID	975_3.R1040
5'-most EST	pmv700888650.h1
Seq. No.	1775
Contig ID	975_4.R1040
5'-most EST	LIB3170-043-Q1-K1-A4
Seq. No.	1776
Contig ID	975_5.R1040
5'-most EST	LIB3106-074-Q1-K1-G9
Method	BLASTX
NCBI GI	g2266994

NCBI Description Drosophila melanogaster DNA sequence (P1 DS07982 (D185)), complete sequence [Drosophila melanogaster]

Seq. No. 1786
Contig ID 997_1.R1040
5'-most EST ASG32442DA-01-Q1-E1-C7

Seq. No. 1787
Contig ID 1004_1.R1040
5'-most EST LIB3028-017-Q1-B1-F12

Seq. No. 1788
Contig ID 1005_1.R1040
5'-most EST LIB3053-012-Q1-N1-A6

Seq. No. 1789
Contig ID 1010_1.R1040
5'-most EST jC-gmle01810088b06d1
Method BLASTN
NCBI GI g12139
BLAST score 387
E value 0.0e+00
Match length 499
% identity 94
NCBI Description Pea plastid genes rps2, atpI, atpH, atpF, atpA, trnR and trnG coding for ribosomal protein S2, one CF(1) and three CF(0) subunits of ATP synthase and tRNA-Arg and tRNA-Gly

Seq. No. 1790
Contig ID 1015_1.R1040
5'-most EST ASG32442DA-01-Q1-E1-E6

Seq. No. 1791
Contig ID 1019_1.R1040
5'-most EST jC-gmro02910031e05d1
Method BLASTN
NCBI GI g2598578
BLAST score 95
E value 5.0e-46
Match length 171
% identity 89
NCBI Description Medicago truncatula mRNA for L-ascorbate oxidase

Seq. No. 1792
Contig ID 1025_1.R1040
5'-most EST ASG32442DA-01-Q1-E1-F4

Seq. No. 1793
Contig ID 1032_1.R1040
5'-most EST LIB3170-087-Q1-J1-B2
Method BLASTX
NCBI GI g4512703
BLAST score 442
E value 2.0e-43
Match length 211
% identity 45
NCBI Description (AC006569) unknown protein [Arabidopsis thaliana]

Seq. No. 1794
 Contig ID 1035_1.R1040
 5'-most EST ASG32442DA-01-Q1-E1-G4
 Method BLASTX
 NCBI GI g2129854
 BLAST score 418
 E value 4.0e-41
 Match length 105
 % identity 72
 NCBI Description early nodulin 8 precursor - alfalfa >gi_304037 (L18899)
 early nodulin [Medicago sativa]

Seq. No. 1795
 Contig ID 1046_1.R1040
 5'-most EST g4299082
 Method BLASTX
 NCBI GI g4510383
 BLAST score 762
 E value 9.0e-81
 Match length 303
 % identity 78
 NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 1796
 Contig ID 1046_2.R1040
 5'-most EST g4305468
 Method BLASTX
 NCBI GI g4510383
 BLAST score 271
 E value 1.0e-23
 Match length 82
 % identity 67
 NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 1797
 Contig ID 1050_1.R1040
 5'-most EST jC-gmro02910007g06d1
 Method BLASTX
 NCBI GI g3953471
 BLAST score 1320
 E value 1.0e-146
 Match length 311
 % identity 79
 NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

Seq. No. 1798
 Contig ID 1050_2.R1040
 5'-most EST LIB3170-029-Q1-J1-A7
 Method BLASTX
 NCBI GI g3953471
 BLAST score 249
 E value 3.0e-21
 Match length 58
 % identity 76
 NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 1805
 Contig ID 1064_2.R1040
 5'-most EST g5126554
 Method BLASTX
 NCBI GI g3868758
 BLAST score 518
 E value 1.0e-52
 Match length 144
 % identity 68

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 1806
 Contig ID 1064_4.R1040
 5'-most EST LIB3139-055-P1-N1-C4
 Method BLASTX
 NCBI GI g3868758
 BLAST score 420
 E value 2.0e-41
 Match length 104
 % identity 75

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 1807
 Contig ID 1064_5.R1040
 5'-most EST LIB3170-036-Q1-K2-D11
 Method BLASTX
 NCBI GI g2160158
 BLAST score 212
 E value 4.0e-17
 Match length 43
 % identity 93

NCBI Description (AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564, gb_T45940, gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No. 1808
 Contig ID 1064_6.R1040
 5'-most EST sat701004617.h1
 Method BLASTN
 NCBI GI g3868757
 BLAST score 73
 E value 5.0e-33
 Match length 209
 % identity 84

NCBI Description Oryza sativa mRNA for elongation factor 1B gamma, complete cds

Seq. No. 1809
 Contig ID 1065_1.R1040
 5'-most EST ASG32442DA-02-Q1-E1-B3
 Method BLASTX
 NCBI GI g4454482
 BLAST score 410
 E value 5.0e-40
 Match length 96

5'-most EST	LIB3167-050-P1-K1-A7
Seq. No.	1835
Contig ID	1135_1.R1040
5'-most EST	LIB3170-087-Q1-K1-A3
Method	BLASTX
NCBI GI	g3036810
BLAST score	381
E value	2.0e-36
Match length	133
% identity	61
NCBI Description	(AL022373) putative Myc-type transcription factor [Arabidopsis thaliana]
Seq. No.	1836
Contig ID	1142_1.R1040
5'-most EST	LIB3109-047-Q1-K1-E2
Method	BLASTX
NCBI GI	g1351838
BLAST score	2125
E value	0.0e+00
Match length	432
% identity	94
NCBI Description	ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA >gi_984309 (U26948) beta-carboxyltransferase subunit [Glycine max]
Seq. No.	1837
Contig ID	1142_2.R1040
5'-most EST	LIB3092-060-Q1-K1-G6
Method	BLASTN
NCBI GI	g984307
BLAST score	1556
E value	0.0e+00
Match length	1664
% identity	98
NCBI Description	Glycine max ribosomal protein S16 (rps16) gene, partial cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229 precursor
Seq. No.	1838
Contig ID	1142_3.R1040
5'-most EST	jC-gmle01810034g10a2
Method	BLASTN
NCBI GI	g984307
BLAST score	324
E value	0.0e+00
Match length	383
% identity	95
NCBI Description	Glycine max ribosomal protein S16 (rps16) gene, partial cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229 precursor

Seq. No. 1839
 Contig ID 1142 7.R1040
 5'-most EST LIB3093-024-Q1-K1-C1
 Method BLASTN
 NCBI GI g984307
 BLAST score 230
 E value 1.0e-126
 Match length 348
 % identity 93
 NCBI Description Glycine max ribosomal protein S16 (rps16) gene, partial cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229 precursor

Seq. No. 1840
 Contig ID 1144 1.R1040
 5'-most EST LIB3139-067-P1-N1-E5
 Method BLASTX
 NCBI GI g3402716
 BLAST score 299
 E value 1.0e-26
 Match length 233
 % identity 34
 NCBI Description (AC004261) unknown protein [Arabidopsis thaliana]

Seq. No. 1841
 Contig ID 1149 1.R1040
 5'-most EST LIB3139-008-P1-N1-C9
 Method BLASTN
 NCBI GI g19500
 BLAST score 164
 E value 1.0e-86
 Match length 433
 % identity 88
 NCBI Description L.polyphyllus mRNA for pPLZ12 protein

Seq. No. 1842
 Contig ID 1149 2.R1040
 5'-most EST LIB3074-031-Q1-K1-B9

Seq. No. 1843
 Contig ID 1155 1.R1040
 5'-most EST gsv701046559.h1
 Method BLASTN
 NCBI GI g396818
 BLAST score 222
 E value 1.0e-121
 Match length 734
 % identity 83
 NCBI Description P.sativum pspor1 mRNA encoding porin

Seq. No. 1844
 Contig ID 1157 1.R1040
 5'-most EST uC-gmrominsoy256g12b1
 Method BLASTN
 NCBI GI g4115332

Contig ID 1158_3.R1040
 5'-most EST wvk700686173.h1
 Method BLASTN
 NCBI GI g2924257
 BLAST score 151
 E value 1.0e-79
 Match length 203
 % identity 94
 NCBI Description Tobacco chloroplast genome DNA

Seq. No. 1850
 Contig ID 1162_1.R1040
 5'-most EST LIB3040-050-Q1-E1-C5
 Method BLASTN
 NCBI GI g2264309
 BLAST score 53
 E value 2.0e-20
 Match length 472
 % identity 82
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No. 1851
 Contig ID 1164_1.R1040
 5'-most EST jC-gmf102220096g11a1
 Method BLASTX
 NCBI GI g461812
 BLAST score 342
 E value 5.0e-32
 Match length 162
 % identity 40
 NCBI Description CYTOCHROME P450 72 (CYPLXXII) (PROBABLE GERANOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] >gi_445604_prf__1909351A cytochrome P450 [Catharanthus roseus]

Seq. No. 1852
 Contig ID 1167_1.R1040
 5'-most EST uC-gmropic032h12b1
 Method BLASTN
 NCBI GI g470126
 BLAST score 220
 E value 1.0e-120
 Match length 536
 % identity 85
 NCBI Description N.tabacum (cv.Samsun NN) L19 mRNA for ribosomal protein L19

Seq. No. 1853
 Contig ID 1167_2.R1040
 5'-most EST LIB3106-051-Q1-K1-H5
 Method BLASTN
 NCBI GI g470126
 BLAST score 170
 E value 3.0e-90
 Match length 566
 % identity 83

NCBI Description	N.tabacum (cv.Samsun NN) L19 mRNA for ribosomal protein L19
Seq. No.	1854
Contig ID	1167_3.R1040
5'-most EST	uC-gmropic010a09b1
Method	BLASTN
NCBI GI	g470126
BLAST score	105
E value	1.0e-51
Match length	333
% identity	83
NCBI Description	N.tabacum (cv.Samsun NN) L19 mRNA for ribosomal protein L19
Seq. No.	1855
Contig ID	1167_4.R1040
5'-most EST	jsh701064147.h1
Method	BLASTX
NCBI GI	g3377797
BLAST score	417
E value	4.0e-79
Match length	174
% identity	89
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara
Seq. No.	1856
Contig ID	1167_5.R1040
5'-most EST	g5688162
Method	BLASTN
NCBI GI	g169928
BLAST score	81
E value	2.0e-37
Match length	89
% identity	98
NCBI Description	Glycine max alpha'-type beta conglycinin storage protein gene, complete cds, clone ch4A
Seq. No.	1857
Contig ID	1167_6.R1040
5'-most EST	LIB3170-035-Q1-K1-G2
Method	BLASTN
NCBI GI	g470126
BLAST score	94
E value	2.0e-45
Match length	242
% identity	85
NCBI Description	N.tabacum (cv.Samsun NN) L19 mRNA for ribosomal protein L19
Seq. No.	1858
Contig ID	1167_7.R1040
5'-most EST	LIB3050-011-Q1-E1-F12
Method	BLASTN
NCBI GI	g470126
BLAST score	90

BLAST score 235
 E value 1.0e-19
 Match length 83
 % identity 61
 NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
 >gi_1076292_pir_S53127 asparaginase - Arabidopsis thaliana
 >gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis thaliana]

Seq. No. 1885
 Contig ID 1203_11.R1040
 5'-most EST zhf700961256.h1
 Method BLASTX
 NCBI GI g1703446
 BLAST score 186
 E value 3.0e-14
 Match length 65
 % identity 63
 NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
 >gi_1076292_pir_S53127 asparaginase - Arabidopsis thaliana
 >gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis thaliana]

Seq. No. 1886
 Contig ID 1204_1.R1040
 5'-most EST awf700839244.h1
 Method BLASTX
 NCBI GI g4204308
 BLAST score 237
 E value 7.0e-20
 Match length 43
 % identity 91
 NCBI Description (AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No. 1887
 Contig ID 1206_1.R1040
 5'-most EST LIB3027-010-Q1-B1-C9

Seq. No. 1888
 Contig ID 1210_1.R1040
 5'-most EST uC-gmflminsoy005a10b1
 Method BLASTX
 NCBI GI g2623309
 BLAST score 702
 E value 2.0e-73
 Match length 435
 % identity 42
 NCBI Description (AC002409) similar to tgacg-specific DNA-binding protein [Arabidopsis thaliana]

Seq. No. 1889
 Contig ID 1212_1.R1040
 5'-most EST LIB3029-006-Q1-B1-H7
 Method BLASTX
 NCBI GI g1710077
 BLAST score 558

Seq. No. 1905
 Contig ID 1248_1.R1040
 5'-most EST LIB3139-026-P1-N1-C10
 Method BLASTX
 NCBI GI g3023832
 BLAST score 1513
 E value 1.0e-169
 Match length 320
 % identity 52
 NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 1
 >gi_1835161_emb_CAB06618_ (Z84820) G protein beta subunit
 [Nicotiana tabacum]

Seq. No. 1906
 Contig ID 1248_2.R1040
 5'-most EST uC-gmrominsoyl67g11b1
 Method BLASTX
 NCBI GI g3023832
 BLAST score 663
 E value 1.0e-69
 Match length 142
 % identity 88
 NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 1
 >gi_1835161_emb_CAB06618_ (Z84820) G protein beta subunit
 [Nicotiana tabacum]

Seq. No. 1907
 Contig ID 1248_3.R1040
 5'-most EST LIB3109-021-Q1-K2-H8
 Method BLASTX
 NCBI GI g3023841
 BLAST score 304
 E value 1.0e-27
 Match length 68
 % identity 87
 NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT
 >gi_1695179_emb_CAA70704_ (Y09513) G protein beta subunit
 [Nicotiana plumbaginifolia]

Seq. No. 1908
 Contig ID 1248_4.R1040
 5'-most EST zpv700762067.h1
 Method BLASTX
 NCBI GI g3023841
 BLAST score 254
 E value 4.0e-22
 Match length 70
 % identity 69
 NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT
 >gi_1695179_emb_CAA70704_ (Y09513) G protein beta subunit
 [Nicotiana plumbaginifolia]

Seq. No. 1909
 Contig ID 1250_1.R1040
 5'-most EST g4305784

Match length 170
 % identity 93
 NCBI Description Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val, NADH dehydrogenase and ORF

Seq. No. 1915
 Contig ID 1267_1.R1040
 5'-most EST awf700842486.h1
 Method BLASTN
 NCBI GI g3046856
 BLAST score 35
 E value 1.0e-09
 Match length 301
 % identity 84
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No. 1916
 Contig ID 1272_1.R1040
 5'-most EST g5688109
 Method BLASTN
 NCBI GI g170005
 BLAST score 1008
 E value 0.0e+00
 Match length 1022
 % identity 100
 NCBI Description Soybean lectin (Le1) gene, complete cds

Seq. No. 1917
 Contig ID 1272_2.R1040
 5'-most EST LIB3092-053-Q1-K1-D3

Seq. No. 1918
 Contig ID 1273_1.R1040
 5'-most EST LIB3107-061-Q1-K1-E4
 Method BLASTX
 NCBI GI g4115934
 BLAST score 593
 E value 3.0e-61
 Match length 128
 % identity 79
 NCBI Description (AF118223) contains similarity to Methanobacterium thermoautotrophicum transcriptional regulator (GB:AE000850) [Arabidopsis thaliana]

Seq. No. 1919
 Contig ID 1273_2.R1040
 5'-most EST LIB3107-016-Q1-K1-D1
 Method BLASTX
 NCBI GI g4115939
 BLAST score 237
 E value 7.0e-20
 Match length 57
 % identity 40
 NCBI Description (AF118223) contains similarity to Methanobacterium thermoautotrophicum transcriptional regulator (GB:AE000850) [Arabidopsis thaliana]

Seq. No.	1920
Contig ID	1274_1.R1040
5'-most EST	LIB3109-001-Q1-K2-B7
Method	BLASTX
NCBI GI	g401188
BLAST score	383
E value	4.0e-48
Match length	305
% identity	22
NCBI Description	NUCLEOLYSIN TIA-1 >gi_107354_pir_A39293 cytotoxic granule-associated RNA-binding protein TIA1 precursor, leukocyte - human
Seq. No.	1921
Contig ID	1274_2.R1040
5'-most EST	LIB3051-001-Q1-E1-D4
Seq. No.	1922
Contig ID	1274_3.R1040
5'-most EST	LIB3170-042-Q1-K1-C2
Seq. No.	1923
Contig ID	1276_1.R1040
5'-most EST	LIB3107-075-Q1-K1-E5
Method	BLASTX
NCBI GI	g3193298
BLAST score	190
E value	6.0e-14
Match length	108
% identity	35
NCBI Description	(AF069298) T14P8.17 gene product [Arabidopsis thaliana]
Seq. No.	1924
Contig ID	1279_1.R1040
5'-most EST	LIB3106-070-P1-K1-F1
Method	BLASTN
NCBI GI	g3603398
BLAST score	336
E value	0.0e+00
Match length	1019
% identity	87
NCBI Description	Medicago sativa cinnamyl-alcohol dehydrogenase (MsaCad2) mRNA, complete cds
Seq. No.	1925
Contig ID	1279_2.R1040
5'-most EST	pmv700890767.h1
Method	BLASTN
NCBI GI	g19594
BLAST score	143
E value	2.0e-74
Match length	338
% identity	88
NCBI Description	M.sativa encoding cinnamyl alcohol dehydrogenase
Seq. No.	1926

Contig ID 1279 3.R1040
 5'-most EST LIB3138-062-Q1-N1-E10
 Method BLASTN
 NCBI GI g3603398
 BLAST score 140
 E value 2.0e-72
 Match length 387
 % identity 89
 NCBI Description Medicago sativa cinnamyl-alcohol dehydrogenase (MsaCad2)
 mRNA, complete cds

Seq. No. 1927
 Contig ID 1279 5.R1040
 5'-most EST sat701009719.h1
 Method BLASTN
 NCBI GI g3603398
 BLAST score 129
 E value 3.0e-66
 Match length 284
 % identity 86
 NCBI Description Medicago sativa cinnamyl-alcohol dehydrogenase (MsaCad2)
 mRNA, complete cds

Seq. No. 1928
 Contig ID 1281_1.R1040
 5'-most EST jC-gmro02800043h04a1
 Method BLASTX
 NCBI GI g2865175
 BLAST score 412
 E value 3.0e-40
 Match length 132
 % identity 61
 NCBI Description (AB010945) AtRer1A [Arabidopsis thaliana]

Seq. No. 1929
 Contig ID 1281_2.R1040
 5'-most EST pxt700941249.h1
 Method BLASTX
 NCBI GI g2642434
 BLAST score 229
 E value 5.0e-19
 Match length 102
 % identity 46
 NCBI Description (AC002391) putative Rer1 protein [Arabidopsis thaliana]

Seq. No. 1930
 Contig ID 1282_1.R1040
 5'-most EST leu701152518.h1
 Method BLASTN
 NCBI GI g343480
 BLAST score 877
 E value 0.0e+00
 Match length 1323
 % identity 92
 NCBI Description tobacco chloroplast atpase gene (b and e subunits) and
 flanks

Seq. No. 1931
 Contig ID 1282_6.R1040
 5'-most EST fde700872028.h1
 Method BLASTN
 NCBI GI g3929530
 BLAST score 168
 E value 1.0e-89
 Match length 244
 % identity 96
 NCBI Description Anisoptera marginata ATP synthase beta subunit (atpB) gene, chloroplast gene encoding chloroplast protein, partial cds

Seq. No. 1932
 Contig ID 1283_1.R1040
 5'-most EST sat701003615.h1
 Method BLASTN
 NCBI GI g3043427
 BLAST score 278
 E value 1.0e-155
 Match length 594
 % identity 87
 NCBI Description Cicer arietinum mRNA for 40S ribosomal protein S5

Seq. No. 1933
 Contig ID 1283_2.R1040
 5'-most EST rca700999874.h1

Seq. No. 1934
 Contig ID 1283_3.R1040
 5'-most EST uC-gmrominsoy068d03b1
 Method BLASTN
 NCBI GI g3043427
 BLAST score 248
 E value 1.0e-137
 Match length 592
 % identity 85
 NCBI Description Cicer arietinum mRNA for 40S ribosomal protein S5

Seq. No. 1935
 Contig ID 1283_4.R1040
 5'-most EST LIB3170-014-Q1-K1-E1
 Method BLASTN
 NCBI GI g3043427
 BLAST score 183
 E value 4.0e-98
 Match length 567
 % identity 86
 NCBI Description Cicer arietinum mRNA for 40S ribosomal protein S5

Seq. No. 1936
 Contig ID 1283_6.R1040
 5'-most EST LIB3051-015-Q1-E1-C1
 Method BLASTN
 NCBI GI g3043427
 BLAST score 117
 E value 4.0e-59
 Match length 279

% identity	87
NCBI Description	Cicer arietinum mRNA for 40S ribosomal protein S5
Seq. No.	1937
Contig ID	1285_1.R1040
5'-most EST	LIB3049-048-Q1-E1-A5
Method	BLASTN
NCBI GI	g20657
BLAST score	362
E value	0.0e+00
Match length	753
% identity	89
NCBI Description	P.sativum Cab II gene for chlorophyll a/b-binding protein
Seq. No.	1938
Contig ID	1285_2.R1040
5'-most EST	LIB3170-023-Q1-J1-B4
Method	BLASTX
NCBI GI	g3560529
BLAST score	194
E value	7.0e-15
Match length	49
% identity	80
NCBI Description	(AF039598) light harvesting chlorophyll A/B binding protein [Prunus persica]
Seq. No.	1939
Contig ID	1285_3.R1040
5'-most EST	hyd700727351.h1
Method	BLASTN
NCBI GI	g20657
BLAST score	229
E value	1.0e-126
Match length	450
% identity	91
NCBI Description	P.sativum Cab II gene for chlorophyll a/b-binding protein
Seq. No.	1940
Contig ID	1287_1.R1040
5'-most EST	LIB3106-019-Q1-K1-H2
Method	BLASTX
NCBI GI	g3183247
BLAST score	1178
E value	1.0e-129
Match length	391
% identity	58
NCBI Description	PUTATIVE GTP-BINDING PROTEIN W08E3.3 >gi_3880615_emb_CAB07131_ (Z92773) predicted using Genefinder; Similarity to Yeast hypothetical 44.2 KD protein, putative GTP-binding protein (SW:P38219); cDNA EST EMBL:D64516 comes from this gene; cDNA EST EMBL:D65777 comes from this gene; cDNA EST EMB
Seq. No.	1941
Contig ID	1290_1.R1040
5'-most EST	kmv700739112.h1
Method	BLASTX

NCBI GI g4056479
BLAST score 291
E value 4.0e-26
Match length 82
% identity 73
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 1942
Contig ID 1291_1.R1040
5'-most EST LIB3027-008-Q1-B1-A3

Seq. No. 1943
Contig ID 1292_1.R1040
5'-most EST LIB3029-012-Q1-B1-B1
Method BLASTX
NCBI GI g1839188
BLAST score 539
E value 7.0e-55
Match length 157
% identity 64
NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No. 1944
Contig ID 1293_1.R1040
5'-most EST leu701153506.h1

Seq. No. 1945
Contig ID 1294_1.R1040
5'-most EST g5687992
Method BLASTX
NCBI GI g729470
BLAST score 1608
E value 1.0e-180
Match length 356
% identity 83
NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
(NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
>gi_542089_pir_JQ2272 formate dehydrogenase (EC 1.2.1.2)
precursor, mitochondrial - potato >gi_297798_emb_CAA79702_
(Z21493) mitochondrial formate dehydrogenase precursor
[Solanum tuberosum]

Seq. No. 1946
Contig ID 1294_2.R1040
5'-most EST kl1701213327.h1
Method BLASTX
NCBI GI g729470
BLAST score 518
E value 1.0e-52
Match length 115
% identity 85
NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
(NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
>gi_542089_pir_JQ2272 formate dehydrogenase (EC 1.2.1.2)
precursor, mitochondrial - potato >gi_297798_emb_CAA79702_
(Z21493) mitochondrial formate dehydrogenase precursor
[Solanum tuberosum]

5'-most EST jC-gmle01810089f02a1
 Method BLASTN
 NCBI GI g19600
 BLAST score 174
 E value 9.0e-93
 Match length 470
 % identity 85
 NCBI Description M.sativa mRNA for eIF-4D

Seq. No. 1964
 Contig ID 1298_6.R1040
 5'-most EST LIB3049-054-Q1-E1-D11
 Method BLASTN
 NCBI GI g19701
 BLAST score 149
 E value 4.0e-78
 Match length 401
 % identity 84
 NCBI Description N.plumbaginifolia mRNA NeIF-5A2 for initiation factor 5A(2)

Seq. No. 1965
 Contig ID 1298_7.R1040
 5'-most EST LIB3051-107-Q1-K1-C3
 Method BLASTN
 NCBI GI g3986749
 BLAST score 96
 E value 2.0e-46
 Match length 243
 % identity 86
 NCBI Description Hevea brasiliensis serine/threonine protein phosphatase type 2A (PP2A) mRNA, complete cds

Seq. No. 1966
 Contig ID 1298_11.R1040
 5'-most EST jex700904182.h1
 Method BLASTN
 NCBI GI g3986749
 BLAST score 34
 E value 1.0e-09
 Match length 66
 % identity 88
 NCBI Description Hevea brasiliensis serine/threonine protein phosphatase type 2A (PP2A) mRNA, complete cds

Seq. No. 1967
 Contig ID 1298_12.R1040
 5'-most EST xpa700793188.h1
 Method BLASTN
 NCBI GI g2225884
 BLAST score 123
 E value 1.0e-62
 Match length 339
 % identity 84
 NCBI Description Solanum tuberosum mRNA for eukaryotic initiation factor 5A5, complete cds

Seq. No. 1968

Contig ID 1299 1.R1040
 5'-most EST djj700606009.h2
 Method BLASTX
 NCBI GI g2194139
 BLAST score 237
 E value 6.0e-20
 Match length 66
 % identity 65
 NCBI Description (AC002062) EST gb_ATTS0887 comes from this gene.
 [Arabidopsis thaliana]

Seq. No. 1969
 Contig ID 1303 1.R1040
 5'-most EST LIB3138-128-Q1-N1-B10
 Method BLASTX
 NCBI GI g2664210
 BLAST score 536
 E value 5.0e-55
 Match length 123
 % identity 80
 NCBI Description (AJ222644) asparaginyl-tRNA synthetase [Arabidopsis
 thaliana]

Seq. No. 1970
 Contig ID 1303 2.R1040
 5'-most EST LIB3138-022-Q1-N1-F2
 Method BLASTN
 NCBI GI g210811
 BLAST score 127
 E value 1.0e-64
 Match length 634
 % identity 88
 NCBI Description Bean pod mottle virus coat protein gene, complete cds,
 complete middle component (M) RNA

Seq. No. 1971
 Contig ID 1304 1.R1040
 5'-most EST LIB3029-006-Q1-B1-G2
 Method BLASTX
 NCBI GI g691752
 BLAST score 1150
 E value 1.0e-126
 Match length 424
 % identity 54
 NCBI Description (D29803) preproMP27-MP32 [Cucurbita sp.]

Seq. No. 1972
 Contig ID 1306 1.R1040
 5'-most EST vwf700676455.h1
 Method BLASTX
 NCBI GI g872116
 BLAST score 1674
 E value 0.0e+00
 Match length 580
 % identity 61
 NCBI Description (X79770) sti (stress inducible protein) [Glycine max]

Seq. No. 1973
 Contig ID 1306_2.R1040
 5'-most EST txt700732045.h1
 Method BLASTX
 NCBI GI g4115918
 BLAST score 502
 E value 2.0e-50
 Match length 154
 % identity 69
 NCBI Description (AF118222) similar to nascent polypeptide associated complex alpha chain [Arabidopsis thaliana]

Seq. No. 1974
 Contig ID 1306_3.R1040
 5'-most EST dpv701101850.h1
 Method BLASTN
 NCBI GI g872115
 BLAST score 93
 E value 2.0e-44
 Match length 277
 % identity 83
 NCBI Description G.max gmsti. mRNA

Seq. No. 1975
 Contig ID 1306_4.R1040
 5'-most EST jC-gmro02910039g01d1
 Method BLASTX
 NCBI GI g4115918
 BLAST score 207
 E value 2.0e-16
 Match length 70
 % identity 63
 NCBI Description (AF118222) similar to nascent polypeptide associated complex alpha chain [Arabidopsis thaliana]

Seq. No. 1976
 Contig ID 1306_5.R1040
 5'-most EST asj700967426.h1
 Method BLASTX
 NCBI GI g4115918
 BLAST score 325
 E value 4.0e-30
 Match length 77
 % identity 82
 NCBI Description (AF118222) similar to nascent polypeptide associated complex alpha chain [Arabidopsis thaliana]

Seq. No. 1977
 Contig ID 1307_1.R1040
 5'-most EST awf700840576.h1
 Method BLASTX
 NCBI GI g2275196
 BLAST score 475
 E value 8.0e-49
 Match length 132
 % identity 81
 NCBI Description (AC002337) water stress-induced protein, WSI76 isolog

[Arabidopsis thaliana]

Seq. No. 1978
 Contig ID 1309_1.R1040
 5'-most EST uC-gmflminsoy045g04b1
 Method BLASTX
 NCBI GI g3063713
 BLAST score 193
 E value 2.0e-14
 Match length 122
 % identity 46
 NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 1979
 Contig ID 1313_1.R1040
 5'-most EST uC-gmrominsoy060b07b1

Seq. No. 1980
 Contig ID 1313_2.R1040
 5'-most EST jC-gmfl02220108a04d1

Seq. No. 1981
 Contig ID 1313_3.R1040
 5'-most EST LIB3106-006-Q1-K1-B4
 Method BLASTN
 NCBI GI g4038468
 BLAST score 157
 E value 1.0e-82
 Match length 409
 % identity 86
 NCBI Description Porteresia coarctata histone H3 mRNA, complete cds

Seq. No. 1982
 Contig ID 1313_4.R1040
 5'-most EST jC-gmfl02220052g08d1
 Method BLASTX
 NCBI GI g1200205
 BLAST score 725
 E value 3.0e-76
 Match length 217
 % identity 65
 NCBI Description (X95753) DAG [Antirrhinum majus]

Seq. No. 1983
 Contig ID 1313_5.R1040
 5'-most EST jC-gmle01810001g08d1
 Method BLASTN
 NCBI GI g4038468
 BLAST score 161
 E value 6.0e-85
 Match length 409
 % identity 86
 NCBI Description Porteresia coarctata histone H3 mRNA, complete cds

Seq. No. 1984
 Contig ID 1314_1.R1040
 5'-most EST crh700852056.h1

BLAST score 105
 E value 1.0e-51
 Match length 240
 % identity 86
 NCBI Description M.sativa MMK4 mRNA for protein kinase

Seq. No. 1997
 Contig ID 1331_8.R1040
 5'-most EST LIB3170-061-Q1-J1-F1

Seq. No. 1998
 Contig ID 1331_9.R1040
 5'-most EST LIB3051-031-Q1-K1-C11
 Method BLASTN
 NCBI GI g1667372
 BLAST score 75
 E value 8.0e-34
 Match length 91
 % identity 96
 NCBI Description M.sativa MMK4 mRNA for protein kinase

Seq. No. 1999
 Contig ID 1331_11.R1040
 5'-most EST jC-gmro02910024c08a1
 Method BLASTN
 NCBI GI g1667372
 BLAST score 133
 E value 2.0e-68
 Match length 293
 % identity 86
 NCBI Description M.sativa MMK4 mRNA for protein kinase

Seq. No. 2000
 Contig ID 1331_12.R1040
 5'-most EST LIB3051-064-Q1-K1-F1

Seq. No. 2001
 Contig ID 1331_14.R1040
 5'-most EST jC-gmst02400060f10d1

Seq. No. 2002
 Contig ID 1331_15.R1040
 5'-most EST uC-gmropic063f01b1
 Method BLASTN
 NCBI GI g1667372
 BLAST score 95
 E value 7.0e-46
 Match length 250
 % identity 83
 NCBI Description M.sativa MMK4 mRNA for protein kinase

Seq. No. 2003
 Contig ID 1331_17.R1040
 5'-most EST LIB3170-051-Q1-J1-B10

Seq. No. 2004
 Contig ID 1331_22.R1040

09654016 101000

Seq. No.	2006
Contig ID	1331_24.R1040
5'-most EST	LIB3051-054-Q1-K2-B8

```
Seq. No.          2008
Contig ID         1338_1.R1040
5'-most EST      LIB3109-034-Q1-K1-C2
Method            BLASTN
NCBI GI           g3025860
BLAST score       35
E value           7.0e-10
Match length      111
% identity        92
NCBI Description  Medicago truncatula Mt4 genomic sequence
```

```
Seq. No.      2009
Contig ID     1341_1.R1040
5'-most EST   LIB3167-078-P1-K2-B7
Method        BLASTX
NCBI GI       g3914472
BLAST score    526
E value       2.0e-53
Match length   129
% identity     78
NCBI Description PHOTOSYSTEM II 10 K $\Delta$  POLYPEPTIDE PRECURSOR (PII10)
                >gi_322764_pir_S32021 photosystem II 10K protein - common
                tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana
                tabacum]
```

```
Seq. No.          2010
Contig ID         1341_2.R1040
5'-most EST      fde700876719.h1
Method            BLASTX
NCBI GI           g3914472
BLAST score       318
E value           2.0e-29
Match length      99
% identity        67
NCBI Description  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)
                  >gi 322764 pir S32021 photosystem II 10K protein - common
```

tobacco >gi_22669_emb_CAA49693_ (X70088) NtpIII10 [Nicotiana tabacum]

Seq. No. 2011
 Contig ID 1341_3.R1040
 5'-most EST LIB3093-012-Q1-K1-A8
 Method BLASTX
 NCBI GI g3914472
 BLAST score 272
 E value 6.0e-24
 Match length 126
 % identity 41
 NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)
 >gi_322764_pir_S32021 photosystem II 10K protein - common
 tobacco >gi_22669_emb_CAA49693_ (X70088) NtpIII10 [Nicotiana tabacum]

Seq. No. 2012
 Contig ID 1341_5.R1040
 5'-most EST uC-gmropic043e05b1
 Method BLASTN
 NCBI GI g1418983
 BLAST score 59
 E value 2.0e-24
 Match length 167
 % identity 84
 NCBI Description L.esculentum mRNA for photosystem II 10 kD protein

Seq. No. 2013
 Contig ID 1341_6.R1040
 5'-most EST LIB3040-027-Q1-E1-A2
 Method BLASTX
 NCBI GI g3914472
 BLAST score 391
 E value 1.0e-37
 Match length 89
 % identity 83
 NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)
 >gi_322764_pir_S32021 photosystem II 10K protein - common
 tobacco >gi_22669_emb_CAA49693_ (X70088) NtpIII10 [Nicotiana tabacum]

Seq. No. 2014
 Contig ID 1343_1.R1040
 5'-most EST LIB3139-052-P1-N1-F3
 Method BLASTX
 NCBI GI g2982303
 BLAST score 1215
 E value 1.0e-133
 Match length 267
 % identity 84
 NCBI Description (AF051236) hypothetical protein [Picea mariana]

Seq. No. 2015
 Contig ID 1343_2.R1040
 5'-most EST jC-gmle01810024e10d1
 Method BLASTX

NCBI GI	g4204315
BLAST score	801
E value	0.0e+00
Match length	717
% identity	50
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]
Seq. No.	2016
Contig ID	1343_4.R1040
5'-most EST	bth700846788.h1
Method	BLASTX
NCBI GI	g4128133
BLAST score	377
E value	5.0e-36
Match length	131
% identity	55
NCBI Description	(AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]
Seq. No.	2017
Contig ID	1343_5.R1040
5'-most EST	LIB3106-028-Q1-K1-H1
Method	BLASTX
NCBI GI	g3337435
BLAST score	158
E value	3.0e-23
Match length	172
% identity	32
NCBI Description	(AF060198) PsbY precursor; putative photosytem II peptide [Spinacia oleracea]
Seq. No.	2018
Contig ID	1343_7.R1040
5'-most EST	LIB3073-016-Q1-K1-C7
Method	BLASTX
NCBI GI	g3337435
BLAST score	265
E value	4.0e-23
Match length	131
% identity	38
NCBI Description	(AF060198) PsbY precursor; putative photosytem II peptide [Spinacia oleracea]
Seq. No.	2019
Contig ID	1343_11.R1040
5'-most EST	vzy700753763.h1
Seq. No.	2020
Contig ID	1343_12.R1040
5'-most EST	jC-gmle01810075b12a1
Method	BLASTX
NCBI GI	g3337435
BLAST score	189
E value	3.0e-14
Match length	56
% identity	43
NCBI Description	(AF060198) PsbY precursor; putative photosytem II peptide [Spinacia oleracea]

Seq. No. 2021
Contig ID 1343_14.R1040
5'-most EST taw700656383.h1

Seq. No. 2022
Contig ID 1343_15.R1040
5'-most EST zhf700963687.h1

Seq. No. 2023
Contig ID 1343_16.R1040
5'-most EST hrw701057276.h1

Seq. No. 2024
Contig ID 1344_1.R1040
5'-most EST LIB3051-026-Q1-K1-B3
Method BLASTX
NCBI GI g3747050
BLAST score 411
E value 5.0e-40
Match length 101
% identity 80
NCBI Description (AF093540) ribosomal protein L26 [Zea mays]

Seq. No. 2025
Contig ID 1344_2.R1040
5'-most EST LIB3106-093-Q1-K1-H2
Method BLASTN
NCBI GI g3747049
BLAST score 92
E value 5.0e-44
Match length 224
% identity 85
NCBI Description Zea mays ribosomal protein L26 mRNA, partial cds

Seq. No. 2026
Contig ID 1345_1.R1040
5'-most EST kl1701215182.h1
Method BLASTX
NCBI GI g4337178
BLAST score 707
E value 1.0e-74
Match length 155
% identity 85
NCBI Description (AC006416) T31J12.5 [Arabidopsis thaliana]

Seq. No. 2027
Contig ID 1345_2.R1040
5'-most EST uC-gmrominsoy265e12b1
Method BLASTX
NCBI GI g4337178
BLAST score 348
E value 6.0e-33
Match length 76
% identity 88
NCBI Description (AC006416) T31J12.5 [Arabidopsis thaliana]

Seq. No. 2028
 Contig ID 1348 1.R1040
 5'-most EST LIB3027-006-Q1-B1-A10
 Method BLASTN
 NCBI GI g3241920
 BLAST score 41
 E value 1.0e-13
 Match length 81
 % identity 88
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAE1, complete sequence [Arabidopsis thaliana]

Seq. No. 2029
 Contig ID 1350 1.R1040
 5'-most EST gsv701052806.h1
 Method BLASTX
 NCBI GI g4539307
 BLAST score 229
 E value 1.0e-18
 Match length 62
 % identity 71
 NCBI Description (AL049480) putative acidic ribosomal protein [Arabidopsis thaliana]

Seq. No. 2030
 Contig ID 1350 2.R1040
 5'-most EST g4397512
 Method BLASTX
 NCBI GI g4539307
 BLAST score 260
 E value 2.0e-22
 Match length 68
 % identity 75
 NCBI Description (AL049480) putative acidic ribosomal protein [Arabidopsis thaliana]

Seq. No. 2031
 Contig ID 1352 1.R1040
 5'-most EST jsh701063775.h1
 Method BLASTN
 NCBI GI g555973
 BLAST score 269
 E value 1.0e-149
 Match length 692
 % identity 85
 NCBI Description Pisum sativum 14-3-3-like protein mRNA, complete cds

Seq. No. 2032
 Contig ID 1352 2.R1040
 5'-most EST LIB3093-015-Q1-K1-C6
 Method BLASTN
 NCBI GI g555973
 BLAST score 313
 E value 1.0e-175
 Match length 786
 % identity 86
 NCBI Description Pisum sativum 14-3-3-like protein mRNA, complete cds

Seq. No. 2033
 Contig ID 1352_3.R1040
 5'-most EST LIB3167-004-P1-K1-A2
 Method BLASTN
 NCBI GI g555973
 BLAST score 224
 E value 1.0e-122
 Match length 706
 % identity 86
 NCBI Description Pisum sativum 14-3-3-like protein mRNA, complete cds

Seq. No. 2034
 Contig ID 1352_4.R1040
 5'-most EST zhf700963441.h1
 Method BLASTN
 NCBI GI g2921511
 BLAST score 70
 E value 4.0e-31
 Match length 146
 % identity 87
 NCBI Description Fritillaria agrestis GF14 protein (GRF) mRNA, complete cds

Seq. No. 2035
 Contig ID 1352_5.R1040
 5'-most EST LIB3055-011-Q1-N1-A8
 Method BLASTX
 NCBI GI g4544412
 BLAST score 303
 E value 2.0e-27
 Match length 82
 % identity 70
 NCBI Description (AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No. 2036
 Contig ID 1352_6.R1040
 5'-most EST LIB3139-084-P1-N1-A1
 Method BLASTN
 NCBI GI g555973
 BLAST score 56
 E value 1.0e-22
 Match length 353
 % identity 86
 NCBI Description Pisum sativum 14-3-3-like protein mRNA, complete cds

Seq. No. 2037
 Contig ID 1352_9.R1040
 5'-most EST g4396272
 Method BLASTX
 NCBI GI g4544412
 BLAST score 464
 E value 2.0e-46
 Match length 111
 % identity 75
 NCBI Description (AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No. 2038

Seq. No. 2043
 Contig ID 1355_4.R1040
 5'-most EST LIB3049-054-Q1-E1-B4
 Method BLASTX
 NCBI GI g1174162
 BLAST score 534
 E value 1.0e-54
 Match length 105
 % identity 90
 NCBI Description (U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No. 2044
 Contig ID 1355_6.R1040
 5'-most EST uC-gmrominsoy050f02b1

Seq. No. 2045
 Contig ID 1356_1.R1040
 5'-most EST LIB3072-060-Q1-K1-G5
 Method BLASTX
 NCBI GI g2832620
 BLAST score 562
 E value 8.0e-58
 Match length 175
 % identity 61
 NCBI Description (AL021711) hypothetical protein [Arabidopsis thaliana]

Seq. No. 2046
 Contig ID 1363_1.R1040
 5'-most EST LIB3139-068-P1-N1-D3
 Method BLASTX
 NCBI GI g4432844
 BLAST score 394
 E value 7.0e-38
 Match length 207
 % identity 41
 NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 2047
 Contig ID 1363_2.R1040
 5'-most EST sat701010967.h1

Seq. No. 2048
 Contig ID 1364_1.R1040
 5'-most EST fde700876671.h1
 Method BLASTX
 NCBI GI g4033838
 BLAST score 1220
 E value 1.0e-134
 Match length 410
 % identity 61
 NCBI Description (Y18550) sigma-like factor [Arabidopsis thaliana]

Seq. No. 2049
 Contig ID 1364_2.R1040
 5'-most EST jC-gmf102220132ab11d1

Method BLASTX
 NCBI GI g4033838
 BLAST score 430
 E value 2.0e-42
 Match length 101
 % identity 84
 NCBI Description (Y18550) sigma-like factor [Arabidopsis thaliana]

Seq. No. 2050
 Contig ID 1364_3.R1040
 5'-most EST jC-gmro02910008c07a1
 Method BLASTX
 NCBI GI g4033838
 BLAST score 317
 E value 4.0e-29
 Match length 185
 % identity 45
 NCBI Description (Y18550) sigma-like factor [Arabidopsis thaliana]

Seq. No. 2051
 Contig ID 1364_4.R1040
 5'-most EST jC-gmle01810004d04a1
 Method BLASTX
 NCBI GI g4033838
 BLAST score 226
 E value 2.0e-18
 Match length 120
 % identity 41
 NCBI Description (Y18550) sigma-like factor [Arabidopsis thaliana]

Seq. No. 2052
 Contig ID 1367_1.R1040
 5'-most EST LIB3027-005-Q1-B1-G11
 Method BLASTX
 NCBI GI g2225877
 BLAST score 211
 E value 1.0e-16
 Match length 76
 % identity 53
 NCBI Description (AB002406) TIP49 [Rattus norvegicus] >gi_4106528 (AF100694)
 Pontin52 [Mus musculus] >gi_4521276_dbj_BAA76313.1_
 (AB001581) DNA helicase p50 [Rattus norvegicus]

Seq. No. 2053
 Contig ID 1368_1.R1040
 5'-most EST wvk700680956.h1
 Method BLASTX
 NCBI GI g2191191
 BLAST score 513
 E value 7.0e-52
 Match length 166
 % identity 61
 NCBI Description (AF007271) A_TM021B04.14 gene product [Arabidopsis thaliana]

Seq. No. 2054
 Contig ID 1372_1.R1040

5'-most EST zsg701123846.h1
 Method BLASTX
 NCBI GI g3250679
 BLAST score 447
 E value 4.0e-44
 Match length 236
 % identity 44
 NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 2055
 Contig ID 1375_1.R1040
 5'-most EST hyd700730420.h1
 Method BLASTX
 NCBI GI g3334299
 BLAST score 1049
 E value 1.0e-114
 Match length 219
 % identity 94
 NCBI Description PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE COMPLEX ALPHA SUBUNIT) >gi_2315211_emb_CAA74725_ (Y14339) proteasome alpha subunit [Lycopersicon esculentum]

Seq. No. 2056
 Contig ID 1376_1.R1040
 5'-most EST kl1701213854.h1
 Method BLASTX
 NCBI GI g3176874
 BLAST score 753
 E value 1.0e-132
 Match length 478
 % identity 52
 NCBI Description (AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No. 2057
 Contig ID 1377_1.R1040
 5'-most EST rca701002041.h1
 Method BLASTX
 NCBI GI g3193314
 BLAST score 906
 E value 1.0e-97
 Match length 328
 % identity 55
 NCBI Description (AF069299) contains similarity to Arabidopsis scarecrow (GB:U62798) [Arabidopsis thaliana]

Seq. No. 2058
 Contig ID 1379_1.R1040
 5'-most EST awf700843166.h1
 Method BLASTX
 NCBI GI g2270990
 BLAST score 200
 E value 3.0e-15
 Match length 116
 % identity 44
 NCBI Description (AF004807) dehydrin [Glycine max]

Seq. No. 2059
 Contig ID 1385_1.R1040
 5'-most EST LIB3050-002-Q1-E1-H4

Seq. No. 2060
 Contig ID 1386_1.R1040
 5'-most EST rca701000271.h1
 Method BLASTN
 NCBI GI g1498327
 BLAST score 272
 E value 1.0e-151
 Match length 276
 % identity 100
 NCBI Description Glycine max actin (Soy70) gene, partial cds

Seq. No. 2061
 Contig ID 1386_2.R1040
 5'-most EST trc700562963.h1
 Method BLASTX
 NCBI GI g1531672
 BLAST score 1602
 E value 0.0e+00
 Match length 377
 % identity 93
 NCBI Description (U68461) actin [Striga asiatica]

Seq. No. 2062
 Contig ID 1386_3.R1040
 5'-most EST hyd700730194.h1
 Method BLASTX
 NCBI GI g4139264
 BLAST score 1157
 E value 0.0e+00
 Match length 376
 % identity 96
 NCBI Description (AF111812) actin [Brassica napus]

Seq. No. 2063
 Contig ID 1386_4.R1040
 5'-most EST kl1701206694.h1
 Method BLASTX
 NCBI GI g1703108
 BLAST score 1856
 E value 0.0e+00
 Match length 369
 % identity 97
 NCBI Description ACTIN 2/7 >gi_2129525_pir_S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir_S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No. 2064
 Contig ID 1386_5.R1040
 5'-most EST LIB3094-054-Q1-K1-E3
 Method BLASTN
 NCBI GI g1498339

09684016-101000

BLAST score 498
 E value 0.0e+00
 Match length 1018
 % identity 95
 NCBI Description Glycine max actin (Soy118) gene, partial cds

Seq. No. 2065
 Contig ID 1386_6.R1040
 5'-most EST uC-gmrominsoy035g05b1
 Method BLASTN
 NCBI GI g1498333
 BLAST score 540
 E value 0.0e+00
 Match length 1020
 % identity 96
 NCBI Description Glycine max actin (Soy57) gene, partial cds

Seq. No. 2066
 Contig ID 1391_1.R1040
 5'-most EST sat701008458.h1
 Method BLASTX
 NCBI GI g3337356
 BLAST score 2273
 E value 0.0e+00
 Match length 476
 % identity 93
 NCBI Description (AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No. 2067
 Contig ID 1391_2.R1040
 5'-most EST asn701140282.h1
 Method BLASTX
 NCBI GI g2827544
 BLAST score 243
 E value 3.0e-20
 Match length 57
 % identity 81
 NCBI Description (AL021635) HSP associated protein like [Arabidopsis thaliana]

Seq. No. 2068
 Contig ID 1391_3.R1040
 5'-most EST LIB3170-053-Q1-J1-B12
 Method BLASTX
 NCBI GI g3337356
 BLAST score 385
 E value 5.0e-37
 Match length 76
 % identity 97
 NCBI Description (AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No. 2069
 Contig ID 1391_4.R1040
 5'-most EST jC-gmfl02220063a06a1
 Method BLASTX

NCBI GI g3337356
 BLAST score 628
 E value 1.0e-65
 Match length 126
 % identity 98
 NCBI Description (AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No. 2070
 Contig ID 1391_5.R1040
 5'-most EST jC-gmro02910040c03a1
 Method BLASTN
 NCBI GI g3766106
 BLAST score 47
 E value 3.0e-17
 Match length 135
 % identity 84
 NCBI Description Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 2071
 Contig ID 1391_6.R1040
 5'-most EST LIB3028-053-Q1-B1-G8
 Method BLASTX
 NCBI GI g3337356
 BLAST score 350
 E value 5.0e-33
 Match length 70
 % identity 97
 NCBI Description (AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No. 2072
 Contig ID 1391_8.R1040
 5'-most EST uC-gmrominsoy174e10b1

Seq. No. 2073
 Contig ID 1391_9.R1040
 5'-most EST hyd700725385.h1
 Method BLASTX
 NCBI GI g3337356
 BLAST score 210
 E value 8.0e-17
 Match length 55
 % identity 78
 NCBI Description (AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No. 2074
 Contig ID 1391_10.R1040
 5'-most EST sat701013338.h1
 Method BLASTX
 NCBI GI g2827544
 BLAST score 213
 E value 3.0e-17
 Match length 50
 % identity 82

NCBI Description (AL021635) HSP associated protein like [Arabidopsis thaliana]

Seq. No. 2075
 Contig ID 1391_11.R1040
 5'-most EST uaw700665063.h1
 Method BLASTX
 NCBI GI g2827544
 BLAST score 241
 E value 3.0e-20
 Match length 54
 % identity 87

NCBI Description (AL021635) HSP associated protein like [Arabidopsis thaliana]

Seq. No. 2076
 Contig ID 1391_18.R1040
 5'-most EST dpv701098828.h1
 Method BLASTX
 NCBI GI g3834321
 BLAST score 248
 E value 4.0e-21
 Match length 143
 % identity 50

NCBI Description (AC005679) Strong similarity to F13P17.9 gi_3337356 transport protein SEC61 alpha subunit homolog from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No. 2077
 Contig ID 1394_1.R1040
 5'-most EST LIB3028-031-Q1-B1-C9
 Method BLASTX
 NCBI GI g3355468
 BLAST score 536
 E value 1.0e-54
 Match length 123
 % identity 89

NCBI Description (AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No. 2078
 Contig ID 1394_2.R1040
 5'-most EST LIB3093-022-Q1-K1-B1
 Method BLASTX
 NCBI GI g4545262
 BLAST score 172
 E value 5.0e-12
 Match length 42
 % identity 71

NCBI Description (AF118230) metallothionein-like protein [Gossypium hirsutum]

Seq. No. 2079
 Contig ID 1394_3.R1040
 5'-most EST LIB3107-060-Q1-K1-C9
 Method BLASTN

NCBI GI g4545261
 BLAST score 40
 E value 4.0e-13
 Match length 142
 % identity 86
 NCBI Description Gossypium hirsutum metallothionein-like protein mRNA,
 complete cds

Seq. No. 2080
 Contig ID 1394 5.R1040
 5'-most EST LIB3093-052-Q1-K1-F5
 Method BLASTX
 NCBI GI g3355468
 BLAST score 186
 E value 1.0e-13
 Match length 50
 % identity 80
 NCBI Description (AC004218) putative ribosomal protein L35 [Arabidopsis
 thaliana]

Seq. No. 2081
 Contig ID 1397 1.R1040
 5'-most EST awf700836730.h1
 Method BLASTX
 NCBI GI g126078
 BLAST score 380
 E value 2.0e-73
 Match length 248
 % identity 51
 NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN D-34 (LEA D-34)
 >gi_81554_pir_S04046 embryonic abundant protein gD-34 -
 upland cotton >gi_18501_emb_CAA31594 (X13206) D-34 Lea
 protein [Gossypium hirsutum] >gi_167385 (M19389) storage
 protein [Gossypium hirsutum] >gi_226556_prf_1601521F Lea
 D-34 gene [Saguinus oedipus]

Seq. No. 2082
 Contig ID 1400 1.R1040
 5'-most EST LIB3051-088-Q1-K1-E7
 Method BLASTX
 NCBI GI g2146740
 BLAST score 435
 E value 5.0e-43
 Match length 133
 % identity 64
 NCBI Description inner mitochondrial membrane protein - Arabidopsis thaliana
 >gi_603056 (U18126) inner mitochondrial membrane protein
 [Arabidopsis thaliana]

Seq. No. 2083
 Contig ID 1401 1.R1040
 5'-most EST uC-gmflminsoy016c08b1
 Method BLASTX
 NCBI GI g4490732
 BLAST score 2599
 E value 0.0e+00
 Match length 666

E value 2.0e-19
Match length 93
% identity 53
NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 2095
Contig ID 1409_2.R1040
5'-most EST zsg701119142.h1
Method BLASTX
NCBI GI g2980760
BLAST score 226
E value 2.0e-18
Match length 58
% identity 67
NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 2096
Contig ID 1409_3.R1040
5'-most EST pcp700995525.h1
Method BLASTX
NCBI GI g421855
BLAST score 1044
E value 1.0e-114
Match length 342
% identity 61
NCBI Description alanine--tRNA ligase (EC 6.1.1.7) - Arabidopsis thaliana (fragment)

Seq. No. 2097
Contig ID 1409_5.R1040
5'-most EST LIB3092-041-Q1-K1-H8
Method BLASTX
NCBI GI g1673366
BLAST score 201
E value 2.0e-15
Match length 86
% identity 51
NCBI Description (Z22673) cytosolic tRNA-Ala synthetase [Arabidopsis thaliana]

Seq. No. 2098
Contig ID 1411_1.R1040
5'-most EST zsg701129392.h1
Method BLASTN
NCBI GI g1372965
BLAST score 387
E value 0.0e+00
Match length 832
% identity 88
NCBI Description Vicia faba CREB-like protein mRNA, complete cds

Seq. No. 2099
Contig ID 1411_2.R1040
5'-most EST uC-gmronoir037g03b1
Method BLASTN
NCBI GI g1372965
BLAST score 50

NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No. 2106
 Contig ID 1416_4.R1040
 5'-most EST pxt700941510.h1
 Method BLASTX
 NCBI GI g1350956
 BLAST score 303
 E value 2.0e-49
 Match length 117
 % identity 85

NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No. 2107
 Contig ID 1416_5.R1040
 5'-most EST kl1701215312.h1
 Method BLASTX
 NCBI GI g1350956
 BLAST score 274
 E value 3.0e-24
 Match length 74
 % identity 70

NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No. 2108
 Contig ID 1416_6.R1040
 5'-most EST taw700655032.h1
 Method BLASTX
 NCBI GI g1350956
 BLAST score 194
 E value 4.0e-15
 Match length 48
 % identity 81

NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No. 2109
 Contig ID 1418_1.R1040
 5'-most EST g4313692
 Method BLASTN
 NCBI GI g20901
 BLAST score 285
 E value 1.0e-159
 Match length 730
 % identity 85

NCBI Description Pisum sativum mRNA for manganese superoxide dismutase

Seq. No. 2110
 Contig ID 1418_2.R1040
 5'-most EST bth700849612.h1
 Method BLASTX
 NCBI GI g3287977
 BLAST score 556
 E value 3.0e-57
 Match length 127
 % identity 82

NCBI Description SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_945044 (U30841)
 manganese superoxide dismutase precursor [Pisum sativum]

Seq. No. 2111
 Contig ID 1422_1.R1040
 5'-most EST LIB3167-050-P1-K1-F9
 Method BLASTX
 NCBI GI g3776572
 BLAST score 449
 E value 2.0e-44
 Match length 171
 % identity 59
 NCBI Description (AC005388) ESTs gb_R65052, gb_AA712146, gb_H76533, gb_H76282, gb_AA650771, gb_H76287, gb_AA650887, gb_N37383, gb_Z29721 and gb_Z29722 come from this gene. [Arabidopsis thaliana]

Seq. No. 2112
 Contig ID 1424_1.R1040
 5'-most EST gsv701056551.h1
 Method BLASTX
 NCBI GI g3193303
 BLAST score 342
 E value 1.0e-31
 Match length 99
 % identity 64
 NCBI Description (AF069298) similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis thaliana]

Seq. No. 2113
 Contig ID 1425_1.R1040
 5'-most EST LIB3107-053-Q1-K1-E3
 Method BLASTX
 NCBI GI g3176690
 BLAST score 1639
 E value 0.0e+00
 Match length 377
 % identity 84
 NCBI Description (AC003671) Similar to ubiquitin ligase gb_D63905 from S. cerevisiae. EST gb_R65295 comes from this gene. [Arabidopsis thaliana]

Seq. No. 2114
 Contig ID 1425_2.R1040
 5'-most EST vwf700678792.h1
 Method BLASTX
 NCBI GI g3176690
 BLAST score 731
 E value 2.0e-77
 Match length 306
 % identity 54
 NCBI Description (AC003671) Similar to ubiquitin ligase gb_D63905 from S. cerevisiae. EST gb_R65295 comes from this gene. [Arabidopsis thaliana]

Seq. No. 2115
 Contig ID 1427_1.R1040

5'-most EST	LIB3072-056-Q1-K1-A9
Seq. No.	2116
Contig ID	1430_1.R1040
5'-most EST	ncj700985904.h1
Method	BLASTX
NCBI GI	g3928869
BLAST score	219
E value	5.0e-17
Match length	306
% identity	27
NCBI Description	(AF093420) Hsp70 binding protein HspBP1 [Homo sapiens]
Seq. No.	2117
Contig ID	1430_2.R1040
5'-most EST	LIB3027-001-Q1-B1-G7
Seq. No.	2118
Contig ID	1430_4.R1040
5'-most EST	jC-gmro02910070c02a1
Seq. No.	2119
Contig ID	1431_1.R1040
5'-most EST	LIB3109-014-Q1-K1-E7
Seq. No.	2120
Contig ID	1433_1.R1040
5'-most EST	LIB3027-003-Q1-B1-E4
Method	BLASTX
NCBI GI	g3243274
BLAST score	148
E value	2.0e-09
Match length	61
% identity	51
NCBI Description	(AF072134) TCP3 [Arabidopsis thaliana]
Seq. No.	2121
Contig ID	1433_2.R1040
5'-most EST	LIB3049-028-Q1-E1-F10
Seq. No.	2122
Contig ID	1434_1.R1040
5'-most EST	LIB3040-048-Q1-E1-F9
Method	BLASTX
NCBI GI	g2852449
BLAST score	927
E value	1.0e-167
Match length	398
% identity	77
NCBI Description	(D88207) protein kinase [Arabidopsis thaliana] >gi_2947061 (AC002521) putative protein kinase [Arabidopsis thaliana]
Seq. No.	2123
Contig ID	1434_2.R1040
5'-most EST	LIB3051-104-Q1-K1-G3
Method	BLASTX
NCBI GI	g2852449

BLAST score 887
 E value 1.0e-95
 Match length 246
 % identity 73
 NCBI Description (D88207) protein kinase [Arabidopsis thaliana] >gi_2947061
 (AC002521) putative protein kinase [Arabidopsis thaliana]

Seq. No. 2124
 Contig ID 1434_3.R1040
 5'-most EST epX701106557.h1
 Method BLASTX
 NCBI GI g2852449
 BLAST score 532
 E value 3.0e-54
 Match length 142
 % identity 75
 NCBI Description (D88207) protein kinase [Arabidopsis thaliana] >gi_2947061
 (AC002521) putative protein kinase [Arabidopsis thaliana]

Seq. No. 2125
 Contig ID 1434_4.R1040
 5'-most EST zsg701126118.h1
 Method BLASTX
 NCBI GI g2852447
 BLAST score 178
 E value 7.0e-13
 Match length 50
 % identity 68
 NCBI Description (D88206) protein kinase [Arabidopsis thaliana]

Seq. No. 2126
 Contig ID 1437_1.R1040
 5'-most EST LIB3065-027-Q1-N1-G9
 Method BLASTX
 NCBI GI g1169200
 BLAST score 195
 E value 6.0e-15
 Match length 59
 % identity 66
 NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR
 >gi_421829_pir_S33706 DNA-damage resistance protein -
 Arabidopsis thaliana >gi_166694 (M98455) [Arabidopsis
 thaliana recombination and DNA-damage resistance protein
 (DRT111) mRNA, complete cds.], gene product [Arabidopsis
 thaliana]

Seq. No. 2127
 Contig ID 1438_1.R1040
 5'-most EST zhf700963184.h1

Seq. No. 2128
 Contig ID 1438_2.R1040
 5'-most EST LIB3107-054-Q1-K1-E1

Seq. No. 2129
 Contig ID 1438_3.R1040
 5'-most EST pmv700891037.h1

Seq. No. 2143
 Contig ID 1457_3.R1040
 5'-most EST LIB3170-005-Q1-K1-F5
 Method BLASTN
 NCBI GI g1008880
 BLAST score 56
 E value 1.0e-22
 Match length 120
 % identity 87
 NCBI Description Phaseolus vulgaris eukaryotic initiation factor 5 (eIF-5) gene, complete cds

Seq. No. 2144
 Contig ID 1457_4.R1040
 5'-most EST uC-gmropic059d08b1
 Method BLASTN
 NCBI GI g1008880
 BLAST score 60
 E value 5.0e-25
 Match length 120
 % identity 88
 NCBI Description Phaseolus vulgaris eukaryotic initiation factor 5 (eIF-5) gene, complete cds

Seq. No. 2145
 Contig ID 1457_5.R1040
 5'-most EST fde700870816.h1

Seq. No. 2146
 Contig ID 1457_7.R1040
 5'-most EST jC-gmst02400073d03d1
 Method BLASTN
 NCBI GI g1008880
 BLAST score 67
 E value 3.0e-29
 Match length 178
 % identity 90
 NCBI Description Phaseolus vulgaris eukaryotic initiation factor 5 (eIF-5) gene, complete cds

Seq. No. 2147
 Contig ID 1458_1.R1040
 5'-most EST LIB3109-021-Q1-K1-A4
 Method BLASTX
 NCBI GI g1694621
 BLAST score 1838
 E value 0.0e+00
 Match length 461
 % identity 78
 NCBI Description (D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]

Seq. No. 2148
 Contig ID 1461_1.R1040
 5'-most EST smc700744304.h1
 Method BLASTX
 NCBI GI g2827552
 BLAST score 136

E value 2.0e-15
Match length 60
% identity 73
NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]

Seq. No. 2149
Contig ID 1464_1.R1040
5'-most EST jC-gmro02910001d10d1

Seq. No. 2150
Contig ID 1466_1.R1040
5'-most EST LIB3074-031-Q1-K2-E8
Method BLASTX
NCBI GI g4102634
BLAST score 255
E value 1.0e-21
Match length 48
% identity 81
NCBI Description (AF014396) Snakin-1 [Solanum tuberosum]

Seq. No. 2151
Contig ID 1466_2.R1040
5'-most EST sat701006340.h1
Method BLASTX
NCBI GI g4102634
BLAST score 255
E value 3.0e-22
Match length 48
% identity 81
NCBI Description (AF014396) Snakin-1 [Solanum tuberosum]

Seq. No. 2152
Contig ID 1469_1.R1040
5'-most EST awf700840524.h1

Seq. No. 2153
Contig ID 1469_2.R1040
5'-most EST uC-gmrominsoy244g10b1

Seq. No. 2154
Contig ID 1469_3.R1040
5'-most EST LIB3073-011-Q1-K1-G3

Seq. No. 2155
Contig ID 1470_1.R1040
5'-most EST xpa700797086.h1
Method BLASTX
NCBI GI g3478637
BLAST score 355
E value 2.0e-33
Match length 181
% identity 40
NCBI Description (AC005546) R29425_1 [Homo sapiens]

Seq. No. 2156
Contig ID 1473_1.R1040
5'-most EST LIB3027-005-Q1-B1-F8

Seq. No.	2157
Contig ID	1477_1.R1040
5'-most EST	ncj700983761.h1
Method	BLASTX
NCBI GI	g4454009
BLAST score	210
E value	2.0e-16
Match length	102
% identity	43
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]
Seq. No.	2158
Contig ID	1477_2.R1040
5'-most EST	uC-gmrominsoy226a03b1
Method	BLASTX
NCBI GI	g2252829
BLAST score	165
E value	3.0e-11
Match length	97
% identity	38
NCBI Description	(AF013293) A_IG005I10.6 gene product [Arabidopsis thaliana]
Seq. No.	2159
Contig ID	1477_3.R1040
5'-most EST	kl1701214748.h1
Seq. No.	2160
Contig ID	1477_4.R1040
5'-most EST	LIB3051-017-Q1-E1-G5
Seq. No.	2161
Contig ID	1479_1.R1040
5'-most EST	jC-gmle01810041h06a1
Method	BLASTX
NCBI GI	g2459448
BLAST score	692
E value	1.0e-105
Match length	311
% identity	59
NCBI Description	(AC002332) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]
Seq. No.	2162
Contig ID	1479_2.R1040
5'-most EST	LIB3106-057-Q1-K1-B9
Method	BLASTX
NCBI GI	g2459446
BLAST score	322
E value	9.0e-30
Match length	145
% identity	60
NCBI Description	(AC002332) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]
Seq. No.	2163
Contig ID	1480_1.R1040

5'-most EST LIB3040-028-Q1-E1-H7
 Method BLASTX
 NCBI GI g4539408
 BLAST score 389
 E value 4.0e-37
 Match length 221
 % identity 46
 NCBI Description (AL049524) putative alpha NAC [Arabidopsis thaliana]

Seq. No. 2164
 Contig ID 1480_2.R1040
 5'-most EST LIB3049-054-Q1-E1-F10
 Method BLASTX
 NCBI GI g4539408
 BLAST score 287
 E value 1.0e-25
 Match length 84
 % identity 69
 NCBI Description (AL049524) putative alpha NAC [Arabidopsis thaliana]

Seq. No. 2165
 Contig ID 1480_3.R1040
 5'-most EST LIB3040-014-Q1-E1-H10

Seq. No. 2166
 Contig ID 1480_4.R1040
 5'-most EST crh700853176.h1
 Method BLASTX
 NCBI GI g4115918
 BLAST score 200
 E value 2.0e-15
 Match length 93
 % identity 49
 NCBI Description (AF118222) similar to nascent polypeptide associated complex alpha chain [Arabidopsis thaliana]

Seq. No. 2167
 Contig ID 1480_7.R1040
 5'-most EST fua701039265.h1

Seq. No. 2168
 Contig ID 1480_8.R1040
 5'-most EST kl1701212553.h1

Seq. No. 2169
 Contig ID 1481_1.R1040
 5'-most EST txt700736308.h1
 Method BLASTX
 NCBI GI g1085622
 BLAST score 1427
 E value 1.0e-175
 Match length 378
 % identity 77
 NCBI Description alcohol dehydrogenase (EC 1.1.1.1) 1F - Phaseolus acutifolius >gi_452769_emb_CAA80691_(Z23170) alcohol dehydrogenase-1F [Phaseolus acutifolius]

BLAST score 160
E value 3.0e-10
Match length 73
% identity 48
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No. 2177
Contig ID 1489_4.R1040
5'-most EST LIB3093-038-Q1-K1-E4

Seq. No. 2178
Contig ID 1489_6.R1040
5'-most EST jC-gmfl02220068b09d1

Seq. No. 2179
Contig ID 1492_1.R1040
5'-most EST LIB3040-030-Q1-E1-A10
Method BLASTX
NCBI GI g3367515
BLAST score 912
E value 1.0e-139
Match length 363
% identity 71
NCBI Description (AC004392) Similar to
glucose-6-phosphate/phosphate-translocator (GPT)
gb_AF020814 from Pisum sativum. [Arabidopsis thaliana]

Seq. No. 2180
Contig ID 1493_1.R1040
5'-most EST LIB3027-002-Q1-B1-B8
Method BLASTX
NCBI GI g4467147
BLAST score 199
E value 2.0e-15
Match length 110
% identity 51
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 2181
Contig ID 1493_2.R1040
5'-most EST sat701013373.h1
Method BLASTX
NCBI GI g4467147
BLAST score 307
E value 5.0e-34
Match length 159
% identity 53
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 2182
Contig ID 1495_1.R1040
5'-most EST crh700850359.h1
Method BLASTX
NCBI GI g2281631
BLAST score 317
E value 1.0e-28
Match length 201

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% identity 46
NCBI Description (AF003096) AP2 domain containing protein RAP2.3
[Arabidopsis thaliana]

Seq. No. 2183
Contig ID 1495_2.R1040
5'-most EST awf700842114.h1
Method BLASTX
NCBI GI g2281631
BLAST score 305
E value 3.0e-27
Match length 140

% identity 52
NCBI Description (AF003096) AP2 domain containing protein RAP2.3
[Arabidopsis thaliana]

Seq. No. 2184
Contig ID 1495_3.R1040
5'-most EST LIB3170-067-Q1-K1-B1
Method BLASTX
NCBI GI g2281631
BLAST score 304
E value 2.0e-27
Match length 83

% identity 73
NCBI Description (AF003096) AP2 domain containing protein RAP2.3
[Arabidopsis thaliana]

Seq. No. 2185
Contig ID 1497_1.R1040
5'-most EST smc700749770.h1

Seq. No. 2186
Contig ID 1498_1.R1040
5'-most EST asj700967459.h1

Seq. No. 2187
Contig ID 1499_1.R1040
5'-most EST uxk700669903.h1

Seq. No. 2188
Contig ID 1500_1.R1040
5'-most EST LIB3028-048-Q1-B1-A3
Method BLASTX
NCBI GI g2213538
BLAST score 191
E value 2.0e-14
Match length 155
% identity 43

NCBI Description (X98740) DNA-binding protein PD2 [Pisum sativum]

Seq. No. 2189
Contig ID 1501_1.R1040
5'-most EST LIB3072-028-Q1-E1-B4
Method BLASTX
NCBI GI g1531756
BLAST score 178

E value 9.0e-13
 Match length 70
 % identity 46
 NCBI Description (X82413) proline-rich-like protein [Asparagus officinalis]

Seq. No. 2190
 Contig ID 1502_1.R1040
 5'-most EST k11701204348.h2
 Method BLASTX
 NCBI GI g3128174
 BLAST score 251
 E value 2.0e-21
 Match length 93
 % identity 59
 NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 2191
 Contig ID 1503_1.R1040
 5'-most EST fua701041667.h1
 Method BLASTX
 NCBI GI g3850581
 BLAST score 648
 E value 2.0e-70
 Match length 185
 % identity 68
 NCBI Description (AC005278) EST gb_N96383 comes from this gene. [Arabidopsis thaliana]

Seq. No. 2192
 Contig ID 1507_1.R1040
 5'-most EST LIB3028-053-Q1-B1-E2

Seq. No. 2193
 Contig ID 1510_1.R1040
 5'-most EST LIB3049-030-Q1-E1-D6
 Method BLASTX
 NCBI GI g266743
 BLAST score 2213
 E value 0.0e+00
 Match length 477
 % identity 87
 NCBI Description PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) /
 DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE
 (GLYCOSYLATION SITE-BINDING CHAIN) (GSBP)
 >gi_68467_pir__ISAASS protein disulfide-isomerase (EC
 5.3.4.1) precursor (clone L1) - alfalfa
 >gi_19654_emb_CAA77575_(Z11499) protein disulfide
 isomerase [Medicago sativa]

Seq. No. 2194
 Contig ID 1510_2.R1040
 5'-most EST ncj700980254.h1
 Method BLASTN
 NCBI GI g166417
 BLAST score 97
 E value 5.0e-47
 Match length 141

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Seq. No. 2200
 Contig ID 1519_1.R1040
 5'-most EST uC-gmropic058g03b1
 Method BLASTX
 NCBI GI g3915847
 BLAST score 898
 E value 6.0e-97
 Match length 180
 % identity 94
 NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative
 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No. 2201
 Contig ID 1519_2.R1040
 5'-most EST uC-gmronoir034a10b1
 Method BLASTX
 NCBI GI g3915847
 BLAST score 1063
 E value 1.0e-116
 Match length 219
 % identity 92
 NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative
 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No. 2202
 Contig ID 1519_3.R1040
 5'-most EST uC-gmrominsoy315d11b1
 Method BLASTX
 NCBI GI g3915847
 BLAST score 474
 E value 2.0e-47
 Match length 103
 % identity 89
 NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative
 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No. 2203
 Contig ID 1519_4.R1040
 5'-most EST jC-gmst02400009e05d1
 Method BLASTX
 NCBI GI g3915847
 BLAST score 184
 E value 2.0e-13
 Match length 53
 % identity 66
 NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative
 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No. 2204
 Contig ID 1519_5.R1040
 5'-most EST LIB3106-062-Q1-K1-D6
 Method BLASTX
 NCBI GI g3915847
 BLAST score 295
 E value 1.0e-26
 Match length 67

Seq. No. 2215
 Contig ID 1529_10.R1040
 5'-most EST jC-gmst02400078b01d1
 Method BLASTX
 NCBI GI g4538963
 BLAST score 349
 E value 7.0e-33
 Match length 80
 % identity 88
 NCBI Description (AL049488) chlorophyll a/b-binding protein-like
 [Arabidopsis thaliana]

Seq. No. 2216
 Contig ID 1529_11.R1040
 5'-most EST ssr700556044.h1
 Method BLASTN
 NCBI GI g1644288
 BLAST score 60
 E value 5.0e-25
 Match length 120
 % identity 88
 NCBI Description B.juncea mRNA for chlorophyll a/b-binding protein

Seq. No. 2217
 Contig ID 1529_12.R1040
 5'-most EST jC-gmst02400023f02d1

Seq. No. 2218
 Contig ID 1529_13.R1040
 5'-most EST LIB3106-093-Q1-K1-A11
 Method BLASTX
 NCBI GI g100200
 BLAST score 514
 E value 3.0e-52
 Match length 114
 % identity 63
 NCBI Description chlorophyll a/b-binding protein type I precursor - tomato

Seq. No. 2219
 Contig ID 1530_1.R1040
 5'-most EST jC-gmle01810041e09a1
 Method BLASTX
 NCBI GI g2407800
 BLAST score 506
 E value 4.0e-51
 Match length 110
 % identity 92
 NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No. 2220
 Contig ID 1538_1.R1040
 5'-most EST LIB3073-019-Q1-K1-G11
 Method BLASTX
 NCBI GI g3935169
 BLAST score 238
 E value 8.0e-20
 Match length 68

% identity 72
 NCBI Description (AC004557) F17L21.12 [Arabidopsis thaliana]

Seq. No. 2221
 Contig ID 1538_2.R1040
 5'-most EST jC-gmle01810020g02d1
 Method BLASTX
 NCBI GI g2739382
 BLAST score 357
 E value 2.0e-33
 Match length 205
 % identity 47
 NCBI Description (AC002505) myosin heavy chain-like protein [Arabidopsis thaliana]

Seq. No. 2222
 Contig ID 1538_3.R1040
 5'-most EST bth700845402.h1
 Method BLASTN
 NCBI GI g3228389
 BLAST score 42
 E value 3.0e-14
 Match length 102
 % identity 43
 NCBI Description Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No. 2223
 Contig ID 1541_1.R1040
 5'-most EST LIB3106-102-Q1-K1-D12
 Method BLASTX
 NCBI GI g2677830
 BLAST score 772
 E value 3.0e-82
 Match length 166
 % identity 90
 NCBI Description (U93168) ribosomal protein L12 [Prunus armeniaca]

Seq. No. 2224
 Contig ID 1541_2.R1040
 5'-most EST jC-gmro02910008a06d1
 Method BLASTX
 NCBI GI g4371282
 BLAST score 236
 E value 9.0e-20
 Match length 52
 % identity 81
 NCBI Description (AC006260) putative 60S ribosomal protein L12 [Arabidopsis thaliana]

Seq. No. 2225
 Contig ID 1543_1.R1040
 5'-most EST LIB3027-003-Q1-B1-C7

Seq. No. 2226
 Contig ID 1548_1.R1040
 5'-most EST LIB3139-004-P1-N1-C7

NCBI Description (AF097938) cytosolic phosphoglucomutase [Populus tremula x Populus tremuloides]

Seq. No. 2231
Contig ID 1562_3.R1040
5'-most EST LIB3139-039-P1-N1-B9
Method BLASTN
NCBI GI g4234940
BLAST score 168
E value 2.0e-89
Match length 491
% identity 84

NCBI Description Populus tremula x Populus tremuloides cytosolic phosphoglucomutase (pgm) mRNA, complete cds

Seq. No. 2232
Contig ID 1563_1.R1040
5'-most EST sat701003565.h1
Method BLASTX
NCBI GI g1353352
BLAST score 1572
E value 1.0e-175
Match length 462
% identity 64

NCBI Description (U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No. 2233
Contig ID 1563_2.R1040
5'-most EST fC-gmle7000743719a1
Method BLASTX
NCBI GI g1353352
BLAST score 401
E value 6.0e-39
Match length 104
% identity 72

NCBI Description (U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No. 2234
Contig ID 1563_3.R1040
5'-most EST LIB3073-025-Q1-K1-B2

Seq. No. 2235
Contig ID 1563_4.R1040
5'-most EST trc700564493.h1
Method BLASTX
NCBI GI g1353352
BLAST score 494
E value 1.0e-49
Match length 146
% identity 68

NCBI Description (U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No. 2236
Contig ID 1563_8.R1040

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Contig ID 1572_6.R1040
5'-most EST LIB3138-015-Q1-N2-D10
Method BLASTN
NCBI GI g951322
BLAST score 90
E value 7.0e-43
Match length 130
% identity 92
NCBI Description Vigna radiata pyrophosphatase mRNA, complete cds

Seq. No. 2249
Contig ID 1572_7.R1040
5'-most EST uaw700664346.h1
Method BLASTX
NCBI GI g4249662
BLAST score 606
E value 4.0e-63
Match length 134
% identity 88
NCBI Description (AF089810) Altered Response to Gravity [Arabidopsis thaliana]

Seq. No. 2250
Contig ID 1572_8.R1040
5'-most EST uc-gmronoir002d10b1
Method BLASTN
NCBI GI g2653445
BLAST score 182
E value 6.0e-98
Match length 238
% identity 94
NCBI Description Vigna radiata mRNA for proton pyrophosphatase, complete cds

Seq. No. 2251
Contig ID 1572_10.R1040
5'-most EST g5057881
Method BLASTN
NCBI GI g2653445
BLAST score 206
E value 1.0e-112
Match length 510
% identity 89
NCBI Description Vigna radiata mRNA for proton pyrophosphatase, complete cds

Seq. No. 2252
Contig ID 1572_12.R1040
5'-most EST LIB3139-006-P1-N1-G12
Method BLASTN
NCBI GI g2653445
BLAST score 115
E value 7.0e-58
Match length 267
% identity 87
NCBI Description Vigna radiata mRNA for proton pyrophosphatase, complete cds

Seq. No. 2253
Contig ID 1572_14.R1040

NCBI GI g4218169
 BLAST score 395
 E value 4.0e-38
 Match length 120
 % identity 69
 NCBI Description (AJ009724) MADs-box protein, GDEF1 [Gerbera hybrida]

Seq. No. 2259
 Contig ID 1576_2.R1040
 5'-most EST kl1701207013.h1
 Method BLASTX
 NCBI GI g4218169
 BLAST score 413
 E value 1.0e-40
 Match length 105
 % identity 77
 NCBI Description (AJ009724) MADs-box protein, GDEF1 [Gerbera hybrida]

Seq. No. 2260
 Contig ID 1577_1.R1040
 5'-most EST LIB3170-048-Q1-J1-B7
 Method BLASTX
 NCBI GI g1729860
 BLAST score 2053
 E value 0.0e+00
 Match length 423
 % identity 95
 NCBI Description 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) (MG(2+)-DEPENDENT ATPASE 1) (LEMA-1) >gi_1362099_pir_S56672 probable 26S proteinase chain MA-1 - tomato >gi_732815_emb_CAA52445_ (X74426) Mg-dependent ATPase 1 [Lycopersicon esculentum]

Seq. No. 2261
 Contig ID 1577_2.R1040
 5'-most EST LIB3092-062-Q1-K1-A4
 Method BLASTX
 NCBI GI g1777386
 BLAST score 853
 E value 2.0e-91
 Match length 369
 % identity 50
 NCBI Description (U39301) caffeic acid O-methyltransferase [Pinus taeda]

Seq. No. 2262
 Contig ID 1577_3.R1040
 5'-most EST cks700764831.h1
 Method BLASTX
 NCBI GI g1729860
 BLAST score 527
 E value 9.0e-54
 Match length 118
 % identity 87
 NCBI Description 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) (MG(2+)-DEPENDENT ATPASE 1) (LEMA-1) >gi_1362099_pir_S56672 probable 26S proteinase chain MA-1 - tomato >gi_732815_emb_CAA52445_ (X74426)

Mg-dependent ATPase 1 [Lycopersicon esculentum]

Seq. No. 2263
 Contig ID 1577_4.R1040
 5'-most EST jC-gmfl02220060e09a1
 Method BLASTX
 NCBI GI g3024434
 BLAST score 470
 E value 8.0e-70
 Match length 167
 % identity 74
 NCBI Description 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) >gi_2564337_dbj_BAA22951_ (D88663) Tat binding protein 1 [Brassica rapa]

Seq. No. 2264
 Contig ID 1577_5.R1040
 5'-most EST zhf700960240.h1

Seq. No. 2265
 Contig ID 1577_7.R1040
 5'-most EST LIB3028-031-Q1-B1-B9
 Method BLASTX
 NCBI GI g1777386
 BLAST score 171
 E value 6.0e-12
 Match length 52
 % identity 60
 NCBI Description (U39301) caffeic acid O-methyltransferase [Pinus taeda]

Seq. No. 2266
 Contig ID 1577_8.R1040
 5'-most EST g4305637
 Method BLASTX
 NCBI GI g3024434
 BLAST score 302
 E value 2.0e-51
 Match length 126
 % identity 93
 NCBI Description 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) >gi_2564337_dbj_BAA22951_ (D88663) Tat binding protein 1 [Brassica rapa]

Seq. No. 2267
 Contig ID 1579_3.R1040
 5'-most EST jC-gmfl02220148g09a1
 Method BLASTN
 NCBI GI g1870205
 BLAST score 265
 E value 1.0e-147
 Match length 576
 % identity 86
 NCBI Description Medicago sativa (clone nmh7) MADS-box protein mRNA, complete cds

Seq. No. 2268
 Contig ID 1580_1.R1040

5'-most EST LIB3107-052-Q1-K1-B8
 Method BLASTX
 NCBI GI g2129933
 BLAST score 691
 E value 5.0e-73
 Match length 131
 % identity 95
 NCBI Description myb-related transcription factor TMH27 - tomato
 >gi_1167484_emb_CAA64614_ (X95296) transcription factor
 [Lycopersicon esculentum]

Seq. No. 2269
 Contig ID 1580_2.R1040
 5'-most EST hyd700730584.h1
 Method BLASTX
 NCBI GI g82308
 BLAST score 412
 E value 3.0e-40
 Match length 120
 % identity 77
 NCBI Description myb protein 308 - garden snapdragon

Seq. No. 2270
 Contig ID 1582_1.R1040
 5'-most EST leu701152088.h1
 Method BLASTX
 NCBI GI g4105772
 BLAST score 301
 E value 2.0e-27
 Match length 67
 % identity 39
 NCBI Description (AF049917) PGP9B [Petunia x hybrida]

Seq. No. 2271
 Contig ID 1584_1.R1040
 5'-most EST wrg700786265.h2
 Method BLASTX
 NCBI GI g399024
 BLAST score 1708
 E value 0.0e+00
 Match length 355
 % identity 93
 NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE 1, CHLOROPLAST PRECURSOR
 >gi_322710_pir_S29047 fructose-bisphosphate aldolase (EC
 4.1.2.13) precursor, chloroplast - garden pea (fragment)
 >gi_169037 (M97476) aldolase [Pisum sativum]

Seq. No. 2272
 Contig ID 1584_2.R1040
 5'-most EST LIB3107-016-Q1-K1-C2
 Method BLASTN
 NCBI GI g169036
 BLAST score 189
 E value 1.0e-102
 Match length 369
 % identity 88
 NCBI Description Pisum sativum L. aldolase gene, 3' end cds

09684016.101000

Seq. No. 2273
Contig ID 1584_3.R1040
5'-most EST fde700877186.h1
Method BLASTN
NCBI GI g169038
BLAST score 238
E value 1.0e-131
Match length 495
% identity 89
NCBI Description Pisum sativum L. aldolase gene, 3' end cds

Seq. No. 2274
Contig ID 1584_6.R1040
5'-most EST LIB3138-096-Q1-N1-B6
Method BLASTN
NCBI GI g169036
BLAST score 240
E value 1.0e-132
Match length 420
% identity 90
NCBI Description Pisum sativum L. aldolase gene, 3' end cds

Seq. No. 2275
Contig ID 1586_1.R1040
5'-most EST LIB3106-057-Q1-K1-D2
Method BLASTX
NCBI GI g4033424
BLAST score 889
E value 8.0e-96
Match length 208
% identity 82
NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic
pyrophosphatase [Zea mays]

Seq. No. 2276
Contig ID 1588_1.R1040
5'-most EST pmv700888137.h1
Method BLASTX
NCBI GI g4105772
BLAST score 818
E value 2.0e-87
Match length 183
% identity 54
NCBI Description (AF049917) PGP9B [Petunia x hybrida]

Seq. No. 2277
Contig ID 1588_2.R1040
5'-most EST LIB3106-005-Q1-K1-H8
Method BLASTX
NCBI GI g4105772
BLAST score 818
E value 2.0e-87
Match length 193
% identity 41
NCBI Description (AF049917) PGP9B [Petunia x hybrida]

Seq. No. 2278
 Contig ID 1590_1.R1040
 5'-most EST kmv700737719.h1
 Method BLASTN
 NCBI GI g2318116
 BLAST score 617
 E value 0.0e+00
 Match length 1267
 % identity 89
 NCBI Description Pisum sativum Mg-chelatase subunit D (ChlD) mRNA, complete cds

Seq. No. 2279
 Contig ID 1591_1.R1040
 5'-most EST zhf700960315.h1
 Method BLASTN
 NCBI GI g1841474
 BLAST score 171
 E value 5.0e-91
 Match length 434
 % identity 88
 NCBI Description P.sativum mRNA for Myb-like protein (Myb26)

Seq. No. 2280
 Contig ID 1591_2.R1040
 5'-most EST zhf700960664.h1
 Method BLASTN
 NCBI GI g1841474
 BLAST score 227
 E value 1.0e-124
 Match length 363
 % identity 91
 NCBI Description P.sativum mRNA for Myb-like protein (Myb26)

Seq. No. 2281
 Contig ID 1592_1.R1040
 5'-most EST LIB3028-039-Q1-B1-E7
 Method BLASTN
 NCBI GI g2104680
 BLAST score 227
 E value 1.0e-124
 Match length 894
 % identity 83
 NCBI Description V.faba mRNA for putative transcription factor (1556bp)

Seq. No. 2282
 Contig ID 1593_1.R1040
 5'-most EST LIB3028-056-Q1-B1-H7
 Method BLASTN
 NCBI GI g1223925
 BLAST score 258
 E value 1.0e-143
 Match length 393
 % identity 92
 NCBI Description Vigna radiata carboxypeptidase II mRNA, partial cds

09684016-101000

Seq. No. 2283
Contig ID 1595_1.R1040
5'-most EST jC-gmf102220055h11a1
Method BLASTX
NCBI GI g2541876
BLAST score 1190
E value 1.0e-131
Match length 465
% identity 53
NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein
[Nicotiana tabacum]

Seq. No. 2284
Contig ID 1595_2.R1040
5'-most EST jC-gmle01810023c07d1

Seq. No. 2285
Contig ID 1595_3.R1040
5'-most EST hyd700726241.h1
Method BLASTX
NCBI GI g2541876
BLAST score 306
E value 1.0e-27
Match length 113
% identity 65
NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein
[Nicotiana tabacum]

Seq. No. 2286
Contig ID 1595_4.R1040
5'-most EST uC-gmflminsoy115h12b1

Seq. No. 2287
Contig ID 1596_1.R1040
5'-most EST kl1701212428.h1
Method BLASTX
NCBI GI g3979665
BLAST score 269
E value 3.0e-23
Match length 102
% identity 53
NCBI Description (X66482) orf [Arabidopsis thaliana]

Seq. No. 2288
Contig ID 1596_2.R1040
5'-most EST hyd700727018.h1

Seq. No. 2289
Contig ID 1596_3.R1040
5'-most EST gsv701046770.h1

Seq. No. 2290
Contig ID 1596_5.R1040
5'-most EST epx701104051.h1

Seq. No. 2291
Contig ID 1600_1.R1040

5'-most EST LIB3028-006-Q1-B1-A7
 Method BLASTX
 NCBI GI g4099921
 BLAST score 451
 E value 1.0e-44
 Match length 219
 % identity 48
 NCBI Description (U91982) EREBP-3 homolog [Stylosanthes hamata]

Seq. No. 2292
 Contig ID 1600_2.R1040
 5'-most EST LIB3087-005-Q1-K1-D1
 Method BLASTN
 NCBI GI g4099920
 BLAST score 95
 E value 7.0e-46
 Match length 179
 % identity 88
 NCBI Description Stylosanthes hamata EREBP-3 homolog mRNA, complete cds

Seq. No. 2293
 Contig ID 1601_1.R1040
 5'-most EST LIB3028-056-Q1-B1-G1
 Method BLASTX
 NCBI GI g2370253
 BLAST score 300
 E value 3.0e-27
 Match length 143
 % identity 51
 NCBI Description (Y13273) putative protein kinase [Lycopersicon esculentum]

Seq. No. 2294
 Contig ID 1602_1.R1040
 5'-most EST g5057999
 Method BLASTX
 NCBI GI g3860247
 BLAST score 1871
 E value 0.0e+00
 Match length 385
 % identity 91
 NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 2295
 Contig ID 1602_2.R1040
 5'-most EST trc700565474.h1
 Method BLASTX
 NCBI GI g3860247
 BLAST score 1863
 E value 0.0e+00
 Match length 383
 % identity 91
 NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 2296
 Contig ID 1602_3.R1040
 5'-most EST uC-gmronoir011h03b1
 Method BLASTX

NCBI GI g3860247
 BLAST score 539
 E value 7.0e-93
 Match length 190
 % identity 89
 NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 2297
 Contig ID 1602_4.R1040
 5'-most EST rlr700895868.h1
 Method BLASTX
 NCBI GI g3860247
 BLAST score 513
 E value 4.0e-52
 Match length 114
 % identity 84
 NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 2298
 Contig ID 1602_10.R1040
 5'-most EST bth700845653.h1
 Method BLASTX
 NCBI GI g3860247
 BLAST score 329
 E value 8.0e-31
 Match length 65
 % identity 94
 NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 2299
 Contig ID 1604_1.R1040
 5'-most EST jC-gmro02910064f06a1
 Method BLASTX
 NCBI GI g1076389
 BLAST score 2747
 E value 0.0e+00
 Match length 587
 % identity 91
 NCBI Description protein phosphatase 2A pDF1 - Arabidopsis thaliana
 >gi_683502_emb_CAA57528_(X82002) protein phosphatase 2A 65
 kDa regulatory subunit [Arabidopsis thaliana]

Seq. No. 2300
 Contig ID 1604_2.R1040
 5'-most EST fC-gmse700668369h1
 Method BLASTX
 NCBI GI g1076389
 BLAST score 1095
 E value 1.0e-160
 Match length 325
 % identity 19
 NCBI Description protein phosphatase 2A pDF1 - Arabidopsis thaliana
 >gi_683502_emb_CAA57528_(X82002) protein phosphatase 2A 65
 kDa regulatory subunit [Arabidopsis thaliana]

Seq. No. 2301
 Contig ID 1604_3.R1040

5'-most EST jC-gmle01810047f12d1
 Method BLASTX
 NCBI GI g1076389
 BLAST score 405
 E value 2.0e-39
 Match length 94
 % identity 26
 NCBI Description protein phosphatase 2A pDF1 - Arabidopsis thaliana
 >gi_683502_emb_CAA57528_ (X82002) protein phosphatase 2A 65
 kDa regulatory subunit [Arabidopsis thaliana]

Seq. No. 2302
 Contig ID 1604_4.R1040
 5'-most EST LIB3170-058-Q1-K1-H1
 Method BLASTX
 NCBI GI g1568511
 BLAST score 299
 E value 5.0e-27
 Match length 162
 % identity 37
 NCBI Description (X97913) protein phosphatase 2A [Nicotiana tabacum]

Seq. No. 2303
 Contig ID 1604_5.R1040
 5'-most EST LIB3109-036-Q1-K1-E3
 Method BLASTX
 NCBI GI g1076389
 BLAST score 326
 E value 2.0e-30
 Match length 78
 % identity 95
 NCBI Description protein phosphatase 2A pDF1 - Arabidopsis thaliana
 >gi_683502_emb_CAA57528_ (X82002) protein phosphatase 2A 65
 kDa regulatory subunit [Arabidopsis thaliana]

Seq. No. 2304
 Contig ID 1606_1.R1040
 5'-most EST g5509172
 Method BLASTX
 NCBI GI g1346812
 BLAST score 1568
 E value 1.0e-175
 Match length 418
 % identity 75
 NCBI Description 26S PROTEASE REGULATORY SUBUNIT 8 (PROTEASOME SUBUNIT P45)
 (THYROID HORMONE RECEPTOR INTERACTING PROTEIN 1) (TRIP1)
 >gi_2136007_pir_I53510 proteasome subunit p45 - human
 >gi_976227_dbj_BAA07919_ (D44467) 26S proteasome subunit
 p45 [Homo sapiens] >gi_1096205_prf_2111282A 26S proteasome
 [Homo sapiens]

Seq. No. 2305
 Contig ID 1606_2.R1040
 5'-most EST jC-gmfl02220071h07a1
 Method BLASTX
 NCBI GI g3747111
 BLAST score 678

E value 6.0e-71
 Match length 237
 % identity 57
 NCBI Description (AF095641) MTN3 homolog [Arabidopsis thaliana]

Seq. No. 2306
 Contig ID 1606_4.R1040
 5'-most EST LIB3051-112-Q1-K1-B12
 Method BLASTX
 NCBI GI g1171978
 BLAST score 1202
 E value 1.0e-133
 Match length 431
 % identity 33
 NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi_304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No. 2307
 Contig ID 1606_5.R1040
 5'-most EST LIB3167-049-P1-K1-G8
 Method BLASTX
 NCBI GI g1171978
 BLAST score 1300
 E value 1.0e-144
 Match length 331
 % identity 28
 NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi_304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No. 2308
 Contig ID 1606_6.R1040
 5'-most EST LIB3170-049-Q1-J1-B1
 Method BLASTX
 NCBI GI g2213871
 BLAST score 295
 E value 1.0e-26
 Match length 73
 % identity 88
 NCBI Description (AF003126) poly(A)-binding protein [Mesembryanthemum crystallinum]

Seq. No. 2309
 Contig ID 1606_12.R1040
 5'-most EST gsv701056823.h1
 Method BLASTX
 NCBI GI g1170767
 BLAST score 221
 E value 7.0e-18
 Match length 94
 % identity 49
 NCBI Description 26S PROTEASE REGULATORY SUBUNIT 8 HOMOLOG (LET1 PROTEIN) >gi_626074_pir_S45176 transcription factor SUG1 homolog - fission yeast (Schizosaccharomyces pombe) >gi_406051

(U02280) Let1 [Schizosaccharomyces pombe]
 >gi_4106689_emb_CAA22628_ (AL035065) 26s protease
 regulatory subunit 8 homolog [Schizosaccharomyces pombe]

Seq. No. 2310
 Contig ID 1606_13.R1040
 5'-most EST ncj700977584.h1

Seq. No. 2311
 Contig ID 1606_14.R1040
 5'-most EST g4397126

Seq. No. 2312
 Contig ID 1606_15.R1040
 5'-most EST gsv701044733.h1

Seq. No. 2313
 Contig ID 1606_16.R1040
 5'-most EST LIB3050-022-Q1-K1-C11

Seq. No. 2314
 Contig ID 1606_19.R1040
 5'-most EST jC-gmfl02220084c12d1
 Method BLASTX
 NCBI GI g2982331
 BLAST score 288
 E value 1.0e-25
 Match length 58
 % identity 98
 NCBI Description (AF051251) TAT-binding protein homolog [Picea mariana]

Seq. No. 2315
 Contig ID 1607_1.R1040
 5'-most EST zpv700757870.h1
 Method BLASTX
 NCBI GI g2213425
 BLAST score 1277
 E value 1.0e-141
 Match length 279
 % identity 84
 NCBI Description (Z97064) hypothetical protein [Citrus x paradisi]

Seq. No. 2316
 Contig ID 1607_3.R1040
 5'-most EST jC-gmro02910073h07a1
 Method BLASTN
 NCBI GI g2213424
 BLAST score 145
 E value 1.0e-75
 Match length 409
 % identity 84
 NCBI Description Citrus paradisi mRNA for hypothetical protein

Seq. No. 2317
 Contig ID 1607_4.R1040
 5'-most EST uC-gmronoir040f06b1

Seq. No. 2318
 Contig ID 1607_5.R1040
 5'-most EST jC-gmro02910005a04d1
 Method BLASTX
 NCBI GI g2213425
 BLAST score 391
 E value 7.0e-38
 Match length 88
 % identity 46
 NCBI Description (Z97064) hypothetical protein [Citrus x paradisi]

Seq. No. 2319
 Contig ID 1607_6.R1040
 5'-most EST LIB3040-059-Q1-E1-B4
 Method BLASTX
 NCBI GI g2213425
 BLAST score 376
 E value 3.0e-36
 Match length 78
 % identity 47
 NCBI Description (Z97064) hypothetical protein [Citrus x paradisi]

Seq. No. 2320
 Contig ID 1607_9.R1040
 5'-most EST zhf700958949.h1
 Method BLASTN
 NCBI GI g2213424
 BLAST score 73
 E value 5.0e-33
 Match length 177
 % identity 86
 NCBI Description Citrus paradisi mRNA for hypothetical protein

Seq. No. 2321
 Contig ID 1608_1.R1040
 5'-most EST uaw700666018.h1
 Method BLASTN
 NCBI GI g3449326
 BLAST score 46
 E value 2.0e-16
 Match length 151
 % identity 86
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No. 2322
 Contig ID 1608_2.R1040
 5'-most EST gsv701049801.h1
 Method BLASTN
 NCBI GI g3869065
 BLAST score 51
 E value 2.0e-19
 Match length 155
 % identity 86
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]

Seq. No. 2323
 Contig ID 1611_1.R1040
 5'-most EST jC-gmro02910016b07a1
 Method BLASTX
 NCBI GI g3935150
 BLAST score 655
 E value 1.0e-68
 Match length 194
 % identity 45
 NCBI Description (AC005106) T25N20.14 [Arabidopsis thaliana]

Seq. No. 2324
 Contig ID 1612_1.R1040
 5'-most EST LIB3039-046-Q1-E1-H12
 Method BLASTN
 NCBI GI g563328
 BLAST score 116
 E value 4.0e-58
 Match length 320
 % identity 86
 NCBI Description A.officinalis mRNA for histone 2B

Seq. No. 2325
 Contig ID 1612_2.R1040
 5'-most EST jC-gmro02910020f12d1
 Method BLASTN
 NCBI GI g3510337
 BLAST score 34
 E value 3.0e-09
 Match length 188
 % identity 84
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence [Arabidopsis thaliana]

Seq. No. 2326
 Contig ID 1613_1.R1040
 5'-most EST LIB3051-053-Q1-K2-D4

Seq. No. 2327
 Contig ID 1613_3.R1040
 5'-most EST zhf700952934.h1
 Method BLASTN
 NCBI GI g1370171
 BLAST score 37
 E value 1.0e-11
 Match length 70
 % identity 89
 NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB1X

Seq. No. 2328
 Contig ID 1614_1.R1040
 5'-most EST LIB3106-039-Q1-K1-A10
 Method BLASTX
 NCBI GI g2253442
 BLAST score 268
 E value 4.0e-23
 Match length 62

Seq. No. 2334
 Contig ID 1617_2.R1040
 5'-most EST zzp700834205.h1
 Method BLASTX
 NCBI GI g1709761
 BLAST score 433
 E value 1.0e-46
 Match length 105
 % identity 95
 NCBI Description PROTEASOME 27 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE COMPLEX 27 KD SUBUNIT) >gi_1262146_emb_CAA65660_ (X96974) proteasome subunit [Spinacia oleracea]

Seq. No. 2335
 Contig ID 1618_1.R1040
 5'-most EST pcp700990455.h1
 Method BLASTX
 NCBI GI g3513727
 BLAST score 2263
 E value 0.0e+00
 Match length 525
 % identity 85
 NCBI Description (AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No. 2336
 Contig ID 1618_2.R1040
 5'-most EST zsg701130248.h1
 Method BLASTX
 NCBI GI g3513727
 BLAST score 385
 E value 5.0e-37
 Match length 148
 % identity 42
 NCBI Description (AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No. 2337
 Contig ID 1620_1.R1040
 5'-most EST LIB3094-083-Q1-K1-C2

Seq. No. 2338
 Contig ID 1620_2.R1040
 5'-most EST leu701152744.h1
 Method BLASTX
 NCBI GI g4249376
 BLAST score 357
 E value 3.0e-33
 Match length 225
 % identity 39

NCBI Description	(U51330) rust resistance kinase Lr10 [Triticum aestivum]
Seq. No.	2347
Contig ID	1621_2.R1040
5'-most EST	LIB3138-008-Q1-N1-A8
Method	BLASTX
NCBI GI	g3025189
BLAST score	799
E value	5.0e-85
Match length	458
% identity	39
NCBI Description	HYPOTHETICAL 67.1 KD PROTEIN SLL1770 >gi_1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis sp.]
Seq. No.	2348
Contig ID	1621_3.R1040
5'-most EST	jC-gmfl02220094b06a1
Seq. No.	2349
Contig ID	1621_8.R1040
5'-most EST	jC-gmle01810006e09a1
Method	BLASTX
NCBI GI	g3025189
BLAST score	192
E value	2.0e-14
Match length	79
% identity	43
NCBI Description	HYPOTHETICAL 67.1 KD PROTEIN SLL1770 >gi_1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis sp.]
Seq. No.	2350
Contig ID	1622_1.R1040
5'-most EST	zhf700961260.h1
Method	BLASTX
NCBI GI	g2144584
BLAST score	329
E value	1.0e-30
Match length	142
% identity	51
NCBI Description	trypsin inhibitor A (Kunitz) precursor - soybean >gi_18770_emb_CAA45777_ (X64447) trypsin inhibitor subtype A [Glycine max]
Seq. No.	2351
Contig ID	1623_1.R1040
5'-most EST	uC-gmrominsoyl77g08b1
Method	BLASTX
NCBI GI	g1346297
BLAST score	1869
E value	0.0e+00
Match length	461
% identity	79
NCBI Description	3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE 1 (HMG-COA REDUCTASE 1) (HMGR1) (HMGR) >gi_2117465_pir_S59944 hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34) -

BLAST score 211
 E value 2.0e-16
 Match length 52
 % identity 79
 NCBI Description (Z73553) core protein [Pisum sativum]

Seq. No. 2363
 Contig ID 1630_1.R1040
 5'-most EST LIB3028-056-Q1-B1-C1

Seq. No. 2364
 Contig ID 1631_1.R1040
 5'-most EST jC-gmfl02220050d12a1

Seq. No. 2365
 Contig ID 1633_1.R1040
 5'-most EST LIB3087-011-Q1-K1-F10
 Method BLASTN
 NCBI GI g510189
 BLAST score 445
 E value 0.0e+00
 Match length 815
 % identity 89
 NCBI Description P.sativum (miranda) mRNA for chloroplast outer envelope protein

Seq. No. 2366
 Contig ID 1633_3.R1040
 5'-most EST leu701144743.h1
 Method BLASTN
 NCBI GI g3293200
 BLAST score 201
 E value 1.0e-109
 Match length 305
 % identity 91
 NCBI Description Pisum sativum GTP-binding protein (IAP34) mRNA, complete cds

Seq. No. 2367
 Contig ID 1634_1.R1040
 5'-most EST uC-gmropic011a08b1
 Method BLASTX
 NCBI GI g2191171
 BLAST score 587
 E value 2.0e-60
 Match length 191
 % identity 60
 NCBI Description (AF007270) similar to A. thaliana DI19 mRNA (NID:g469110) [Arabidopsis thaliana]

Seq. No. 2368
 Contig ID 1636_1.R1040
 5'-most EST jC-gmfl02220053f02a1
 Method BLASTX
 NCBI GI g2239262
 BLAST score 576
 E value 3.0e-59

Seq. No. 2374
 Contig ID 1640_2.R1040
 5'-most EST wrg700790238.h2
 Method BLASTN
 NCBI GI g391604
 BLAST score 134
 E value 6.0e-69
 Match length 350
 % identity 85
 NCBI Description Arabidopsis thaliana ATPK15D mRNA for casein kinase II catalytic subunit, complete cds

Seq. No. 2375
 Contig ID 1640_4.R1040
 5'-most EST jC-gmle01810021e08a1
 Method BLASTN
 NCBI GI g3169169
 BLAST score 47
 E value 5.0e-17
 Match length 95
 % identity 53
 NCBI Description Arabidopsis thaliana chromosome II BAC F21P24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 2376
 Contig ID 1640_5.R1040
 5'-most EST g5677543
 Method BLASTX
 NCBI GI g585350
 BLAST score 730
 E value 2.0e-77
 Match length 144
 % identity 94
 NCBI Description CASEIN KINASE II, ALPHA CHAIN 2 (CK II)
 >gi_419753_pir_S31099 casein kinase II (EC 2.7.1.-)
 alpha-type chain (clone ATCKA2) - Arabidopsis thaliana
 >gi_391605_dbj_BAA01091_ (D10247) casein kinase II
 catalytic subunit [Arabidopsis thaliana]

Seq. No. 2377
 Contig ID 1642_1.R1040
 5'-most EST jsh701067642.h1
 Method BLASTX
 NCBI GI g4056468
 BLAST score 359
 E value 8.0e-34
 Match length 154
 % identity 46
 NCBI Description (AC005990) Contains similarity to gb_X66426
 polygalacturonase from Persea americana and is a member of
 the signal peptidase family PF_00461 and polygalacturonase
 family PF_00295. [Arabidopsis thaliana]

Seq. No. 2378
 Contig ID 1643_1.R1040
 5'-most EST g5509675
 Method BLASTX

NCBI GI g2497492
 BLAST score 364
 E value 2.0e-34
 Match length 101
 % identity 68
 NCBI Description URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) >gi_1653646_dbj_BAA18558_ (D90915) uridine monophosphate kinase [Synechocystis sp.]

Seq. No. 2379
 Contig ID 1644_1.R1040
 5'-most EST g5677499
 Method BLASTX
 NCBI GI g4539400
 BLAST score 824
 E value 2.0e-88
 Match length 208
 % identity 75
 NCBI Description (AL035526) putative protein [Arabidopsis thaliana]

Seq. No. 2380
 Contig ID 1645_1.R1040
 5'-most EST pmv700893145.h1
 Method BLASTX
 NCBI GI g1723242
 BLAST score 152
 E value 2.0e-09
 Match length 74
 % identity 50
 NCBI Description HYPOTHETICAL 36.8 KD PROTEIN C26A3.16 IN CHROMOSOME I >gi_1177363_emb_CAA93239_ (Z69240) yeast dsk2 homolog, ubiquitin-like protein [Schizosaccharomyces pombe]

Seq. No. 2381
 Contig ID 1646_1.R1040
 5'-most EST gsv701051466.h1
 Method BLASTX
 NCBI GI g4510345
 BLAST score 355
 E value 4.0e-33
 Match length 164
 % identity 45
 NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 2382
 Contig ID 1646_2.R1040
 5'-most EST sat701008658.h1

Seq. No. 2383
 Contig ID 1646_3.R1040
 5'-most EST LIB3170-007-Q1-K1-G8

Seq. No. 2384
 Contig ID 1646_4.R1040
 5'-most EST LIB3051-032-Q1-K1-F1

Seq. No. 2385

Contig ID	1646_5.R1040
5'-most EST	pxt700945341.h1
Method	BLASTX
NCBI GI	g4510345
BLAST score	145
E value	5.0e-09
Match length	36
% identity	67
NCBI Description	(AC006921) unknown protein. [Arabidopsis thaliana]
Seq. No.	2386
Contig ID	1646_6.R1040
5'-most EST	LIB3138-021-Q1-N1-H12
Seq. No.	2387
Contig ID	1646_8.R1040
5'-most EST	LIB3139-090-P1-N1-H4
Method	BLASTX
NCBI GI	g1172650
BLAST score	164
E value	6.0e-11
Match length	74
% identity	47
NCBI Description	EXTRACELLULAR METALLOPROTEASE PRECURSOR >gi_95576_pir_A41048 extracellular metalloproteinase (EC 3.4.24.-) precursor - Erwinia carotovora subsp. carotovora >gi_148480 (M36651) extracellular protease (prt) [Erwinia carotovora]
Seq. No.	2388
Contig ID	1646_11.R1040
5'-most EST	jC-gmf102220148b01d1
Seq. No.	2389
Contig ID	1646_12.R1040
5'-most EST	bth700844489.h1
Method	BLASTX
NCBI GI	g3123056
BLAST score	152
E value	1.0e-09
Match length	174
% identity	33
NCBI Description	HYPOTHETICAL PROTEIN KIAA0039 >gi_436222_dbj_BAA05039_ (D26018) KIAA0039 [Homo sapiens]
Seq. No.	2390
Contig ID	1646_17.R1040
5'-most EST	LIB3138-001-Q1-N1-A12
Seq. No.	2391
Contig ID	1646_18.R1040
5'-most EST	fua701037588.h1
Seq. No.	2392
Contig ID	1647_1.R1040
5'-most EST	LIB3093-038-Q1-K1-A3
Method	BLASTN

Seq. No. 2405
 Contig ID 1654_2.R1040
 5'-most EST V4R_01-Q1-B1-B10
 Method BLASTX
 NCBI GI g1076287
 BLAST score 155
 E value 2.0e-10
 Match length 56
 % identity 57
 NCBI Description amine acid permease - Arabidopsis thaliana
 >gi_510236_emb_CAA50672_ (X71787) amine acid permease
 [Arabidopsis thaliana]

Seq. No. 2406
 Contig ID 1656_1.R1040
 5'-most EST ncj700980372.h1
 Method BLASTX
 NCBI GI g4056480
 BLAST score 724
 E value 3.0e-91
 Match length 224
 % identity 76
 NCBI Description (AC005896) putative adenylate kinase [Arabidopsis thaliana]

Seq. No. 2407
 Contig ID 1656_2.R1040
 5'-most EST LIB3170-024-Q1-K1-C5
 Method BLASTX
 NCBI GI g4056480
 BLAST score 453
 E value 4.0e-45
 Match length 113
 % identity 81
 NCBI Description (AC005896) putative adenylate kinase [Arabidopsis thaliana]

Seq. No. 2408
 Contig ID 1656_3.R1040
 5'-most EST uC-gmropic101b11b1
 Method BLASTX
 NCBI GI g4056480
 BLAST score 417
 E value 7.0e-41
 Match length 146
 % identity 62
 NCBI Description (AC005896) putative adenylate kinase [Arabidopsis thaliana]

Seq. No. 2409
 Contig ID 1656_4.R1040
 5'-most EST sat701006284.h2
 Method BLASTX
 NCBI GI g4056480
 BLAST score 227
 E value 1.0e-18
 Match length 82
 % identity 63
 NCBI Description (AC005896) putative adenylate kinase [Arabidopsis thaliana]


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% identity                83
NCBI Description          (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No.                  2424
Contig ID                 1669_1.R1040
5'-most EST              eep700865012.h1
Method                   BLASTX
NCBI GI                   g2194132
BLAST score               1103
E value                  1.0e-120
Match length              355
% identity                66
NCBI Description          (AC002062) No definition line found [Arabidopsis thaliana]

Seq. No.                  2425
Contig ID                 1670_1.R1040
5'-most EST              LIB3139-116-P1-N1-E11
Method                   BLASTX
NCBI GI                   g3763918
BLAST score               701
E value                  6.0e-74
Match length              194
% identity                69
NCBI Description          (AC004450) putative isopropylmalate dehydratase
                          [Arabidopsis thaliana]

Seq. No.                  2426
Contig ID                 1670_2.R1040
5'-most EST              LIB3049-027-Q1-E1-D3
Method                   BLASTX
NCBI GI                   g3763918
BLAST score               214
E value                  3.0e-17
Match length              48
% identity                81
NCBI Description          (AC004450) putative isopropylmalate dehydratase
                          [Arabidopsis thaliana]

Seq. No.                  2427
Contig ID                 1672_1.R1040
5'-most EST              wrg700788550.h1
Method                   BLASTX
NCBI GI                   g2262116
BLAST score               218
E value                  1.0e-17
Match length              120
% identity                39
NCBI Description          (AC002343) cellulose synthase isolog [Arabidopsis thaliana]

Seq. No.                  2428
Contig ID                 1673_1.R1040
5'-most EST              leu701150051.h1

Seq. No.                  2429
Contig ID                 1673_2.R1040
5'-most EST              jC-qmf102220127d06d1

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E value	1.0e-79
Match length	379
% identity	87
NCBI Description	Phaseolus vulgaris proline-rich 14 kDa protein mRNA, complete cds
Seq. No.	2458
Contig ID	1700_8.R1040
5'-most EST	g4313847
Method	BLASTX
NCBI GI	g462195
BLAST score	368
E value	6.0e-35
Match length	88
% identity	81
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir_S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_(X51910) GOS2 [Oryza sativa] >gi_3789950_(AF094774) translation initiation factor [Oryza sativa]
Seq. No.	2459
Contig ID	1700_12.R1040
5'-most EST	hrw701059318.hl
Method	BLASTX
NCBI GI	g3659907
BLAST score	167
E value	6.0e-12
Match length	38
% identity	79
NCBI Description	(AF091857) protein translation factor SUI1 homolog [Pimpinella brachycarpa]
Seq. No.	2460
Contig ID	1701_1.R1040
5'-most EST	LIB3109-037-Q1-K1-E3
Method	BLASTX
NCBI GI	g3183088
BLAST score	316
E value	1.0e-28
Match length	96
% identity	56
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir_S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_(X79604) lipid transfer like protein [Vigna unguiculata]
Seq. No.	2461
Contig ID	1701_2.R1040
5'-most EST	LIB3107-040-Q1-K1-B8
Method	BLASTX
NCBI GI	g3183088
BLAST score	309
E value	6.0e-28
Match length	96
% identity	59
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR

5'-most EST LIB3028-020-Q1-B1-D3
 Method BLASTX
 NCBI GI g2129774
 BLAST score 1095
 E value 1.0e-120
 Match length 292
 % identity 68
 NCBI Description xyloglucan endotransglycosylase-related protein XTR4 -
 Arabidopsis thaliana (fragment) >gi_1244754 (U43486)
 xyloglucan endotransglycosylase-related protein
 [Arabidopsis thaliana]

Seq. No. 2472
 Contig ID 1709_5.R1040
 5'-most EST jex700905796.h1
 Method BLASTX
 NCBI GI g3980400
 BLAST score 872
 E value 1.0e-93
 Match length 261
 % identity 66
 NCBI Description (AC004561) putative tropinone reductase [Arabidopsis
 thaliana]

Seq. No. 2473
 Contig ID 1709_6.R1040
 5'-most EST jC-gmle01810084f07a1
 Method BLASTN
 NCBI GI g20680
 BLAST score 180
 E value 2.0e-96
 Match length 344
 % identity 88
 NCBI Description P.sativum mRNA of cDNA clone 26g

Seq. No. 2474
 Contig ID 1709_7.R1040
 5'-most EST dpv701099710.h1
 Method BLASTX
 NCBI GI g2980793
 BLAST score 506
 E value 3.0e-51
 Match length 161
 % identity 56
 NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 2475
 Contig ID 1709_8.R1040
 5'-most EST jC-gmle01810029a07d1
 Method BLASTX
 NCBI GI g2129774
 BLAST score 214
 E value 8.0e-17
 Match length 75
 % identity 52
 NCBI Description xyloglucan endotransglycosylase-related protein XTR4 -
 Arabidopsis thaliana (fragment) >gi_1244754 (U43486)

Method	BLASTX
NCBI GI	g3236259
BLAST score	1249
E value	1.0e-138
Match length	289
% identity	80
NCBI Description	(AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.	2487
Contig ID	1717_1.R1040
5'-most EST	LIB3139-086-P1-N1-C11
Seq. No.	2488
Contig ID	1717_2.R1040
5'-most EST	jex700904932.h1
Method	BLASTX
NCBI GI	g3122139
BLAST score	327
E value	3.0e-30
Match length	137
% identity	48
NCBI Description	GLYCEROL KINASE (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE) (GLYCEROKINASE) (GK) (ATP-STIMULATED GLUCOCORTICOID-RECEPTOR TRANSLOCATON PROMOTER) (ASTP) >gi_484372_pir_JN0606 ATP-stimulated glucocorticoid-receptor translocation promoter protein - rat >gi_433211_dbj_BAA03677_ (D16102) ATP-stimulated glucocorticoid-receptor translocaton promoter [Rattus rattus]
Seq. No.	2489
Contig ID	1717_3.R1040
5'-most EST	fde700874271.h1
Method	BLASTX
NCBI GI	g631174
BLAST score	291
E value	1.0e-26
Match length	78
% identity	69
NCBI Description	glycerol kinase - human >gi_515029_emb_CAA55364_ (X78711) glycerol kinase [Homo sapiens]
Seq. No.	2490
Contig ID	1717_4.R1040
5'-most EST	eep700863731.h1
Seq. No.	2491
Contig ID	1719_1.R1040
5'-most EST	LIB3170-034-Q1-J1-C12
Seq. No.	2492
Contig ID	1719_2.R1040
5'-most EST	LIB3074-031-Q1-K1-F3
Seq. No.	2493
Contig ID	1719_3.R1040

BLAST score 239
 E value 1.0e-131
 Match length 550
 % identity 87
 NCBI Description P.vulgaris gene for cyclophilin

Seq. No. 2511
 Contig ID 1735_2.R1040
 5'-most EST LIB3139-050-P1-N1-H3
 Method BLASTN
 NCBI GI g829118
 BLAST score 303
 E value 1.0e-169
 Match length 631
 % identity 88
 NCBI Description P.vulgaris gene for cyclophilin

Seq. No. 2512
 Contig ID 1735_3.R1040
 5'-most EST dpv701101486.h1
 Method BLASTX
 NCBI GI g1703292
 BLAST score 357
 E value 2.0e-33
 Match length 187
 % identity 70
 NCBI Description HIGH AFFINITY AMMONIUM TRANSPORTER >gi_551219_emb_CAA53473_(X75879) amt1 [Arabidopsis thaliana]

Seq. No. 2513
 Contig ID 1735_5.R1040
 5'-most EST jC-gmro02910046f04d1
 Method BLASTX
 NCBI GI g4324714
 BLAST score 938
 E value 0.0e+00
 Match length 516
 % identity 67
 NCBI Description (AF110771) ammonium transporter [Arabidopsis thaliana]

Seq. No. 2514
 Contig ID 1735_7.R1040
 5'-most EST LIB3029-009-Q1-B1-G10
 Method BLASTX
 NCBI GI g1703292
 BLAST score 762
 E value 5.0e-81
 Match length 225
 % identity 64
 NCBI Description HIGH AFFINITY AMMONIUM TRANSPORTER >gi_551219_emb_CAA53473_(X75879) amt1 [Arabidopsis thaliana]

Seq. No. 2515
 Contig ID 1735_8.R1040
 5'-most EST jC-gmle01810000c04a1
 Method BLASTX
 NCBI GI g1703292

09634013 107000

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Seq. No.          2527
Contig ID         1741_11.R1040
5'-most EST      zhf700953944.h1
Method            BLASTX
NCBI GI           g124224
BLAST score       528
E value           5.0e-54
Match length      102
% identity         96
NCBI Description  INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)
                  >gi_100345_pir_S21060 translation initiation factor eIF-5A
                  - common tobacco >gi_19887_emb_CAA45105_ (X63543)
                  eukaryotic initiation factor 5A (3) [Nicotiana tabacum]
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Seq. No.          2529
Contig ID         1742_2.R1040
5'-most EST      uC-gmropic099d01b1
Method            BLASTX
NCBI GI           g4580398
BLAST score       253
E value           1.0e-21
Match length      74
% identity        68
NCBI Description  (AC007171) putative protein kinase APK1A [Arabidopsis
                  thaliana]
```


Seq. No. 2542
 Contig ID 1755_3.R1040
 5'-most EST LIB3107-005-Q1-K1-H11
 Method BLASTX
 NCBI GI g533121
 BLAST score 201
 E value 1.0e-15
 Match length 44
 % identity 86
 NCBI Description (U13151) S-adenosyl-L-methionine:trans-caffeoyl-CoA
 3-O-methyltransferase [Zinnia elegans]

Seq. No. 2543
 Contig ID 1755_6.R1040
 5'-most EST g5753226
 Method BLASTN
 NCBI GI g2995933
 BLAST score 34
 E value 2.0e-09
 Match length 58
 % identity 90
 NCBI Description Mesembryanthemum crystallinum caffeoyl-CoA
 O-methyltransferase mRNA, complete cds

Seq. No. 2544
 Contig ID 1756_1.R1040
 5'-most EST LIB3139-017-P1-N1-A11
 Method BLASTX
 NCBI GI g3860249
 BLAST score 432
 E value 4.0e-42
 Match length 194
 % identity 49
 NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 2545
 Contig ID 1756_3.R1040
 5'-most EST dpv701097848.h1

Seq. No. 2546
 Contig ID 1757_1.R1040
 5'-most EST uC-gmflminsoy040g12b1
 Method BLASTX
 NCBI GI g1652601
 BLAST score 264
 E value 2.0e-22
 Match length 235
 % identity 35
 NCBI Description (D90906) hypothetical protein [Synechocystis sp.]

Seq. No. 2547
 Contig ID 1757_2.R1040
 5'-most EST jsh701068824.h1

Seq. No. 2548
 Contig ID 1759_1.R1040
 5'-most EST rca701001537.h1

Seq. No. 2549
 Contig ID 1759_3.R1040
 5'-most EST LIB3073-007-Q1-K1-B3

Seq. No. 2550
 Contig ID 1760_1.R1040
 5'-most EST LIB3049-030-Q1-E1-E4
 Method BLASTX
 NCBI GI g2983997
 BLAST score 426
 E value 1.0e-41
 Match length 159
 % identity 52
 NCBI Description (AE000749) hypothetical protein [Aquifex aeolicus]

Seq. No. 2551
 Contig ID 1762_1.R1040
 5'-most EST smc700748901.h1
 Method BLASTX
 NCBI GI g3176664
 BLAST score 510
 E value 2.0e-51
 Match length 153
 % identity 60
 NCBI Description (AC004393) Contains similarity to beta scruin gb_Z47541 from *Limulus polyphemus*. ESTs gb_T04493 and gb_AA585955 come from this gene. [Arabidopsis thaliana]

Seq. No. 2552
 Contig ID 1764_1.R1040
 5'-most EST txt700733348.h1

Seq. No. 2553
 Contig ID 1765_1.R1040
 5'-most EST zhf700960918.h1
 Method BLASTX
 NCBI GI g1652856
 BLAST score 300
 E value 8.0e-27
 Match length 162
 % identity 41
 NCBI Description (D90909) hypothetical protein [Synechocystis sp.]

Seq. No. 2554
 Contig ID 1766_1.R1040
 5'-most EST LIB3028-053-Q1-B1-E7
 Method BLASTX
 NCBI GI g4006896
 BLAST score 162
 E value 2.0e-15
 Match length 76
 % identity 64
 NCBI Description (Z99708) SCARECROW-like protein [Arabidopsis thaliana]

Seq. No. 2555
 Contig ID 1767_1.R1040

5'-most EST epx701108250.h1
 Method BLASTX
 NCBI GI g4158221
 BLAST score 1715
 E value 0.0e+00
 Match length 354
 % identity 86
 NCBI Description (Y18624) reversibly glycosylated polypeptide [Oryza sativa]

Seq. No. 2556
 Contig ID 1768_1.R1040
 5'-most EST jC-gmro02910054c10a1
 Method BLASTX
 NCBI GI g3763933
 BLAST score 283
 E value 5.0e-25
 Match length 67
 % identity 84
 NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]

Seq. No. 2557
 Contig ID 1769_1.R1040
 5'-most EST ncj700983042.h1
 Method BLASTN
 NCBI GI g2827081
 BLAST score 601
 E value 0.0e+00
 Match length 1016
 % identity 91
 NCBI Description Medicago sativa cytosolic malate dehydrogenase (cmdh) mRNA, complete cds

Seq. No. 2558
 Contig ID 1769_2.R1040
 5'-most EST fua701043420.h1
 Method BLASTX
 NCBI GI g4115534
 BLAST score 1466
 E value 1.0e-176
 Match length 400
 % identity 75
 NCBI Description (AB012114) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]

Seq. No. 2559
 Contig ID 1769_3.R1040
 5'-most EST g4405695
 Method BLASTN
 NCBI GI g2827081
 BLAST score 94
 E value 4.0e-45
 Match length 303
 % identity 88
 NCBI Description Medicago sativa cytosolic malate dehydrogenase (cmdh) mRNA, complete cds

Seq. No. 2560

Contig ID 1770_1.R1040
 5'-most EST fua701036901.h1
 Method BLASTX
 NCBI GI g1209020
 BLAST score 285
 E value 7.0e-25
 Match length 223
 % identity 34
 NCBI Description (U09584) PL6 protein [Homo sapiens]

Seq. No. 2561
 Contig ID 1770_2.R1040
 5'-most EST leu701144340.h1

Seq. No. 2562
 Contig ID 1771_1.R1040
 5'-most EST LIB3167-050-P1-K1-C12
 Method BLASTX
 NCBI GI g1363479
 BLAST score 742
 E value 1.0e-78
 Match length 205
 % identity 72
 NCBI Description photosystem I protein psaL - cucumber
 >gi_801740_dbj_BAA09047_ (D50456) PsaL [Cucumis sativus]

Seq. No. 2563
 Contig ID 1771_3.R1040
 5'-most EST LIB3138-087-P1-N1-A8
 Method BLASTX
 NCBI GI g1363479
 BLAST score 254
 E value 3.0e-25
 Match length 100
 % identity 63
 NCBI Description photosystem I protein psaL - cucumber
 >gi_801740_dbj_BAA09047_ (D50456) PsaL [Cucumis sativus]

Seq. No. 2564
 Contig ID 1771_4.R1040
 5'-most EST zhf700960439.h1
 Method BLASTX
 NCBI GI g1363479
 BLAST score 266
 E value 3.0e-23
 Match length 74
 % identity 76
 NCBI Description photosystem I protein psaL - cucumber
 >gi_801740_dbj_BAA09047_ (D50456) PsaL [Cucumis sativus]

Seq. No. 2565
 Contig ID 1771_5.R1040
 5'-most EST vzy700752230.h1

Seq. No. 2566
 Contig ID 1773_1.R1040
 5'-most EST jC-gmro02910029d07a1

05084019 101000

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Seq. No.          2597
Contig ID         1793_5.R1040
5'-most EST      LIB3170-002-Q1-K1-A4
Method           BLASTN
NCBI GI          g1806284
BLAST score      193
E value          1.0e-104
Match length     313
% identity       90
NCBI Description  S.rostrata mRNA coding for histone H4 homologue
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Seq. No.          2599
Contig ID         1793_7.R1040
5'-most EST      LIB3051-095-Q1-K1-E8
Method           BLASTX
NCBI GI          g730526
BLAST score       502
E value          6.0e-90
Match length      192
% identity        84
NCBI Description  60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
                  >gi_480787_pir_S37271 ribosomal protein L13 - Arabidopsis
                  thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein
                  [Arabidopsis thaliana]
```

552

Method BLASTN
 NCBI GI g2351070
 BLAST score 115
 E value 1.0e-57
 Match length 303
 % identity 84
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 MTH12, complete sequence [Arabidopsis thaliana]

Seq. No. 2601
 Contig ID 1793_9.R1040
 5'-most EST LIB3092-006-Q1-K1-H1
 Method BLASTX
 NCBI GI g131166
 BLAST score 574
 E value 4.0e-59
 Match length 172
 % identity 69
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
 (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_82100_pir_S00449
 photosystem I chain II precursor - tomato >gi_170492
 (M21344) photosystem I subunit II protein precursor
 [Lycopersicon esculentum] >gi_226544_prf_1601516A
 photosystem I reaction center II [Lycopersicon esculentum]

Seq. No. 2602
 Contig ID 1793_10.R1040
 5'-most EST LIB3049-007-Q1-E1-B3
 Method BLASTN
 NCBI GI g166739
 BLAST score 97
 E value 6.0e-47
 Match length 209
 % identity 87
 NCBI Description A.thaliana histone H4 gene, complete cds

Seq. No. 2603
 Contig ID 1793_11.R1040
 5'-most EST LIB3167-078-P1-K2-H6
 Method BLASTX
 NCBI GI g487046
 BLAST score 433
 E value 1.0e-46
 Match length 117
 % identity 85
 NCBI Description photosystem I chain II precursor - wood tobacco
 >gi_407769_dbj_BAA02871_ (D13718) PSI-D1 precursor
 [Nicotiana sylvestris]

Seq. No. 2604
 Contig ID 1793_12.R1040
 5'-most EST LIB3040-042-Q1-E1-G10
 Method BLASTN
 NCBI GI g1806284
 BLAST score 185
 E value 2.0e-99
 Match length 313

E value 4.0e-69
Match length 286
% identity 87
NCBI Description Pea mRNA for the 33kDa polypeptide of the water-oxidizing complex of photosystem II

Seq. No. 2620
Contig ID 1794_5.R1040
5'-most EST jC-gmle01810047h09d1
Method BLASTN
NCBI GI g344003
BLAST score 119
E value 3.0e-60
Match length 271
% identity 86
NCBI Description Pisum sativum mRNA for precursor for 33-kDa protein of photosystem II, complete cds

Seq. No. 2621
Contig ID 1795_1.R1040
5'-most EST all1700863141.h1
Method BLASTX
NCBI GI g3608152
BLAST score 202
E value 5.0e-16
Match length 78
% identity 54
NCBI Description (AC005314) hypothetical protein [Arabidopsis thaliana]

Seq. No. 2622
Contig ID 1798_1.R1040
5'-most EST g4299089
Method BLASTX
NCBI GI g3152585
BLAST score 323
E value 1.0e-29
Match length 140
% identity 55
NCBI Description (AC002986) Contains similarity to auxin-induced protein TM018A10.6 from A. thaliana BAC gb_AF013294. [Arabidopsis thaliana]

Seq. No. 2623
Contig ID 1798_2.R1040
5'-most EST uC-gmrominsoy216f03b1
Method BLASTX
NCBI GI g3152585
BLAST score 278
E value 3.0e-24
Match length 141
% identity 48
NCBI Description (AC002986) Contains similarity to auxin-induced protein TM018A10.6 from A. thaliana BAC gb_AF013294. [Arabidopsis thaliana]

Seq. No. 2624
Contig ID 1799_1.R1040

5'-most EST uC-gmrominsoy048a03b1
 Method BLASTX
 NCBI GI g3123295
 BLAST score 339
 E value 2.0e-31
 Match length 136
 % identity 52
 NCBI Description CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi_2583169
 (AF026473) calmodulin-related protein [Arabidopsis
 thaliana]

Seq. No. 2636
 Contig ID 1805_2.R1040
 5'-most EST LIB3028-042-Q1-B1-H10
 Method BLASTX
 NCBI GI g3123295
 BLAST score 198
 E value 3.0e-15
 Match length 64
 % identity 61
 NCBI Description CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi_2583169
 (AF026473) calmodulin-related protein [Arabidopsis
 thaliana]

Seq. No. 2637
 Contig ID 1810_1.R1040
 5'-most EST zhf700955314.h1

Seq. No. 2638
 Contig ID 1811_1.R1040
 5'-most EST g4291898

Seq. No. 2639
 Contig ID 1811_2.R1040
 5'-most EST jC-gmro02910023d08d1

Seq. No. 2640
 Contig ID 1812_1.R1040
 5'-most EST LIB3028-053-Q1-B1-A5

Seq. No. 2641
 Contig ID 1814_1.R1040
 5'-most EST zhf700955022.h1

Seq. No. 2642
 Contig ID 1815_1.R1040
 5'-most EST uC-gmrominsoy275h01b1

Seq. No. 2643
 Contig ID 1815_2.R1040
 5'-most EST uC-gmrominsoy157d05b1

Seq. No. 2644
 Contig ID 1815_3.R1040
 5'-most EST LIB3092-006-Q1-K1-C12

Seq. No. 2645

E value 3.0e-60
Match length 134
% identity 87
NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No. 2665
Contig ID 1830_2.R1040
5'-most EST leu701156037.h1
Method BLASTX
NCBI GI g2407800
BLAST score 179
E value 3.0e-13
Match length 62
% identity 61
NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No. 2666
Contig ID 1831_1.R1040
5'-most EST LIB3049-002-Q1-E1-H1
Method BLASTN
NCBI GI g2598656
BLAST score 304
E value 1.0e-170
Match length 551
% identity 89
NCBI Description Vicia faba mRNA for elongation factor 1-alpha (EF1-a)

Seq. No. 2667
Contig ID 1833_1.R1040
5'-most EST LIB3106-006-Q1-K1-D6
Method BLASTX
NCBI GI g2262170
BLAST score 1117
E value 1.0e-122
Match length 350
% identity 65
NCBI Description (AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana]

Seq. No. 2668
Contig ID 1833_2.R1040
5'-most EST ssr700558633.h1
Method BLASTX
NCBI GI g2262170
BLAST score 423
E value 2.0e-41
Match length 183
% identity 51
NCBI Description (AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana]

Seq. No. 2669
Contig ID 1833_8.R1040
5'-most EST gsv701045546.h1

Seq. No. 2670
Contig ID 1834_1.R1040

NCBI GI g2894603
 BLAST score 189
 E value 1.0e-14
 Match length 56
 % identity 22
 NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 2697
 Contig ID 1856_1.R1040
 5'-most EST LIB3040-059-Q1-E1-H6
 Method BLASTX
 NCBI GI g3786005
 BLAST score 845
 E value 2.0e-90
 Match length 363
 % identity 40
 NCBI Description (AC005499) putative phosphoethanolamine
 cytidyltransferase [Arabidopsis thaliana]

Seq. No. 2698
 Contig ID 1856_2.R1040
 5'-most EST jex700909340.h1
 Method BLASTX
 NCBI GI g3786005
 BLAST score 584
 E value 4.0e-60
 Match length 191
 % identity 38
 NCBI Description (AC005499) putative phosphoethanolamine
 cytidyltransferase [Arabidopsis thaliana]

Seq. No. 2699
 Contig ID 1857_1.R1040
 5'-most EST pcp700991629.h1

Seq. No. 2700
 Contig ID 1859_1.R1040
 5'-most EST LIB3106-077-P1-K1-G5
 Method BLASTX
 NCBI GI g1706082
 BLAST score 379
 E value 3.0e-36
 Match length 131
 % identity 60
 NCBI Description SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3)
 >gi_629787_pir_S44191 serine-type carboxypeptidase (EC
 3.4.16.1) II-3 - barley >gi_619350_bbs_153536
 CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley,
 cv. Alexis, aleurone, Peptide, 516 aa]
 >gi_474392_emb_CAA55478_ (X78877) serine carboxylase II-3
 [Hordeum vulgare]

Seq. No. 2701
 Contig ID 1860_1.R1040
 5'-most EST LIB3087-009-Q1-K1-G2
 Method BLASTX
 NCBI GI g4539454

BLAST score 276
 E value 6.0e-24
 Match length 208
 % identity 37
 NCBI Description (AL049500) contains EST gb:AA728416 [Arabidopsis thaliana]

Seq. No. 2702
 Contig ID 1860_2.R1040
 5'-most EST LIB3072-052-Q1-E1-F8

Seq. No. 2703
 Contig ID 1861_1.R1040
 5'-most EST jex700904613.h1

Seq. No. 2704
 Contig ID 1862_1.R1040
 5'-most EST LIB3107-024-Q1-K1-A10

Seq. No. 2705
 Contig ID 1864_1.R1040
 5'-most EST LIB3028-052-Q1-B1-B12

Seq. No. 2706
 Contig ID 1864_2.R1040
 5'-most EST seb700647923.h1
 Method BLASTX
 NCBI GI g1439625
 BLAST score 174
 E value 1.0e-12
 Match length 91
 % identity 37
 NCBI Description (U64598) weakly similar to S. cerevisiae PTM1 precursor (SP:P32857) [Caenorhabditis elegans]

Seq. No. 2707
 Contig ID 1865_1.R1040
 5'-most EST jC-gmle01810028a08a1

Seq. No. 2708
 Contig ID 1869_1.R1040
 5'-most EST uC-gmrominsoy283c08b1
 Method BLASTX
 NCBI GI g4432869
 BLAST score 552
 E value 1.0e-56
 Match length 157
 % identity 66
 NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No. 2709
 Contig ID 1869_2.R1040
 5'-most EST LIB3106-113-Q1-K1-E5
 Method BLASTX
 NCBI GI g4432869
 BLAST score 362
 E value 4.0e-34
 Match length 113

% identity 60
 NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No. 2710
 Contig ID 1877 1.R1040
 5'-most EST awf700842923.h1

Seq. No. 2711
 Contig ID 1877 2.R1040
 5'-most EST LIB3072-060-Q1-K1-F5

Seq. No. 2712
 Contig ID 1882 1.R1040
 5'-most EST LIB3055-013-Q1-N1-A7

Seq. No. 2713
 Contig ID 1884 1.R1040
 5'-most EST rlr700898336.h1
 Method BLASTX
 NCBI GI g3128177
 BLAST score 258
 E value 2.0e-22
 Match length 102
 % identity 46
 NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 2714
 Contig ID 1885 1.R1040
 5'-most EST LIB3049-027-Q1-E1-F4
 Method BLASTX
 NCBI GI g266945
 BLAST score 893
 E value 2.0e-96
 Match length 192
 % identity 90
 NCBI Description 60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
 >gi_100065_pir_S19978 ribosomal protein L9 - garden pea
 >gi_20727_emb_CAA46273_(X65155) GA [Pisum sativum]
 >gi_1279645_emb_CAA65987_(X97322) ribosomal protein L9
 [Pisum sativum]

Seq. No. 2715
 Contig ID 1885 2.R1040
 5'-most EST sat701009469.h1
 Method BLASTX
 NCBI GI g266945
 BLAST score 874
 E value 3.0e-94
 Match length 192
 % identity 88
 NCBI Description 60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
 >gi_100065_pir_S19978 ribosomal protein L9 - garden pea
 >gi_20727_emb_CAA46273_(X65155) GA [Pisum sativum]
 >gi_1279645_emb_CAA65987_(X97322) ribosomal protein L9
 [Pisum sativum]

Seq. No. 2716

Match length 104
 % identity 88
 NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No. 2735
 Contig ID 1891_1.R1040
 5'-most EST leu701146963.h1
 Method BLASTX
 NCBI GI g2088651
 BLAST score 250
 E value 8.0e-32
 Match length 222
 % identity 42
 NCBI Description (AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No. 2736
 Contig ID 1891_2.R1040
 5'-most EST LIB3170-006-Q1-K1-H3
 Method BLASTN
 NCBI GI g2264316
 BLAST score 50
 E value 8.0e-19
 Match length 137
 % identity 88
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MR011, complete sequence [Arabidopsis thaliana]

Seq. No. 2737
 Contig ID 1891_3.R1040
 5'-most EST g5753333
 Method BLASTX
 NCBI GI g2088651
 BLAST score 169
 E value 1.0e-11
 Match length 57
 % identity 51
 NCBI Description (AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No. 2738
 Contig ID 1892_1.R1040
 5'-most EST uC-gmronoir032g02b1
 Method BLASTX
 NCBI GI g4006899
 BLAST score 410
 E value 4.0e-40
 Match length 112
 % identity 63
 NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 2739
 Contig ID 1892_2.R1040
 5'-most EST g4294695
 Method BLASTX
 NCBI GI g4006899
 BLAST score 203

Seq. No. 2751
 Contig ID 1898_1.R1040
 5'-most EST leu701149544.h1
 Method BLASTX
 NCBI GI g2129636
 BLAST score 328
 E value 4.0e-30
 Match length 219
 % identity 39
 NCBI Description lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]

Seq. No. 2752
 Contig ID 1899_1.R1040
 5'-most EST bth700844448.h1
 Method BLASTX
 NCBI GI g4263048
 BLAST score 622
 E value 1.0e-64
 Match length 209
 % identity 61
 NCBI Description (AC005142) putative hydrolase [Arabidopsis thaliana]

Seq. No. 2753
 Contig ID 1899_2.R1040
 5'-most EST fua701038150.h1
 Method BLASTX
 NCBI GI g4263048
 BLAST score 278
 E value 1.0e-24
 Match length 108
 % identity 56
 NCBI Description (AC005142) putative hydrolase [Arabidopsis thaliana]

Seq. No. 2754
 Contig ID 1900_1.R1040
 5'-most EST LIB3107-061-Q1-K1-G1
 Method BLASTN
 NCBI GI g456567
 BLAST score 275
 E value 1.0e-153
 Match length 451
 % identity 90
 NCBI Description Pisum sativum ubiquitin conjugating enzyme (UBC4), complete cds

Seq. No. 2755
 Contig ID 1900_3.R1040
 5'-most EST LIB3049-023-Q1-E1-B9
 Method BLASTN
 NCBI GI g456567
 BLAST score 67
 E value 3.0e-29
 Match length 187
 % identity 84
 NCBI Description Pisum sativum ubiquitin conjugating enzyme (UBC4), complete

cds

Seq. No. 2756
 Contig ID 1900_4.R1040
 5'-most EST bth700846257.h1
 Method BLASTN
 NCBI GI g456567
 BLAST score 65
 E value 4.0e-28
 Match length 178
 % identity 90
 NCBI Description Pisum sativum ubiquitin conjugating enzyme (UBC4), complete cds

Seq. No. 2757
 Contig ID 1901_1.R1040
 5'-most EST ujr700646501.h1
 Method BLASTN
 NCBI GI g4193381
 BLAST score 85
 E value 8.0e-40
 Match length 261
 % identity 83
 NCBI Description Arabidopsis thaliana ribosomal protein S27 (ARS27A) mRNA, complete cds

Seq. No. 2758
 Contig ID 1901_2.R1040
 5'-most EST LIB3106-088-Q1-K1-G8
 Method BLASTN
 NCBI GI g4193381
 BLAST score 91
 E value 2.0e-43
 Match length 239
 % identity 85
 NCBI Description Arabidopsis thaliana ribosomal protein S27 (ARS27A) mRNA, complete cds

Seq. No. 2759
 Contig ID 1901_3.R1040
 5'-most EST g5606680
 Method BLASTX
 NCBI GI g4193382
 BLAST score 367
 E value 4.0e-35
 Match length 83
 % identity 84
 NCBI Description (AF083336) ribosomal protein S27 [Arabidopsis thaliana]
 >gi_4193384 (AF083337) ribosomal protein S27 [Arabidopsis thaliana]

Seq. No. 2760
 Contig ID 1902_1.R1040
 5'-most EST LIB3049-016-Q1-E1-D12

Seq. No. 2761
 Contig ID 1902_2.R1040

5'-most EST bth700849686.h1

Seq. No. 2762
Contig ID 1902_3.R1040
5'-most EST LIB3107-006-Q1-K1-C9

Seq. No. 2763
Contig ID 1902_5.R1040
5'-most EST LIB3139-006-P1-N1-H2

Seq. No. 2764
Contig ID 1905_1.R1040
5'-most EST LIB3049-011-Q1-E1-F10
Method BLASTX
NCBI GI g3608481
BLAST score 610
E value 3.0e-63
Match length 146
% identity 78
NCBI Description (AF088913) ribosomal protein L27a [Petunia x hybrida]

Seq. No. 2765
Contig ID 1905_3.R1040
5'-most EST txt700735894.h1
Method BLASTN
NCBI GI g1881580
BLAST score 60
E value 4.0e-25
Match length 124
% identity 88
NCBI Description Drosophila melanogaster ribosomal protein RpL27a gene,
complete cds

Seq. No. 2766
Contig ID 1906_1.R1040
5'-most EST LIB3028-051-Q1-B1-F9

Seq. No. 2767
Contig ID 1907_1.R1040
5'-most EST kl1701208895.h1
Method BLASTX
NCBI GI g2583108
BLAST score 643
E value 9.0e-67
Match length 311
% identity 45
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No. 2768
Contig ID 1907_2.R1040
5'-most EST jC-gmst02400070b04d1

Seq. No. 2769
Contig ID 1908_1.R1040
5'-most EST fua701042926.h1
Method BLASTX
NCBI GI g2129648

Contig ID	1909_3.R1040
5'-most EST	LIB3093-040-Q1-K1-F9
Method	BLASTN
NCBI GI	g1326162
BLAST score	139
E value	6.0e-72
Match length	267
% identity	88
NCBI Description	Phaseolus vulgaris stress related protein PvSRP mRNA, complete cds
Seq. No.	2775
Contig ID	1912_1.R1040
5'-most EST	LIB3107-075-Q1-K1-C9
Method	BLASTX
NCBI GI	g3077640
BLAST score	852
E value	1.0e-91
Match length	268
% identity	63
NCBI Description	(AJ223151) O-methyltransferase [Prunus dulcis]
Seq. No.	2776
Contig ID	1912_2.R1040
5'-most EST	zhf700954691.h1
Method	BLASTX
NCBI GI	g1174621
BLAST score	879
E value	1.0e-94
Match length	330
% identity	52
NCBI Description	T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA) (CCT-THETA) >gi_1083259_pir_JC4073 TCP-1 containing cytosolic chaperonin (CCT) theta chain - mouse >gi_695625_emb_CAA85521_ (Z37164) CCTtheta, theta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus]
Seq. No.	2777
Contig ID	1915_1.R1040
5'-most EST	zhf700952177.h1
Method	BLASTX
NCBI GI	g2739389
BLAST score	1268
E value	1.0e-140
Match length	450
% identity	57
NCBI Description	(AC002505) Cf-2.2 like protein [Arabidopsis thaliana]
Seq. No.	2778
Contig ID	1916_1.R1040
5'-most EST	leu701150759.h1
Method	BLASTX
NCBI GI	g4559334
BLAST score	1197
E value	1.0e-132
Match length	326
% identity	63

NCBI GI g2499553
 BLAST score 1797
 E value 0.0e+00
 Match length 476
 % identity 75
 NCBI Description CRYPTOCHROME 1 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR)
 >gi_629524_pir_S39058 probable deoxyribodipyrimidine
 photo-lyase (EC 4.1.99.3) - Arabidopsis thaliana
 >gi_442529_bbs_139743 (S66907) flavin-type blue-light
 photoreceptor, HY4=DNA photolyase/tropomyosin A homolog
 [Arabidopsis thaliana, ecotype Columbia, Peptide, 681 aa]
 [Arabidopsis thaliana]

Seq. No. 2791
 Contig ID 1927_2.R1040
 5'-most EST kl1701204912.h1
 Method BLASTX
 NCBI GI g4325368
 BLAST score 271
 E value 1.0e-23
 Match length 157
 % identity 46
 NCBI Description (AF128396) Arabidopsis thaliana flavin-type blue-light
 photoreceptor (SW:Q43125) (Pfam: PF00875, Score=765.2,
 E=2.6e-226, N=1) [Arabidopsis thaliana]

Seq. No. 2792
 Contig ID 1927_3.R1040
 5'-most EST LIB3093-018-Q1-K1-E1

Seq. No. 2793
 Contig ID 1929_1.R1040
 5'-most EST leu701146395.h1
 Method BLASTX
 NCBI GI g2222777
 BLAST score 301
 E value 3.0e-27
 Match length 106
 % identity 58
 NCBI Description (Y13986) GTP-binding protein [Ostertagia circumcincta]

Seq. No. 2794
 Contig ID 1930_1.R1040
 5'-most EST LIB3028-051-Q1-B1-B4
 Method BLASTX
 NCBI GI g3426036
 BLAST score 239
 E value 5.0e-20
 Match length 128
 % identity 47
 NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 2795
 Contig ID 1931_1.R1040
 5'-most EST LIB3028-019-Q1-B1-A3

Seq. No. 2796

09684016.101000

Contig ID 1933_1.R1040
5'-most EST LIB3028-051-Q1-B1-B7

Seq. No. 2797
Contig ID 1934_1.R1040
5'-most EST LIB3028-051-Q1-B1-B8
Method BLASTX
NCBI GI g4309969
BLAST score 241
E value 2.0e-20
Match length 89
% identity 52
NCBI Description (AC002983) putative phosphoglyceride transfer protein
[Arabidopsis thaliana]

Seq. No. 2798
Contig ID 1934_2.R1040
5'-most EST LIB3049-045-Q1-E1-F12

Seq. No. 2799
Contig ID 1936_1.R1040
5'-most EST leu701155657.h1
Method BLASTX
NCBI GI g100347
BLAST score 383
E value 9.0e-37
Match length 141
% identity 53
NCBI Description monosaccharide transport protein MST1 - common tobacco
>gi_19885_emb_CAA47324_ (X66856) monosaccharid transporter
[Nicotiana tabacum]

Seq. No. 2800
Contig ID 1936_2.R1040
5'-most EST uC-gmflminsoy079f01b1
Method BLASTX
NCBI GI g100347
BLAST score 312
E value 1.0e-28
Match length 98
% identity 59
NCBI Description monosaccharide transport protein MST1 - common tobacco
>gi_19885_emb_CAA47324_ (X66856) monosaccharid transporter
[Nicotiana tabacum]

Seq. No. 2801
Contig ID 1940_1.R1040
5'-most EST LIB3170-078-Q1-J1-D1

Seq. No. 2802
Contig ID 1941_1.R1040
5'-most EST uC-gmrominsoy180d02b1
Method BLASTX
NCBI GI g3860263
BLAST score 1554
E value 1.0e-173
Match length 460

00684016-101000

% identity 65
NCBI Description (AC005824) putative cytochrome p450 protein [Arabidopsis thaliana]

Seq. No. 2803
Contig ID 1941_2.R1040
5'-most EST uC-gmrominsoy243e12b1
Method BLASTX
NCBI GI g3860263
BLAST score 658
E value 5.0e-70
Match length 241
% identity 58

NCBI Description (AC005824) putative cytochrome p450 protein [Arabidopsis thaliana]

Seq. No. 2804
Contig ID 1941_4.R1040
5'-most EST LIB3092-058-Q1-K1-E8
Method BLASTX
NCBI GI g3860263
BLAST score 288
E value 8.0e-26
Match length 91
% identity 59

NCBI Description (AC005824) putative cytochrome p450 protein [Arabidopsis thaliana]

Seq. No. 2805
Contig ID 1942_1.R1040
5'-most EST LIB3028-043-Q1-B1-E4
Method BLASTX
NCBI GI g2244956
BLAST score 307
E value 1.0e-27
Match length 146
% identity 43

NCBI Description (Z97340) strong similarity to pectinesterase [Arabidopsis thaliana]

Seq. No. 2806
Contig ID 1942_2.R1040
5'-most EST jC-gmfl02220130e04d1

Seq. No. 2807
Contig ID 1944_1.R1040
5'-most EST LIB3107-044-Q1-K1-E9

Seq. No. 2808
Contig ID 1944_3.R1040
5'-most EST zhf700964515.h1

Seq. No. 2809
Contig ID 1946_1.R1040
5'-most EST sat701015379.h1
Method BLASTX
NCBI GI g2760320

BLAST score 162
 E value 1.0e-85
 Match length 354
 % identity 86
 NCBI Description M.sativa (Nagyszenasi) mRNA for ribosomal protein RL5

Seq. No. 2817
 Contig ID 1947_4.R1040
 5'-most EST LIB3028-009-Q1-B1-F12
 Method BLASTN
 NCBI GI g4512656
 BLAST score 67
 E value 4.0e-29
 Match length 115
 % identity 90
 NCBI Description Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No. 2818
 Contig ID 1947_5.R1040
 5'-most EST LIB3170-016-Q1-K1-G1
 Method BLASTN
 NCBI GI g463251
 BLAST score 241
 E value 1.0e-133
 Match length 553
 % identity 86
 NCBI Description M.sativa (Nagyszenasi) mRNA for ribosomal protein RL5

Seq. No. 2819
 Contig ID 1947_7.R1040
 5'-most EST LIB3040-019-Q1-E1-F10
 Method BLASTX
 NCBI GI g1173055
 BLAST score 462
 E value 3.0e-46
 Match length 124
 % identity 81
 NCBI Description 60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir_S42497
 ribosomal protein L11.e - alfalfa >gi_1076504_pir_S51819
 RL5 ribosomal protein - alfalfa >gi_463252_emb_CAA55090_
 (X78284) RL5 ribosomal protein [Medicago sativa]

Seq. No. 2820
 Contig ID 1947_9.R1040
 5'-most EST zzp700829957.h1
 Method BLASTN
 NCBI GI g1944341
 BLAST score 87
 E value 3.0e-41
 Match length 147
 % identity 90
 NCBI Description Glycine max DNA for cysteine proteinase inhibitor, complete cds

Seq. No. 2821
 Contig ID 1947_12.R1040

E value 0.0e+00
 Match length 374
 % identity 89
 NCBI Description (U81288) PsRT17-1 [Pisum sativum]

Seq. No. 2828
 Contig ID 1950_2.R1040
 5'-most EST jC-gmst02400050d06a1
 Method BLASTN
 NCBI GI g1778375
 BLAST score 50
 E value 7.0e-19
 Match length 86
 % identity 90
 NCBI Description Pisum sativum PsRT17-1 mRNA, complete cds

Seq. No. 2829
 Contig ID 1950_5.R1040
 5'-most EST LIB3065-006-Q1-N1-E7
 Method BLASTN
 NCBI GI g1778375
 BLAST score 36
 E value 7.0e-11
 Match length 74
 % identity 93
 NCBI Description Pisum sativum PsRT17-1 mRNA, complete cds

Seq. No. 2830
 Contig ID 1950_6.R1040
 5'-most EST zhf700962217.h1
 Method BLASTN
 NCBI GI g1778375
 BLAST score 159
 E value 4.0e-84
 Match length 377
 % identity 87
 NCBI Description Pisum sativum PsRT17-1 mRNA, complete cds

Seq. No. 2831
 Contig ID 1950_9.R1040
 5'-most EST wrg700786756.h2

Seq. No. 2832
 Contig ID 1951_1.R1040
 5'-most EST LIB3139-087-P1-N1-D6
 Method BLASTX
 NCBI GI g2654358
 BLAST score 494
 E value 1.0e-49
 Match length 175
 % identity 54
 NCBI Description (Y15522) MNUDC protein [Mus musculus]
 >gi_2808636_emb_CAA57201_ (X81443) Sig 92 [Mus musculus]

Seq. No. 2833
 Contig ID 1951_2.R1040
 5'-most EST leu701151540.h1

NCBI Description (AL031369) putative protein [Arabidopsis thaliana]
 >gi_4567258_gb_AAD23672.1 AC007070_21 (AC007070)
 hypothetical protein [Arabidopsis thaliana]

Seq. No. 2839
 Contig ID 1956_1.R1040
 5'-most EST crh700854558.h1
 Method BLASTX
 NCBI GI g133872
 BLAST score 1491
 E value 1.0e-166
 Match length 363
 % identity 80
 NCBI Description 30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)
 >gi_282838_pir_S26494 ribosomal protein S1, chloroplast -
 spinach >gi_322404_pir_A44121 small subunit ribosomal
 protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_
 (X66135) ribosomal protein S1 [Spinacia oleracea]
 >gi_170143 (M82923) chloroplast ribosomal protein S1
 [Spinacia oleracea]

Seq. No. 2840
 Contig ID 1956_2.R1040
 5'-most EST LIB3106-006-Q1-K1-G8
 Method BLASTX
 NCBI GI g133872
 BLAST score 469
 E value 5.0e-47
 Match length 101
 % identity 93
 NCBI Description 30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)
 >gi_282838_pir_S26494 ribosomal protein S1, chloroplast -
 spinach >gi_322404_pir_A44121 small subunit ribosomal
 protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_
 (X66135) ribosomal protein S1 [Spinacia oleracea]
 >gi_170143 (M82923) chloroplast ribosomal protein S1
 [Spinacia oleracea]

Seq. No. 2841
 Contig ID 1957_1.R1040
 5'-most EST bth700848861.h1
 Method BLASTX
 NCBI GI g1076610
 BLAST score 1404
 E value 1.0e-156
 Match length 355
 % identity 70
 NCBI Description cathepsin B-like cysteine proteinase (EC 3.4.22.-) - Aztec
 tobacco >gi_609175_emb_CAA57522_ (X81995) cathepsin B-like
 cysteine proteinase [Nicotiana rustica]

Seq. No. 2842
 Contig ID 1957_2.R1040
 5'-most EST jC-gmf102220056d01d1

Seq. No. 2843
 Contig ID 1957_3.R1040

Seq. No. 2849
 Contig ID 1958_1.R1040
 5'-most EST LIB3028-051-Q1-B1-A8
 Method BLASTX
 NCBI GI g3256035
 BLAST score 956
 E value 1.0e-107
 Match length 458
 % identity 46
 NCBI Description (Y14274) putative serine/threonine protein kinase [Sorghum
 bicolor]

Seq. No. 2850
 Contig ID 1958_2.R1040
 5'-most EST fC-gmse700855803a1
 Method BLASTX
 NCBI GI g2980770
 BLAST score 576
 E value 5.0e-59
 Match length 284
 % identity 45
 NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 2851
 Contig ID 1958_4.R1040
 5'-most EST uC-gmropic107g01b1

Seq. No. 2852
 Contig ID 1958_5.R1040
 5'-most EST seb700653353.h1

Seq. No. 2853
 Contig ID 1958_6.R1040
 5'-most EST 6HC-01-Q1-B1-E11
 Method BLASTX
 NCBI GI g1777312
 BLAST score 153
 E value 7.0e-10
 Match length 45
 % identity 64
 NCBI Description (D30622) novel serine/threonine protein kinase [Arabidopsis
 thaliana]

Seq. No. 2854
 Contig ID 1958_8.R1040
 5'-most EST jC-gmro02910020g05d1
 Method BLASTX
 NCBI GI g2980770
 BLAST score 183
 E value 2.0e-13
 Match length 65
 % identity 54
 NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 2855
 Contig ID 1959_1.R1040
 5'-most EST LIB3028-051-Q1-B1-A9

Method BLASTX
 NCBI GI g3080391
 BLAST score 679
 E value 5.0e-71
 Match length 292
 % identity 67
 NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

Seq. No. 2856
 Contig ID 1961_1.R1040
 5'-most EST wvk700681379.h2
 Method BLASTX
 NCBI GI g3341899
 BLAST score 185
 E value 4.0e-13
 Match length 110
 % identity 45
 NCBI Description (AB009285) BCNT [Homo sapiens]

Seq. No. 2857
 Contig ID 1962_1.R1040
 5'-most EST jC-gmro02800033c10a1
 Method BLASTX
 NCBI GI g2129956
 BLAST score 467
 E value 2.0e-46
 Match length 155
 % identity 55
 NCBI Description photoassimilate-responsive protein PAR-1c precursor - common tobacco >gi_871489_emb_CAA58732_ (X83852) mRNA inducible by sucrose and salicylic acid and potato virus Y expressed in sugar-accumulating plants [Nicotiana tabacum]

Seq. No. 2858
 Contig ID 1962_2.R1040
 5'-most EST ncj700982510.h1
 Method BLASTX
 NCBI GI g2129956
 BLAST score 353
 E value 2.0e-33
 Match length 115
 % identity 54
 NCBI Description photoassimilate-responsive protein PAR-1c precursor - common tobacco >gi_871489_emb_CAA58732_ (X83852) mRNA inducible by sucrose and salicylic acid and potato virus Y expressed in sugar-accumulating plants [Nicotiana tabacum]

Seq. No. 2859
 Contig ID 1962_3.R1040
 5'-most EST g4437054
 Method BLASTX
 NCBI GI g4544412
 BLAST score 384
 E value 1.0e-36
 Match length 173
 % identity 40
 NCBI Description (AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No. 2860
 Contig ID 1965_1.R1040
 5'-most EST epv701106858.h1
 Method BLASTX
 NCBI GI g4388726
 BLAST score 1425
 E value 1.0e-158
 Match length 383
 % identity 71
 NCBI Description (AC006413) putative 12-oxophytodienoate-10,11-reductase
 [Arabidopsis thaliana]

Seq. No. 2861
 Contig ID 1965_2.R1040
 5'-most EST pmv700893580.h1
 Method BLASTX
 NCBI GI g4388726
 BLAST score 811
 E value 7.0e-87
 Match length 198
 % identity 76
 NCBI Description (AC006413) putative 12-oxophytodienoate-10,11-reductase
 [Arabidopsis thaliana]

Seq. No. 2862
 Contig ID 1965_3.R1040
 5'-most EST LIB3170-037-Q1-J1-C12

Seq. No. 2863
 Contig ID 1965_4.R1040
 5'-most EST LIB3109-009-Q1-K1-G10
 Method BLASTX
 NCBI GI g4388726
 BLAST score 390
 E value 9.0e-38
 Match length 97
 % identity 76
 NCBI Description (AC006413) putative 12-oxophytodienoate-10,11-reductase
 [Arabidopsis thaliana]

Seq. No. 2864
 Contig ID 1966_1.R1040
 5'-most EST vzy700756786.h1
 Method BLASTX
 NCBI GI g4220512
 BLAST score 229
 E value 3.0e-19
 Match length 57
 % identity 72
 NCBI Description (AL035356) putative pectate lyase [Arabidopsis thaliana]

Seq. No. 2865
 Contig ID 1967_1.R1040
 5'-most EST LIB3028-052-Q1-B2-E1
 Method BLASTX
 NCBI GI g3608412

Seq. No. 2873
 Contig ID 1975_1.R1040
 5'-most EST uC-gmrominsoy302h05b1
 Method BLASTX
 NCBI GI g4262233
 BLAST score 460
 E value 1.0e-45
 Match length 246
 % identity 46
 NCBI Description (AC006200) hypothetical protein [Arabidopsis thaliana]

Seq. No. 2874
 Contig ID 1976_1.R1040
 5'-most EST jC-gmro02910046b07a1
 Method BLASTX
 NCBI GI g4567281
 BLAST score 201
 E value 3.0e-15
 Match length 114
 % identity 43
 NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]

Seq. No. 2875
 Contig ID 1976_3.R1040
 5'-most EST leu701150855.h1

Seq. No. 2876
 Contig ID 1977_1.R1040
 5'-most EST LIB3028-050-Q1-B1-G9

Seq. No. 2877
 Contig ID 1979_1.R1040
 5'-most EST LIB3028-026-Q1-B1-H2
 Method BLASTX
 NCBI GI g4204466
 BLAST score 582
 E value 8.0e-60
 Match length 222
 % identity 56
 NCBI Description (AF067417) mannose lectin [Dolichos lablab]

Seq. No. 2878
 Contig ID 1980_1.R1040
 5'-most EST epX701107594.h1
 Method BLASTN
 NCBI GI g3551246
 BLAST score 181
 E value 6.0e-97
 Match length 499
 % identity 85
 NCBI Description Daucus carota mRNA for 181, partial cds

Seq. No. 2879
 Contig ID 1983_1.R1040
 5'-most EST jC-gmle01810018c12a2
 Method BLASTX

NCBI GI g2911799
 BLAST score 1303
 E value 1.0e-144
 Match length 328
 % identity 75
 NCBI Description (AF008184) 4-coumarate:CoA ligase 1 [Populus balsamifera
 subsp. trichocarpa X Populus deltoides]

Seq. No. 2880
 Contig ID 1984_1.R1040
 5'-most EST zhf700956267.h1
 Method BLASTX
 NCBI GI g2262110
 BLAST score 235
 E value 7.0e-20
 Match length 65
 % identity 63
 NCBI Description (AC002343) zinc finger protein isolog [Arabidopsis
 thaliana]

Seq. No. 2881
 Contig ID 1986_1.R1040
 5'-most EST asn701131155.h1
 Method BLASTN
 NCBI GI g2970050
 BLAST score 380
 E value 0.0e+00
 Match length 692
 % identity 89
 NCBI Description Vigna radiata mRNA for ARG10, complete cds

Seq. No. 2882
 Contig ID 1986_2.R1040
 5'-most EST pxt700944387.h1

Seq. No. 2883
 Contig ID 1986_3.R1040
 5'-most EST zzp700833378.h1
 Method BLASTN
 NCBI GI g2970050
 BLAST score 320
 E value 1.0e-180
 Match length 727
 % identity 88
 NCBI Description Vigna radiata mRNA for ARG10, complete cds

Seq. No. 2884
 Contig ID 1986_4.R1040
 5'-most EST fua701040205.h1
 Method BLASTN
 NCBI GI g2970050
 BLAST score 215
 E value 1.0e-117
 Match length 351
 % identity 90
 NCBI Description Vigna radiata mRNA for ARG10, complete cds

Seq. No. 2885
 Contig ID 1986_9.R1040
 5'-most EST jC-gmf102220097h01a1
 Method BLASTN
 NCBI GI g2970050
 BLAST score 78
 E value 9.0e-36
 Match length 355
 % identity 87
 NCBI Description Vigna radiata mRNA for ARG10, complete cds

Seq. No. 2886
 Contig ID 1987_1.R1040
 5'-most EST g5753538
 Method BLASTX
 NCBI GI g2967456
 BLAST score 473
 E value 2.0e-47
 Match length 164
 % identity 54
 NCBI Description (AB012048) sulfate transporter [Arabidopsis thaliana]

Seq. No. 2887
 Contig ID 1988_1.R1040
 5'-most EST LIB3028-040-Q1-B1-G1

Seq. No. 2888
 Contig ID 1988_2.R1040
 5'-most EST zsg701118956.h1

Seq. No. 2889
 Contig ID 1989_1.R1040
 5'-most EST jC-gmro02910024d07a1
 Method BLASTX
 NCBI GI g3193330
 BLAST score 510
 E value 2.0e-51
 Match length 208
 % identity 55
 NCBI Description (AF069299) contains similarity to Medicago sativa corC (GB:L22305) [Arabidopsis thaliana]

Seq. No. 2890
 Contig ID 1989_2.R1040
 5'-most EST 6HA-01-Q1-B1-G3

Seq. No. 2891
 Contig ID 1989_4.R1040
 5'-most EST zhf700962925.h1
 Method BLASTX
 NCBI GI g3738316
 BLAST score 156
 E value 1.0e-10
 Match length 42
 % identity 74
 NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 2892
 Contig ID 1991_1.R1040
 5'-most EST zzp700830841.h1
 Method BLASTX
 NCBI GI g3790581
 BLAST score 237
 E value 3.0e-19
 Match length 157
 % identity 37
 NCBI Description (AF079179) RING-H2 finger protein RHB1a [Arabidopsis thaliana]

Seq. No. 2893
 Contig ID 1991_2.R1040
 5'-most EST LIB3051-102-Q1-K1-C7
 Method BLASTX
 NCBI GI g3790581
 BLAST score 214
 E value 6.0e-17
 Match length 111
 % identity 38
 NCBI Description (AF079179) RING-H2 finger protein RHB1a [Arabidopsis thaliana]

Seq. No. 2894
 Contig ID 1991_3.R1040
 5'-most EST sat701009081.h1

Seq. No. 2895
 Contig ID 1993_1.R1040
 5'-most EST LIB3039-048-Q1-E1-D8
 Method BLASTX
 NCBI GI g4512671
 BLAST score 381
 E value 3.0e-36
 Match length 162
 % identity 57
 NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]

Seq. No. 2896
 Contig ID 1993_2.R1040
 5'-most EST LIB3039-006-Q1-E1-H10

Seq. No. 2897
 Contig ID 1993_3.R1040
 5'-most EST asn701138996.h1
 Method BLASTX
 NCBI GI g4512671
 BLAST score 333
 E value 1.0e-30
 Match length 146
 % identity 47
 NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]

Seq. No. 2898
 Contig ID 1994_1.R1040
 5'-most EST leu701150696.h1

Method	BLASTN
NCBI GI	g1658196
BLAST score	475
E value	0.0e+00
Match length	1107
% identity	86
NCBI Description	Ricinus communis calreticulin mRNA, complete cds
Seq. No.	2899
Contig ID	1994_2.R1040
5'-most EST	LIB3087-001-Q1-K1-A11
Method	BLASTX
NCBI GI	g4467153
BLAST score	550
E value	3.0e-56
Match length	126
% identity	78
NCBI Description	(AL035540) putative thaumatin-like protein [Arabidopsis thaliana]
Seq. No.	2900
Contig ID	1997_1.R1040
5'-most EST	LIB3040-042-Q1-E1-A8
Method	BLASTN
NCBI GI	g2465009
BLAST score	98
E value	1.0e-47
Match length	170
% identity	89
NCBI Description	Fragaria vesca mRNA for putative acyl carrier protein
Seq. No.	2901
Contig ID	1997_2.R1040
5'-most EST	g5607168
Method	BLASTN
NCBI GI	g1838960
BLAST score	91
E value	3.0e-43
Match length	215
% identity	86
NCBI Description	C.glauca mRNA for acyl carrier protein
Seq. No.	2902
Contig ID	1998_1.R1040
5'-most EST	uC-gmronoir037d06b1
Seq. No.	2903
Contig ID	1998_2.R1040
5'-most EST	zzp700832963.h1
Seq. No.	2904
Contig ID	1999_1.R1040
5'-most EST	LIB3028-050-Q1-B1-F1
Method	BLASTX
NCBI GI	g4249386
BLAST score	166
E value	1.0e-11

Match length 37
 % identity 86
 NCBI Description (AC005966) Strong similarity to gb_AF061286 gamma-adaptin 1 from Arabidopsis thaliana. EST gb_H37393 comes from this gene. [Arabidopsis thaliana]

Seq. No. 2905
 Contig ID 2002_1.R1040
 5'-most EST LIB3028-050-Q1-B1-A8
 Method BLASTX
 NCBI GI g3928089
 BLAST score 670
 E value 4.0e-70
 Match length 188
 % identity 66
 NCBI Description (AC005770) putative osr40 [Arabidopsis thaliana]

Seq. No. 2906
 Contig ID 2002_2.R1040
 5'-most EST LIB3049-014-Q1-E1-H9
 Method BLASTX
 NCBI GI g3928089
 BLAST score 390
 E value 2.0e-37
 Match length 101
 % identity 68
 NCBI Description (AC005770) putative osr40 [Arabidopsis thaliana]

Seq. No. 2907
 Contig ID 2003_1.R1040
 5'-most EST LIB3139-094-P1-N1-B6
 Method BLASTX
 NCBI GI g2191150
 BLAST score 852
 E value 1.0e-149
 Match length 355
 % identity 45
 NCBI Description (AF007269) similar to mitochondrial carrier family [Arabidopsis thaliana]

Seq. No. 2908
 Contig ID 2003_2.R1040
 5'-most EST LIB3170-073-Q1-K1-G9
 Method BLASTX
 NCBI GI g2191150
 BLAST score 345
 E value 2.0e-32
 Match length 81
 % identity 37
 NCBI Description (AF007269) similar to mitochondrial carrier family [Arabidopsis thaliana]

Seq. No. 2909
 Contig ID 2003_3.R1040
 5'-most EST LIB3106-090-Q1-K1-C6
 Method BLASTX
 NCBI GI g2191150

BLAST score 263
E value 8.0e-23
Match length 91
% identity 67
NCBI Description (AF007269) similar to mitochondrial carrier family
[Arabidopsis thaliana]

Seq. No. 2910
Contig ID 2004_1.R1040
5'-most EST LIB3030-009-Q1-B1-H9
Method BLASTX
NCBI GI g728867
BLAST score 736
E value 1.0e-77
Match length 325
% identity 44
NCBI Description ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR
>gi_99694_pir_S21961 proline-rich protein APG -
Arabidopsis thaliana >gi_22599_emb_CAA42925_ (X60377) APG
[Arabidopsis thaliana]

Seq. No. 2911
Contig ID 2005_1.R1040
5'-most EST vwf700674514.h1
Method BLASTX
NCBI GI g2583108
BLAST score 218
E value 2.0e-17
Match length 79
% identity 57
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No. 2912
Contig ID 2005_2.R1040
5'-most EST LIB3106-004-Q1-K1-E8
Method BLASTX
NCBI GI g2507093
BLAST score 340
E value 3.0e-31
Match length 154
% identity 2
NCBI Description PERIOD CLOCK PROTEIN >gi_1196649 (M12039) ORF starts at 87,
first start codon is found at 210.; putative [Mus musculus]

Seq. No. 2913
Contig ID 2005_3.R1040
5'-most EST LIB3094-048-Q1-K1-H6
Method BLASTX
NCBI GI g2583108
BLAST score 765
E value 2.0e-81
Match length 233
% identity 65
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No. 2914
Contig ID 2006_1.R1040

NCBI GI g3953473
 BLAST score 504
 E value 9.0e-51
 Match length 140
 % identity 71
 NCBI Description (AC002328) F2202.18 [Arabidopsis thaliana]

Seq. No. 2925
 Contig ID 2017_3.R1040
 5'-most EST LIB3106-043-Q1-K1-F4
 Method BLASTX
 NCBI GI g131194
 BLAST score 387
 E value 3.0e-37
 Match length 89
 % identity 85
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR
 (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi_72686_pir_F1SP5
 photosystem I chain V precursor - spinach
 >gi_21299_emb_CAA31524_(X13134) PSI subunit V preprotein
 (AA -69 to 98) [Spinacia oleracea] >gi_226167_prf_1413236B
 photosystem I reaction center V [Spinacia oleracea]

Seq. No. 2926
 Contig ID 2017_4.R1040
 5'-most EST LIB3138-010-Q1-N1-H6

Seq. No. 2927
 Contig ID 2019_1.R1040
 5'-most EST LIB3028-050-Q1-B1-C8
 Method BLASTX
 NCBI GI g1076398
 BLAST score 186
 E value 8.0e-14
 Match length 48
 % identity 73
 NCBI Description ribosomal protein L2 - Arabidopsis thaliana
 >gi_572523_emb_CAA57902_(X82556) ribosomal protein L2
 [Arabidopsis thaliana]

Seq. No. 2928
 Contig ID 2021_1.R1040
 5'-most EST LIB3051-012-Q1-E1-H12
 Method BLASTX
 NCBI GI g2498973
 BLAST score 288
 E value 3.0e-25
 Match length 270
 % identity 31
 NCBI Description SURFEIT LOCUS PROTEIN 1 >gi_1362943_pir_S57749 SURF-1
 protein - human >gi_895849_emb_CAA84476_(Z35093) SURF-1
 [Homo sapiens] >gi_4507319_ref_NP_003163.1_pSURF1_surfeit

Seq. No. 2929
 Contig ID 2022_1.R1040
 5'-most EST LIB3028-049-Q1-B1-H6

Seq. No. 2930
Contig ID 2024_1.R1040
5'-most EST jC-gmst02400048g07a1

Seq. No. 2931
Contig ID 2024_2.R1040
5'-most EST jsh701066682.h1

Seq. No. 2932
Contig ID 2025_1.R1040
5'-most EST uC-gmrominsoy271f10b1
Method BLASTX
NCBI GI g1362093
BLAST score 675
E value 1.0e-70
Match length 212
% identity 63
NCBI Description hypothetical protein (clone TPP15) - tomato (fragment)
>gi_924632 (U20595) unknown [Solanum lycopersicum]

Seq. No. 2933
Contig ID 2025_2.R1040
5'-most EST LIB3106-112-Q1-K1-G9
Method BLASTX
NCBI GI g1362093
BLAST score 222
E value 1.0e-17
Match length 100
% identity 64
NCBI Description hypothetical protein (clone TPP15) - tomato (fragment)
>gi_924632 (U20595) unknown [Solanum lycopersicum]

Seq. No. 2934
Contig ID 2025_3.R1040
5'-most EST awf700842920.h1
Method BLASTN
NCBI GI g924631
BLAST score 59
E value 2.0e-24
Match length 119
% identity 87
NCBI Description Solanum lycopersicum predominantly pistil-, sepal-, and fruit-expressed unknown protein mRNA, partial cds

Seq. No. 2935
Contig ID 2025_4.R1040
5'-most EST uC-gmrominsoy243b12b1
Method BLASTX
NCBI GI g1362093
BLAST score 636
E value 3.0e-66
Match length 163
% identity 72
NCBI Description hypothetical protein (clone TPP15) - tomato (fragment)
>gi_924632 (U20595) unknown [Solanum lycopersicum]

Seq. No. 2936

Contig ID 2025_5.R1040
 5'-most EST LIB3106-049-Q1-K1-G2
 Method BLASTN
 NCBI GI g924631
 BLAST score 51
 E value 2.0e-19
 Match length 119
 % identity 86
 NCBI Description Solanum lycopersicum predominantly pistil-, sepal-, and fruit-expressed unknown protein mRNA, partial cds

Seq. No. 2937
 Contig ID 2025_7.R1040
 5'-most EST LIB3139-085-P4-N4-F12

Seq. No. 2938
 Contig ID 2028_2.R1040
 5'-most EST jex700909111.h1
 Method BLASTX
 NCBI GI g1834288
 BLAST score 149
 E value 2.0e-09
 Match length 149
 % identity 28
 NCBI Description (AB000475) S.pombe TFA2 homolog [Schizosaccharomyces pombe]

Seq. No. 2939
 Contig ID 2030_1.R1040
 5'-most EST jC-gmf102220073c06a1
 Method BLASTX
 NCBI GI g2832625
 BLAST score 337
 E value 4.0e-31
 Match length 194
 % identity 38
 NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 2940
 Contig ID 2030_2.R1040
 5'-most EST LIB3039-032-Q1-E1-D4
 Method BLASTX
 NCBI GI g2832625
 BLAST score 605
 E value 1.0e-62
 Match length 257
 % identity 45
 NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 2941
 Contig ID 2032_1.R1040
 5'-most EST LIB3028-049-Q1-B1-H11

Seq. No. 2942
 Contig ID 2034_1.R1040
 5'-most EST LIB3106-060-Q1-K1-F3

Seq. No. 2943

Seq. No.	2948
Contig ID	2040_1.R1040
5'-most EST	LIB3028-020-Q1-B1-A1
Method	BLASTX
NCBI GI	g419963
BLAST score	285
E value	4.0e-25
Match length	85
% identity	59
NCBI Description	snRNP protein B - fruit fly (<i>Drosophila melanogaster</i>) >gi_290272 (L02919) ribonucleoprotein [<i>Drosophila melanogaster</i>]
Seq. No.	2949
Contig ID	2040_2.R1040
5'-most EST	g4397638
Method	BLASTN
NCBI GI	g3510341
BLAST score	46
E value	1.0e-16
Match length	114
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC16, complete sequence [<i>Arabidopsis thaliana</i>]
Seq. No.	2950
Contig ID	2042_1.R1040
5'-most EST	LIB3039-014-Q1-E1-A3
Method	BLASTX
NCBI GI	g2565429
BLAST score	144
E value	1.0e-08
Match length	36
% identity	75
NCBI Description	(AF027686) glycine-rich protein [<i>Onobrychis viciifolia</i>]
Seq. No.	2951
Contig ID	2042_2.R1040
5'-most EST	LIB3039-035-Q1-E1-H4
Method	BLASTX
NCBI GI	g2565429
BLAST score	150
E value	2.0e-09
Match length	61
% identity	49
NCBI Description	(AF027686) glycine-rich protein [<i>Onobrychis viciifolia</i>]
Seq. No.	2952
Contig ID	2043_1.R1040
5'-most EST	uC-gmropic027h11b1
Method	BLASTX
NCBI GI	g1706130
BLAST score	830
E value	6.0e-89
Match length	189
% identity	83

Match length	118
% identity	44
NCBI Description	(AC002130) F1N21.10 [Arabidopsis thaliana]
Seq. No.	2959
Contig ID	2047_2.R1040
5'-most EST	LIB3170-047-Q1-J1-A2
Method	BLASTX
NCBI GI	g2648692
BLAST score	160
E value	2.0e-10
Match length	262
% identity	28
NCBI Description	(AE000975) NADH oxidase (noxA-5) [Archaeoglobus fulgidus]
Seq. No.	2960
Contig ID	2047_3.R1040
5'-most EST	pcp700995722.h1
Seq. No.	2961
Contig ID	2047_4.R1040
5'-most EST	jC-gmro02910067h12a1
Seq. No.	2962
Contig ID	2048_1.R1040
5'-most EST	LIB3028-049-Q1-B1-E5
Method	BLASTX
NCBI GI	g3377517
BLAST score	346
E value	2.0e-32
Match length	149
% identity	46
NCBI Description	(AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]
Seq. No.	2963
Contig ID	2050_1.R1040
5'-most EST	LIB3028-049-Q1-B1-E8
Seq. No.	2964
Contig ID	2051_1.R1040
5'-most EST	dpr701101734.h1
Method	BLASTX
NCBI GI	g4262236
BLAST score	830
E value	4.0e-92
Match length	256
% identity	66
NCBI Description	(AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]
Seq. No.	2965
Contig ID	2051_2.R1040
5'-most EST	jC-gmle01810073a01a1
Method	BLASTX
NCBI GI	g4262236
BLAST score	362
E value	3.0e-34

Match length	106
% identity	73
NCBI Description	(AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]
Seq. No.	2966
Contig ID	2053_1.R1040
5'-most EST	LIB3072-021-Q1-E1-B12
Seq. No.	2967
Contig ID	2053_2.R1040
5'-most EST	LIB3050-003-Q1-E1-B7
Seq. No.	2968
Contig ID	2054_1.R1040
5'-most EST	uC-gmrominsoy244e12b1
Method	BLASTN
NCBI GI	g4159704
BLAST score	50
E value	8.0e-19
Match length	320
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence [Arabidopsis thaliana]
Seq. No.	2969
Contig ID	2054_2.R1040
5'-most EST	LIB3028-049-Q1-B1-F11
Method	BLASTN
NCBI GI	g4159704
BLAST score	50
E value	6.0e-19
Match length	187
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence [Arabidopsis thaliana]
Seq. No.	2970
Contig ID	2054_3.R1040
5'-most EST	leu701152121.h1
Seq. No.	2971
Contig ID	2055_1.R1040
5'-most EST	LIB3092-041-Q1-K1-G3
Method	BLASTX
NCBI GI	g1854443
BLAST score	1598
E value	1.0e-179
Match length	376
% identity	79
NCBI Description	(D83970) CPRD8 protein [Vigna unguiculata]
Seq. No.	2972
Contig ID	2055_2.R1040
5'-most EST	LIB3051-068-Q1-K1-A4
Method	BLASTX
NCBI GI	g2232254

Seq. No. 2978
 Contig ID 2059_3.R1040
 5'-most EST txt700734209.h1
 Method BLASTX
 NCBI GI g2982463
 BLAST score 146
 E value 2.0e-09
 Match length 37
 % identity 76
 NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

Seq. No. 2979
 Contig ID 2060_1.R1040
 5'-most EST LIB3109-014-Q1-K1-B11
 Method BLASTX
 NCBI GI g4580397
 BLAST score 498
 E value 3.0e-50
 Match length 204
 % identity 50
 NCBI Description (AC007171) putative RNA helicase [Arabidopsis thaliana]

Seq. No. 2980
 Contig ID 2061_1.R1040
 5'-most EST zhf700962048.h1

Seq. No. 2981
 Contig ID 2061_3.R1040
 5'-most EST leu701156542.h1
 Method BLASTN
 NCBI GI g1924955
 BLAST score 57
 E value 2.0e-23
 Match length 57
 % identity 100
 NCBI Description L.luteus 5S rRNA gene

Seq. No. 2982
 Contig ID 2061_5.R1040
 5'-most EST zhf700954372.h1

Seq. No. 2983
 Contig ID 2061_6.R1040
 5'-most EST jC-gmst02400040c11a1

Seq. No. 2984
 Contig ID 2063_1.R1040
 5'-most EST fC-gmfl700905086f4
 Method BLASTX
 NCBI GI g2598587
 BLAST score 2091
 E value 0.0e+00
 Match length 464
 % identity 80
 NCBI Description (Y15366) cycloartenol synthase [Medicago truncatula]

Seq. No. 2985

Contig ID	2065 1.R1040
5'-most EST	LIB3028-048-Q1-B1-F7
Seq. No.	2986
Contig ID	2068 1.R1040
5'-most EST	LIB3028-049-Q1-B1-D7
Seq. No.	2987
Contig ID	2069 1.R1040
5'-most EST	sat701009654.h1
Seq. No.	2988
Contig ID	2070 1.R1040
5'-most EST	g5510085
Seq. No.	2989
Contig ID	2070 2.R1040
5'-most EST	g4396899
Method	BLASTX
NCBI GI	g2583123
BLAST score	525
E value	2.0e-53
Match length	145
% identity	68
NCBI Description	(AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]
Seq. No.	2990
Contig ID	2073 1.R1040
5'-most EST	LIB3028-039-Q1-B2-C1
Seq. No.	2991
Contig ID	2074 1.R1040
5'-most EST	LIB3028-049-Q1-B1-B4
Method	BLASTX
NCBI GI	g4468979
BLAST score	590
E value	9.0e-61
Match length	243
% identity	55
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]
Seq. No.	2992
Contig ID	2074 2.R1040
5'-most EST	fua701041905.h1
Method	BLASTX
NCBI GI	g4468979
BLAST score	416
E value	7.0e-41
Match length	86
% identity	90
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]
Seq. No.	2993
Contig ID	2075 1.R1040
5'-most EST	LIB3028-049-Q1-B1-B5

Seq. No. 3005
 Contig ID 2083_1.R1040
 5'-most EST hyd700724953.h1
 Method BLASTX
 NCBI GI g3292814
 BLAST score 1095
 E value 1.0e-120
 Match length 317
 % identity 70
 NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 3006
 Contig ID 2083_2.R1040
 5'-most EST LIB3138-059-Q1-N1-C8
 Method BLASTX
 NCBI GI g3292814
 BLAST score 452
 E value 6.0e-45
 Match length 128
 % identity 70
 NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 3007
 Contig ID 2083_3.R1040
 5'-most EST LIB3028-049-Q1-B1-B3

Seq. No. 3008
 Contig ID 2083_4.R1040
 5'-most EST g5606500
 Method BLASTX
 NCBI GI g3292814
 BLAST score 316
 E value 4.0e-29
 Match length 94
 % identity 68
 NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 3009
 Contig ID 2085_1.R1040
 5'-most EST kl1701203522.h2
 Method BLASTX
 NCBI GI g4457221
 BLAST score 372
 E value 5.0e-35
 Match length 161
 % identity 56
 NCBI Description (AF127797) putative bZIP DNA-binding protein [Capsicum chinense]

Seq. No. 3010
 Contig ID 2085_2.R1040
 5'-most EST LIB3087-011-Q1-K1-C12
 Method BLASTX
 NCBI GI g4457221
 BLAST score 361
 E value 7.0e-34

Match length	496
% identity	75
NCBI Description	(AJ005042) beta-galactosidase [<i>Cicer arietinum</i>]
Seq. No.	3023
Contig ID	2096_4.R1040
5'-most EST	uC-gmflminsoy001a11b1
Method	BLASTX
NCBI GI	g3860420
BLAST score	1813
E value	0.0e+00
Match length	383
% identity	84
NCBI Description	(AJ011047) exo galactanase [<i>Lupinus angustifolius</i>]
Seq. No.	3024
Contig ID	2096_5.R1040
5'-most EST	uC-gmflminsoy034h12b1
Seq. No.	3025
Contig ID	2096_6.R1040
5'-most EST	LIB3072-052-Q1-E1-D10
Method	BLASTN
NCBI GI	g3860419
BLAST score	65
E value	6.0e-28
Match length	117
% identity	90
NCBI Description	<i>Lupinus angustifolius</i> mRNA for exo galactanase
Seq. No.	3026
Contig ID	2096_8.R1040
5'-most EST	sat701007604.h1
Method	BLASTN
NCBI GI	g3860419
BLAST score	119
E value	3.0e-60
Match length	199
% identity	90
NCBI Description	<i>Lupinus angustifolius</i> mRNA for exo galactanase
Seq. No.	3027
Contig ID	2097_1.R1040
5'-most EST	LIB3028-048-Q1-B1-G12
Method	BLASTX
NCBI GI	g2760326
BLAST score	1178
E value	1.0e-129
Match length	531
% identity	46
NCBI Description	(AC002130) F1N21.11 [<i>Arabidopsis thaliana</i>]
Seq. No.	3028
Contig ID	2097_2.R1040
5'-most EST	g5676937
Method	BLASTX
NCBI GI	g2760326

5'-most EST jC-gmro02800036a04d1
 Method BLASTN
 NCBI GI g516248
 BLAST score 97
 E value 4.0e-47
 Match length 177
 % identity 89
 NCBI Description A.thaliana gene for porphobilinogen deaminase

Seq. No. 3035
 Contig ID 2102_1.R1040
 5'-most EST LIB3049-042-Q1-E1-A8

Seq. No. 3036
 Contig ID 2102_2.R1040
 5'-most EST LIB3049-004-Q1-E1-G5

Seq. No. 3037
 Contig ID 2103_1.R1040
 5'-most EST LIB3093-029-Q1-K1-E5
 Method BLASTN
 NCBI GI g3928149
 BLAST score 412
 E value 0.0e+00
 Match length 852
 % identity 87
 NCBI Description Cicer arietinum mRNA for hypothetical protein

Seq. No. 3038
 Contig ID 2103_2.R1040
 5'-most EST uC-gmropic028g12b1
 Method BLASTX
 NCBI GI g3928150
 BLAST score 230
 E value 2.0e-40
 Match length 124
 % identity 72
 NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]

Seq. No. 3039
 Contig ID 2103_3.R1040
 5'-most EST kl1701203849.h1
 Method BLASTN
 NCBI GI g3928149
 BLAST score 69
 E value 1.0e-30
 Match length 197
 % identity 84
 NCBI Description Cicer arietinum mRNA for hypothetical protein

Seq. No. 3040
 Contig ID 2105_1.R1040
 5'-most EST txt700735241.h1
 Method BLASTX
 NCBI GI g3641837
 BLAST score 1027
 E value 0.0e+00

Match length 94
 % identity 43
 NCBI Description (X94625) amp-binding protein [Brassica napus]

Seq. No. 3052
 Contig ID 2120_1.R1040
 5'-most EST jC-gmst02400060f04a1

Seq. No. 3053
 Contig ID 2120_2.R1040
 5'-most EST uC-gmflminsoy028d12b1
 Method BLASTX
 NCBI GI g3063710
 BLAST score 208
 E value 3.0e-16
 Match length 150
 % identity 37
 NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 3054
 Contig ID 2123_1.R1040
 5'-most EST zsg701123264.h1
 Method BLASTX
 NCBI GI g3319340
 BLAST score 231
 E value 5.0e-19
 Match length 91
 % identity 54
 NCBI Description (AF077407) contains similarity to E. coli cation transport protein ChaC (GB:D90756) [Arabidopsis thaliana]

Seq. No. 3055
 Contig ID 2125_1.R1040
 5'-most EST uC-gmflminsoy078e04b1

Seq. No. 3056
 Contig ID 2126_1.R1040
 5'-most EST LIB3028-048-Q1-B1-D9
 Method BLASTX
 NCBI GI g3513738
 BLAST score 149
 E value 2.0e-09
 Match length 37
 % identity 68
 NCBI Description (AF080118) similar to the GDSL family of lipolytic enzymes [Arabidopsis thaliana]

Seq. No. 3057
 Contig ID 2131_1.R1040
 5'-most EST LIB3087-009-Q1-K1-E1
 Method BLASTX
 NCBI GI g2618721
 BLAST score 716
 E value 2.0e-75
 Match length 231
 % identity 67
 NCBI Description (U49072) IAA16 [Arabidopsis thaliana]

Seq. No. 3058
 Contig ID 2131_2.R1040
 5'-most EST LIB3039-034-Q1-E1-F1
 Method BLASTX
 NCBI GI g114734
 BLAST score 655
 E value 2.0e-68
 Match length 226
 % identity 65
 NCBI Description AUXIN-INDUCED PROTEIN AUX28 >gi_81759_pir_A28993_aux28
 protein - soybean >gi_169921 (J03919) auxin-regulated
 protein (Aux28) [Glycine max]

Seq. No. 3059
 Contig ID 2131_3.R1040
 5'-most EST LIB3107-066-Q1-K1-D4
 Method BLASTX
 NCBI GI g2618721
 BLAST score 660
 E value 6.0e-69
 Match length 234
 % identity 61
 NCBI Description (U49072) IAA16 [Arabidopsis thaliana]

Seq. No. 3060
 Contig ID 2131_4.R1040
 5'-most EST sat701006155.h1
 Method BLASTX
 NCBI GI g2618721
 BLAST score 116
 E value 1.0e-08
 Match length 69
 % identity 61
 NCBI Description (U49072) IAA16 [Arabidopsis thaliana]

Seq. No. 3061
 Contig ID 2132_1.R1040
 5'-most EST LIB3028-048-Q1-B1-C8
 Method BLASTX
 NCBI GI g2352492
 BLAST score 488
 E value 6.0e-49
 Match length 115
 % identity 78
 NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis
 thaliana] >gi_2352494 (AF005048) transport inhibitor
 response 1 [Arabidopsis thaliana]

Seq. No. 3062
 Contig ID 2132_2.R1040
 5'-most EST uC-gmrominsoyl25g04b1
 Method BLASTX
 NCBI GI g2352492
 BLAST score 329
 E value 2.0e-30
 Match length 83

% identity 71
 NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No. 3063
 Contig ID 2134_1.R1040
 5'-most EST LIB3139-039-P1-N1-H4
 Method BLASTX
 NCBI GI g2947062
 BLAST score 550
 E value 8.0e-56
 Match length 534
 % identity 35
 NCBI Description (AC002521) unknown protein [Arabidopsis thaliana]

Seq. No. 3064
 Contig ID 2134_2.R1040
 5'-most EST uC-gmropic083d02b1

Seq. No. 3065
 Contig ID 2134_3.R1040
 5'-most EST pmv700894820.h1

Seq. No. 3066
 Contig ID 2135_1.R1040
 5'-most EST LIB3167-023-P4-K4-B8
 Method BLASTX
 NCBI GI g2495180
 BLAST score 1073
 E value 1.0e-117
 Match length 251
 % identity 84
 NCBI Description PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG) (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN SYNTHASE) >gi_421882_pir_S35873 hydroxymethylbilane synthase (EC 4.3.1.8) - garden pea >gi_541971_pir_JQ2278 hydroxymethylbilane synthase (EC 4.3.1.8) precursor - garden pea chloroplast >gi_313724_emb_CAA51820_ (X73418) hydroxymethylbilane synthase [Pisum sativum]

Seq. No. 3067
 Contig ID 2135_2.R1040
 5'-most EST LIB3028-048-Q1-B1-D10
 Method BLASTN
 NCBI GI g313723
 BLAST score 134
 E value 3.0e-69
 Match length 322
 % identity 85
 NCBI Description P.sativum hemC mRNA for hydroxymethylbilane synthase

Seq. No. 3068
 Contig ID 2135_5.R1040
 5'-most EST gsv701054125.h1
 Method BLASTX
 NCBI GI g2495179

BLAST score 268
 E value 1.0e-37
 Match length 146
 % identity 79
 NCBI Description PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG)
 (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN
 SYNTHASE) >gi_1084340_pir_S50762 hydroxymethylbilane
 synthase (EC 4.3.1.8) precursor - Arabidopsis thaliana
 >gi_313150_emb_CAA51941_ (X73535) hydroxymethylbilane
 synthase [Arabidopsis thaliana] >gi_313838_emb_CAA52061_
 (X73839) hydroxymethylbilane synthase [Arabidopsis
 thaliana]

Seq. No. 3069
 Contig ID 2135_6.R1040
 5'-most EST ncj700975534.h1
 Method BLASTX
 NCBI GI g2495180
 BLAST score 271
 E value 5.0e-36
 Match length 89
 % identity 90
 NCBI Description PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG)
 (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN
 SYNTHASE) >gi_421882_pir_S35873 hydroxymethylbilane
 synthase (EC 4.3.1.8) - garden pea >gi_541971_pir_JQ2278
 hydroxymethylbilane synthase (EC 4.3.1.8) precursor -
 garden pea chloroplast >gi_313724_emb_CAA51820_ (X73418)
 hydroxymethylbilane synthase [Pisum sativum]

Seq. No. 3070
 Contig ID 2136_1.R1040
 5'-most EST LIB3138-022-Q1-N1-D5
 Method BLASTN
 NCBI GI g1381085
 BLAST score 322
 E value 0.0e+00
 Match length 578
 % identity 89
 NCBI Description Pisum sativum imidazoleglycerol-phosphate dehydratase
 (PSHIS3) mRNA, complete cds

Seq. No. 3071
 Contig ID 2137_1.R1040
 5'-most EST LIB3028-048-Q1-B1-D12

Seq. No. 3072
 Contig ID 2138_1.R1040
 5'-most EST LIB3093-027-Q1-K1-B1
 Method BLASTN
 NCBI GI g3885514
 BLAST score 178
 E value 3.0e-95
 Match length 334
 % identity 88
 NCBI Description Medicago sativa clone MS56 unknown mRNA

Method BLASTN
 NCBI GI g297877
 BLAST score 102
 E value 5.0e-50
 Match length 290
 % identity 84
 NCBI Description A.thaliana UBC10 mRNA for ubiquitin conjugating enzyme homolog >gi_349212_gb_L00640_ATHUBCC Arabidopsis thaliana ubiquitin conjugating enzyme mRNA, complete cds

Seq. No. 3083
 Contig ID 2141_1.R1040
 5'-most EST kl1701212974.h1
 Method BLASTX
 NCBI GI g2464855
 BLAST score 551
 E value 2.0e-56
 Match length 176
 % identity 66
 NCBI Description (Z99707). myb-related protein [Arabidopsis thaliana]

Seq. No. 3084
 Contig ID 2144_2.R1040
 5'-most EST jC-gmfl02220108a01a1

Seq. No. 3085
 Contig ID 2144_3.R1040
 5'-most EST jC-gmfl02220090d03a1
 Method BLASTN
 NCBI GI g3033512
 BLAST score 557
 E value 0.0e+00
 Match length 1251
 % identity 87
 NCBI Description Phaseolus vulgaris rubisco activase (Rcal) mRNA, complete cds

Seq. No. 3086
 Contig ID 2144_4.R1040
 5'-most EST LIB3138-105-Q1-N1-F11
 Method BLASTN
 NCBI GI g4406529
 BLAST score 499
 E value 0.0e+00
 Match length 1411
 % identity 88
 NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No. 3087
 Contig ID 2148_1.R1040
 5'-most EST uC-gmrominsoy176b07b1
 Method BLASTX
 NCBI GI g4115925
 BLAST score 798
 E value 6.0e-85
 Match length 270

% identity 60
 NCBI Description (AF118222) contains similarity to RNA recognition motifs
 (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
 >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein
 [Arabidopsis thaliana]

Seq. No. 3088
 Contig ID 2148_2.R1040
 5'-most EST jC-gmst02400014a06a1
 Method BLASTX
 NCBI GI g4115925
 BLAST score 683
 E value 9.0e-72
 Match length 231
 % identity 43

NCBI Description (AF118222) contains similarity to RNA recognition motifs
 (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
 >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein
 [Arabidopsis thaliana]

Seq. No. 3089
 Contig ID 2150_1.R1040
 5'-most EST pmv700894902.h1

Seq. No. 3090
 Contig ID 2150_2.R1040
 5'-most EST sat701013106.h1

Seq. No. 3091
 Contig ID 2151_1.R1040
 5'-most EST dpv701103482.h1
 Method BLASTX
 NCBI GI g2462927
 BLAST score 178
 E value 6.0e-13
 Match length 64
 % identity 52
 NCBI Description (Y10342) putative amidase [Arabidopsis thaliana]

Seq. No. 3092
 Contig ID 2152_1.R1040
 5'-most EST kl1701205744.h1
 Method BLASTX
 NCBI GI g285741
 BLAST score 694
 E value 1.0e-72
 Match length 376
 % identity 45
 NCBI Description (D14550) EDGP precursor [Daucus carota]

Seq. No. 3093
 Contig ID 2152_2.R1040
 5'-most EST jC-gmro02910034c10d1
 Method BLASTX
 NCBI GI g285741
 BLAST score 320
 E value 2.0e-29

Match length	104
% identity	60
NCBI Description	(D14550) EDGP precursor [Daucus. carota]
Seq. No.	3094
Contig ID	2152_3.R1040
5'-most EST	uC-gmropic116e09b1
Seq. No.	3095
Contig ID	2153_1.R1040
5'-most EST	has700548121.h1
Method	BLASTX
NCBI GI	g4006816
BLAST score	166
E value	4.0e-11
Match length	99
% identity	43
NCBI Description	(AC005970) hypothetical protein, 3' partial [Arabidopsis thaliana]
Seq. No.	3096
Contig ID	2153_2.R1040
5'-most EST	ncj700984512.h1
Seq. No.	3097
Contig ID	2154_1.R1040
5'-most EST	LIB3028-048-Q1-B1-B2
Method	BLASTX
NCBI GI	g3201619
BLAST score	557
E value	4.0e-57
Match length	163
% identity	65
NCBI Description	(AC004669) dihydroxypolyprenylbenzoate methyltransferase [Arabidopsis thaliana]
Seq. No.	3098
Contig ID	2155_1.R1040
5'-most EST	g4294625
Seq. No.	3099
Contig ID	2156_1.R1040
5'-most EST	uC-gmrominsoy173a11b1
Method	BLASTX
NCBI GI	g2181180
BLAST score	1149
E value	1.0e-125
Match length	699
% identity	38
NCBI Description	(Z84377) xylosidase [Aspergillus niger]
Seq. No.	3100
Contig ID	2158_1.R1040
5'-most EST	zhf700955352.h1
Method	BLASTX
NCBI GI	g4115547
BLAST score	282

E value 7.0e-32
 Match length 155
 % identity 51
 NCBI Description (AB012634) lectin [Robinia pseudoacacia]

Seq. No. 3101
 Contig ID 2161_1.R1040
 5'-most EST jC-gmle01810044a01d1
 Method BLASTX
 NCBI GI g1388078
 BLAST score 307
 E value 1.0e-27
 Match length 104
 % identity 47
 NCBI Description (U35826) thioredoxin h [Arabidopsis thaliana]

Seq. No. 3102
 Contig ID 2161_2.R1040
 5'-most EST uC-gmrominsoyl01a09b1
 Method BLASTX
 NCBI GI g1388078
 BLAST score 265
 E value 7.0e-23
 Match length 106
 % identity 42
 NCBI Description (U35826) thioredoxin h [Arabidopsis thaliana]

Seq. No. 3103
 Contig ID 2161_3.R1040
 5'-most EST zsg701119390.h1
 Method BLASTX
 NCBI GI g129960
 BLAST score 494
 E value 2.0e-49
 Match length 282
 % identity 42
 NCBI Description 4-NITROPHENYLPHOSPHATASE (PNPPASE)

Seq. No. 3104
 Contig ID 2161_4.R1040
 5'-most EST LIB3139-033-P1-N1-F1
 Method BLASTX
 NCBI GI g1388078
 BLAST score 269
 E value 1.0e-23
 Match length 88
 % identity 57
 NCBI Description (U35826) thioredoxin h [Arabidopsis thaliana]

Seq. No. 3105
 Contig ID 2163_1.R1040
 5'-most EST g4297823
 Method BLASTX
 NCBI GI g3372230
 BLAST score 461
 E value 9.0e-46
 Match length 140

% identity	62
NCBI Description	(AF017074) RNA polymerase I, II and III 16.5 kDa subunit [Arabidopsis thaliana]
Seq. No.	3106
Contig ID	2164_1.R1040
5'-most EST	LIB3049-050-Q1-E1-B5
Method	BLASTX
NCBI GI	g1041825
BLAST score	228
E value	4.0e-18
Match length	283
% identity	25
NCBI Description	(U26175) LPG2 [Leishmania donovani] >gi_1583457_prf__2120442A LPG2 gene [Leishmania donovani]
Seq. No.	3107
Contig ID	2166_1.R1040
5'-most EST	txt700735601.h1
Seq. No.	3108
Contig ID	2167_1.R1040
5'-most EST	LIB3028-047-Q1-B1-H1
Seq. No.	3109
Contig ID	2168_1.R1040
5'-most EST	LIB3170-057-Q1-K1-A4
Seq. No.	3110
Contig ID	2168_2.R1040
5'-most EST	jC-gmf102220104a05a1
Seq. No.	3111
Contig ID	2168_3.R1040
5'-most EST	LIB3039-046-Q1-E1-E4
Seq. No.	3112
Contig ID	2169_1.R1040
5'-most EST	jC-gmst02400026h10a1
Method	BLASTX
NCBI GI	g4115386
BLAST score	317
E value	3.0e-29
Match length	120
% identity	62
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.	3113
Contig ID	2169_3.R1040
5'-most EST	g4396207
Method	BLASTX
NCBI GI	g4115386
BLAST score	212
E value	7.0e-17
Match length	59
% identity	76
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 3114
 Contig ID 2171_1.R1040
 5'-most EST LIB3109-048-Q1-K1-A2
 Method BLASTX
 NCBI GI g2288981
 BLAST score 512
 E value 7.0e-52
 Match length 148
 % identity 67
 NCBI Description (AC002335) calcium binding protein isolog [Arabidopsis thaliana] >gi_3763938 (AC004450) putative calcium binding protein [Arabidopsis thaliana]

Seq. No. 3115
 Contig ID 2171_2.R1040
 5'-most EST dpv701099410.h1
 Method BLASTX
 NCBI GI g2288981
 BLAST score 527
 E value 3.0e-53
 Match length 148
 % identity 69
 NCBI Description (AC002335) calcium binding protein isolog [Arabidopsis thaliana] >gi_3763938 (AC004450) putative calcium binding protein [Arabidopsis thaliana]

Seq. No. 3116
 Contig ID 2171_3.R1040
 5'-most EST rca701000403.h1

Seq. No. 3117
 Contig ID 2174_1.R1040
 5'-most EST LIB3040-061-Q1-E1-H9
 Method BLASTX
 NCBI GI g4512699
 BLAST score 1164
 E value 1.0e-128
 Match length 300
 % identity 75
 NCBI Description (AC006569) putative NADH-ubiquinone oxireductase [Arabidopsis thaliana]

Seq. No. 3118
 Contig ID 2175_1.R1040
 5'-most EST LIB3028-047-Q1-B1-H7
 Method BLASTX
 NCBI GI g2088650
 BLAST score 244
 E value 2.0e-20
 Match length 74
 % identity 68
 NCBI Description (AF002109) peroxisomal ATP/ADP carrier protein isolog [Arabidopsis thaliana]

Seq. No. 3119
 Contig ID 2176_1.R1040

3.6.1.34) gamma chain precursor - sweet potato
 >gi_303626_dbj_BAA03526_ (D14699) F1-ATPase gamma subunit
 [Ipomoea batatas]

Seq. No. 3124
 Contig ID 2179_5.R1040
 5'-most EST LIB3073-015-Q1-K1-C10
 Method BLASTN
 NCBI GI g397556
 BLAST score 158
 E value 2.0e-83
 Match length 306
 % identity 88
 NCBI Description N.tabacum psaH gene for photosystem I psaH protein

Seq. No. 3125
 Contig ID 2179_6.R1040
 5'-most EST LIB3073-016-Q1-K1-B2
 Method BLASTN
 NCBI GI g397554
 BLAST score 124
 E value 5.0e-63
 Match length 284
 % identity 86
 NCBI Description N.sylvestris psaH gene for photosystem I psaH protein

Seq. No. 3126
 Contig ID 2179_7.R1040
 5'-most EST LIB3074-004-Q1-K1-H1
 Method BLASTN
 NCBI GI g397554
 BLAST score 85
 E value 9.0e-40
 Match length 249
 % identity 85
 NCBI Description N.sylvestris psaH gene for photosystem I psaH protein

Seq. No. 3127
 Contig ID 2179_8.R1040
 5'-most EST q5677856

Seq. No. 3128
 Contig ID 2179_9.R1040
 5'-most EST jC-gmro02910030a06d1
 Method BLASTN
 NCBI GI g286033
 BLAST score 44
 E value 2.0e-15
 Match length 104
 % identity 86
 NCBI Description Ipomoea batatas (sweet potato) mRNA for F1-ATPase gamma-subunit

Seq. No. 3129
 Contig ID 2179_11.R1040
 5'-most EST pmv700892366.h1
 Method BLASTN

% identity 69
NCBI Description (AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No. 3136
Contig ID 2186_2.R1040
5'-most EST LIB3028-012-Q1-B1-C9
Method BLASTX
NCBI GI g4455223
BLAST score 651
E value 8.0e-68
Match length 180
% identity 45

NCBI Description (AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No. 3137
Contig ID 2186_3.R1040
5'-most EST pcp700991124.h1
Method BLASTX
NCBI GI g4455223
BLAST score 424
E value 4.0e-59
Match length 209
% identity 32

NCBI Description (AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No. 3138
Contig ID 2186_4.R1040
5'-most EST LIB3167-023-P4-K4-G9
Method BLASTX
NCBI GI g1899188
BLAST score 266
E value 4.0e-23
Match length 72
% identity 23

NCBI Description (U90212) DNA binding protein ACBF [Nicotiana tabacum]

Seq. No. 3139
Contig ID 2186_5.R1040
5'-most EST uC-gmropic068b09b1
Method BLASTX
NCBI GI g4455223
BLAST score 331
E value 3.0e-31
Match length 100
% identity 28

NCBI Description (AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No. 3140
Contig ID 2186_7.R1040
5'-most EST uxk700669935.h1
Method BLASTX
NCBI GI g4455223
BLAST score 229

Method BLASTX
 NCBI GI g4263712
 BLAST score 373
 E value 4.0e-38
 Match length 107
 % identity 74
 NCBI Description (AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]

Seq. No. 3148
 Contig ID 2193_5.R1040
 5'-most EST LIB3139-075-P1-N1-D5
 Method BLASTX
 NCBI GI g4263712
 BLAST score 401
 E value 9.0e-39
 Match length 121
 % identity 65
 NCBI Description (AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]

Seq. No. 3149
 Contig ID 2193_7.R1040
 5'-most EST LIB3040-009-Q1-E1-A6

Seq. No. 3150
 Contig ID 2194_1.R1040
 5'-most EST fua701040372.h1
 Method BLASTX
 NCBI GI g2369714
 BLAST score 2838
 E value 0.0e+00
 Match length 865
 % identity 89
 NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 3151
 Contig ID 2194_2.R1040
 5'-most EST rlr700899150.h1
 Method BLASTN
 NCBI GI g2369713
 BLAST score 54
 E value 2.0e-21
 Match length 162
 % identity 85
 NCBI Description Beta vulgaris cDNA for elongation factor

Seq. No. 3152
 Contig ID 2194_4.R1040
 5'-most EST LIB3093-010-Q1-K1-H2
 Method BLASTX
 NCBI GI g2369714
 BLAST score 208
 E value 3.0e-16
 Match length 55
 % identity 73
 NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 3153
 Contig ID 2196_1.R1040
 5'-most EST uC-gmrominsoy199h08b1
 Method BLASTX
 NCBI GI g2492519
 BLAST score 2180
 E value 0.0e+00
 Match length 426
 % identity 99
 NCBI Description 26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase subunit [Spinacia oleracea]

Seq. No. 3154
 Contig ID 2196_2.R1040
 5'-most EST jC-gmro02910005d08d1
 Method BLASTN
 NCBI GI g1395190
 BLAST score 45
 E value 5.0e-16
 Match length 85
 % identity 88
 NCBI Description Spinacia oleracea L. mRNA for 26S proteasome ATPase subunit, complete cds

Seq. No. 3155
 Contig ID 2196_3.R1040
 5'-most EST rca701001049.h1
 Method BLASTX
 NCBI GI g2492519
 BLAST score 272
 E value 3.0e-24
 Match length 58
 % identity 90
 NCBI Description 26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase subunit [Spinacia oleracea]

Seq. No. 3156
 Contig ID 2196_4.R1040
 5'-most EST zzp700831319.h1
 Method BLASTN
 NCBI GI g1395190
 BLAST score 46
 E value 7.0e-17
 Match length 86
 % identity 88
 NCBI Description Spinacia oleracea L. mRNA for 26S proteasome ATPase subunit, complete cds

Seq. No. 3157
 Contig ID 2197_1.R1040
 5'-most EST epx701110235.h1
 Method BLASTN
 NCBI GI g1707656
 BLAST score 65

E value 5.0e-28
 Match length 105
 % identity 90
 NCBI Description P.sativum mRNA for DnaJ-like protein

Seq. No. 3158
 Contig ID 2198 1.R1040
 5'-most EST LIB3109-014-Q1-K1-D7
 Method BLASTX
 NCBI GI g4106538
 BLAST score 1078
 E value 1.0e-118
 Match length 282
 % identity 72
 NCBI Description (AF104220) gamma-tocopherol methyltransferase [Arabidopsis thaliana]

Seq. No. 3159
 Contig ID 2198 2.R1040
 5'-most EST taw700655856.h1
 Method BLASTX
 NCBI GI g4106538
 BLAST score 244
 E value 1.0e-20
 Match length 60
 % identity 75
 NCBI Description (AF104220) gamma-tocopherol methyltransferase [Arabidopsis thaliana]

Seq. No. 3160
 Contig ID 2200 1.R1040
 5'-most EST vwf700678153.h1
 Method BLASTX
 NCBI GI g1350680
 BLAST score 1614
 E value 1.0e-180
 Match length 404
 % identity 76
 NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 3161
 Contig ID 2200 3.R1040
 5'-most EST gsv701051391.h1
 Method BLASTX
 NCBI GI g2459420
 BLAST score 716
 E value 1.0e-75
 Match length 140
 % identity 98
 NCBI Description (AC002332) putative ribosomal protein L17 [Arabidopsis thaliana]

Seq. No. 3162
 Contig ID 2200 4.R1040
 5'-most EST LIB3106-005-Q1-K1-D8
 Method BLASTN
 NCBI GI g310932

BLAST score 161
 E value 4.0e-85
 Match length 421
 % identity 85
 NCBI Description Nicotiana tabacum ribosomal protein L17 mRNA, complete cds

Seq. No. 3163
 Contig ID 2200_5.R1040
 5'-most EST LIB3051-015-Q1-E1-G11
 Method BLASTN
 NCBI GI g310932
 BLAST score 145
 E value 1.0e-75
 Match length 413
 % identity 84
 NCBI Description Nicotiana tabacum ribosomal protein L17 mRNA, complete cds

Seq. No. 3164
 Contig ID 2200_8.R1040
 5'-most EST kwa701015594.h1

Seq. No. 3165
 Contig ID 2201_1.R1040
 5'-most EST LIB3093-044-Q1-K1-G2
 Method BLASTX
 NCBI GI g3249071
 BLAST score 560
 E value 3.0e-57
 Match length 164
 % identity 60
 NCBI Description (AC004473) Contains similarity to protein-tyrosine phosphatase 2 gb_L15420 from Dictyostelium discoideum. EST gb_N38718 comes from this g [Arabidopsis thaliana]

Seq. No. 3166
 Contig ID 2201_2.R1040
 5'-most EST asn701134505.h1
 Method BLASTX
 NCBI GI g3249071
 BLAST score 155
 E value 1.0e-10
 Match length 41
 % identity 68
 NCBI Description (AC004473) Contains similarity to protein-tyrosine phosphatase 2 gb_L15420 from Dictyostelium discoideum. EST gb_N38718 comes from this g [Arabidopsis thaliana]

Seq. No. 3167
 Contig ID 2204_1.R1040
 5'-most EST ssr700561073.h1
 Method BLASTN
 NCBI GI g938299
 BLAST score 690
 E value 0.0e+00
 Match length 1290
 % identity 89
 NCBI Description V.ungiculata mRNA for unknown protein (A3 gene)

09634016 101000

NCBI GI g2149051
 BLAST score 631
 E value 1.0e-116
 Match length 222
 % identity 93
 NCBI Description (U73810) small Ras-like GTP-binding protein [Arabidopsis thaliana]

Seq. No. 3175
 Contig ID 2206_10.R1040
 5'-most EST pxt700944036.h1
 Method BLASTN
 NCBI GI g1370202
 BLAST score 149
 E value 3.0e-78
 Match length 209
 % identity 93
 NCBI Description L.japonicus mRNA for small GTP-binding protein, RAN1A

Seq. No. 3176
 Contig ID 2206_11.R1040
 5'-most EST hrw701060904.h1
 Method BLASTN
 NCBI GI g1370202
 BLAST score 112
 E value 4.0e-56
 Match length 234
 % identity 94
 NCBI Description L.japonicus mRNA for small GTP-binding protein, RAN1A

Seq. No. 3177
 Contig ID 2206_13.R1040
 5'-most EST uxk700672208.h1
 Method BLASTN
 NCBI GI g1370204
 BLAST score 56
 E value 1.0e-22
 Match length 153
 % identity 92
 NCBI Description L.japonicus mRNA for small GTP-binding protein, RAN1B

Seq. No. 3178
 Contig ID 2208_1.R1040
 5'-most EST LIB3039-031-Q1-E1-A3
 Method BLASTX
 NCBI GI g4538897
 BLAST score 539
 E value 5.0e-55
 Match length 154
 % identity 63
 NCBI Description (AL049482) AX110P-like protein [Arabidopsis thaliana]

Seq. No. 3179
 Contig ID 2210_1.R1040
 5'-most EST sat701007262.h2
 Method BLASTX
 NCBI GI g2505876

Seq. No. 3184
Contig ID 2216_1.R1040
5'-most EST pxt700943374.h1

Seq. No. 3185
Contig ID 2217_1.R1040
5'-most EST LIB3051-050-Q1-K1-A10
Method BLASTX
NCBI GI g4263722
BLAST score 766
E value 1.0e-81
Match length 203
% identity 70
NCBI Description (AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No. 3186
Contig ID 2218_1.R1040
5'-most EST LIB3039-049-Q1-E1-D2
Method BLASTX
NCBI GI g4185505
BLAST score 266
E value 6.0e-23
Match length 91
% identity 54
NCBI Description (AF101038) nonspecific lipid-transfer protein precursor [Brassica napus]

Seq. No. 3187
Contig ID 2220_1.R1040
5'-most EST g5752955
Method BLASTX
NCBI GI g549750
BLAST score 233
E value 5.0e-19
Match length 96
% identity 48
NCBI Description HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION
>gi_539221_pir_S38045 hypothetical protein YKL207w - yeast (Saccharomyces cerevisiae) >gi_486369_emb_CAA82052_ (Z28207) ORF YKL207w [Saccharomyces cerevisiae]

Seq. No. 3188
Contig ID 2220_2.R1040
5'-most EST LIB3051-028-Q1-K1-G7

Seq. No. 3189
Contig ID 2220_3.R1040
5'-most EST k11701209834.h1
Method BLASTX
NCBI GI g549750
BLAST score 218
E value 2.0e-17
Match length 147
% identity 37
NCBI Description HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION
>gi_539221_pir_S38045 hypothetical protein YKL207w - yeast (Saccharomyces cerevisiae) >gi_486369_emb_CAA82052_

(Z28207) ORF YKL207w [Saccharomyces cerevisiae]

Seq. No. 3190
Contig ID 2220_4.R1040
5'-most EST sat701004550.h1

Seq. No. 3191
Contig ID 2220_5.R1040
5'-most EST LIB3050-024-Q1-K1-D10

Seq. No. 3192
Contig ID 2221_1.R1040
5'-most EST LIB3028-049-Q1-B1-A12
Method BLASTX
NCBI GI g3142301
BLAST score 1220
E value 1.0e-134
Match length 497
% identity 53
NCBI Description (AC002411) Contains similarity to neural cell adhesion molecule 2, large isoform precursor gb_M76710 from *Xenopus laevis*, and beta transducin from *S. cerevisiae* gb_Q05946. ESTs gb_N65081 gb_Z30910, gb_Z34190, gb_Z34611, gb_R30101, gb_H3630

Seq. No. 3193
Contig ID 2222_1.R1040
5'-most EST zsg701121747.h1
Method BLASTX
NCBI GI g2351374
BLAST score 821
E value 5.0e-88
Match length 180
% identity 90
NCBI Description (U54560) putative 26S proteasome subunit athMOV34 [Arabidopsis thaliana]

Seq. No. 3194
Contig ID 2224_1.R1040
5'-most EST crh700850891.h1
Method BLASTX
NCBI GI g3269287
BLAST score 751
E value 5.0e-80
Match length 177
% identity 78
NCBI Description (AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No. 3195
Contig ID 2225_1.R1040
5'-most EST zhf700955393.h1
Method BLASTX
NCBI GI g3819099
BLAST score 450
E value 1.0e-44
Match length 172
% identity 49

09684016-101000

NCBI Description (AJ009825) copper amine oxidase [Cicer arietinum]

Seq. No. 3196
Contig ID 2226_1.R1040
5'-most EST k11701205002.h1
Method BLASTX
NCBI GI g2829911
BLAST score 1328
E value 1.0e-147
Match length 363
% identity 70

NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No. 3197
Contig ID 2226_2.R1040
5'-most EST LIB3051-067-Q1-K1-E5
Method BLASTX
NCBI GI g2829911
BLAST score 212
E value 9.0e-17
Match length 87
% identity 56

NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No. 3198
Contig ID 2226_4.R1040
5'-most EST g4291800
Method BLASTX
NCBI GI g2829911
BLAST score 788
E value 5.0e-84
Match length 206
% identity 44

NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No. 3199
Contig ID 2226_5.R1040
5'-most EST jC-gmf102220063d08a1
Method BLASTX
NCBI GI g2829911
BLAST score 296
E value 8.0e-27
Match length 105
% identity 61

NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No. 3200
Contig ID 2226_6.R1040
5'-most EST LIB3049-004-Q1-E1-E12
Method BLASTX
NCBI GI g2829911
BLAST score 125
E value 8.0e-12
Match length 77
% identity 57

NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No. 3201
 Contig ID 2227_1.R1040
 5'-most EST uC-gmropic009b10b1
 Method BLASTX
 NCBI GI g2065531
 BLAST score 2076
 E value 0.0e+00
 Match length 484
 % identity 77
 NCBI Description (U78526) endo-1,4-beta-glucanase [*Lycopersicon esculentum*]

Seq. No. 3202
 Contig ID 2227_2.R1040
 5'-most EST sat701012015.h1
 Method BLASTX
 NCBI GI g2065531
 BLAST score 1055
 E value 1.0e-154
 Match length 365
 % identity 72
 NCBI Description (U78526) endo-1,4-beta-glucanase [*Lycopersicon esculentum*]

Seq. No. 3203
 Contig ID 2227_3.R1040
 5'-most EST LIB3051-041-Q1-K1-B12
 Method BLASTX
 NCBI GI g2065531
 BLAST score 363
 E value 3.0e-34
 Match length 92
 % identity 71
 NCBI Description (U78526) endo-1,4-beta-glucanase [*Lycopersicon esculentum*]

Seq. No. 3204
 Contig ID 2229_1.R1040
 5'-most EST asn701139633.h1
 Method BLASTN
 NCBI GI g3366929
 BLAST score 35
 E value 5.0e-10
 Match length 71
 % identity 87
 NCBI Description *Solanum tuberosum* putative phosphatidylinositol 4-kinase (PI4KI) mRNA, partial cds

Seq. No. 3205
 Contig ID 2230_1.R1040
 5'-most EST jex700908180.h1
 Method BLASTX
 NCBI GI g118158
 BLAST score 1697
 E value 0.0e+00
 Match length 362
 % identity 87
 NCBI Description VIGNAIN PRECURSOR (BEAN ENDOPEPTIDASE) (CYSTEINE PROTEINASE) (SULFHYDRYL-ENDOPEPTIDASE) (SH-EP)
 >gi_82006_pir__S12581 cysteine proteinase (EC 3.4.22.-) -

Seq. No.	3212
Contig ID	2234_2.R1040
5'-most EST	zsg701118222.h1
Method	BLASTN
NCBI GI	g3341671
BLAST score	42
E value	3.0e-14
Match length	122
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	3213
Contig ID	2237_1.R1040
5'-most EST	uC-gmrominsoy093g12b1
Method	BLASTX
NCBI GI	g1171577
BLAST score	745
E value	3.0e-79
Match length	173
% identity	82
NCBI Description	(X95343) hypersensitivity-related gene [Nicotiana tabacum]
Seq. No.	3214
Contig ID	2238_1.R1040
5'-most EST	jC-gmf102220114g03a1
Seq. No.	3215
Contig ID	2245_1.R1040
5'-most EST	LIB3028-046-Q1-B1-G11
Method	BLASTX
NCBI GI	g4455337
BLAST score	290
E value	8.0e-26
Match length	213
% identity	31
NCBI Description	(AL035525) pectinesterase-like protein [Arabidopsis thaliana]
Seq. No.	3216
Contig ID	2247_1.R1040
5'-most EST	LIB3106-021-Q1-K1-C9
Method	BLASTX
NCBI GI	g478409
BLAST score	491
E value	2.0e-73
Match length	256
% identity	56
NCBI Description	peroxidase (EC 1.11.1.7), cationic - adzuki bean >gi_218328_dbj_BAA01950_ (D11337) peroxidase [Vigna angularis]
Seq. No.	3217
Contig ID	2249_1.R1040
5'-most EST	wrg700789411.h2
Seq. No.	3218

Contig ID 2250 1.R1040
 5'-most EST pmv700894288.h1
 Method BLASTX
 NCBI GI g3164115
 BLAST score 231
 E value 1.0e-18
 Match length 133
 % identity 37
 NCBI Description (AJ224145) major latex-like protein [Rubus idaeus]

Seq. No. 3219
 Contig ID 2251 1.R1040
 5'-most EST LIB3028-046-Q1-B1-G6

Seq. No. 3220
 Contig ID 2253 1.R1040
 5'-most EST smc700748727.h1
 Method BLASTX
 NCBI GI g2154609
 BLAST score 390
 E value 1.0e-37
 Match length 136
 % identity 51
 NCBI Description (D63509) endoxyloglucan transferase related protein [Arabidopsis thaliana] >gi_4522010_gb_AAD21783.1 (AC007069) endoxyloglucan transferase [Arabidopsis thaliana]

Seq. No. 3221
 Contig ID 2254 1.R1040
 5'-most EST LIB3051-045-Q1-K1-C5
 Method BLASTX
 NCBI GI g1019946
 BLAST score 852
 E value 2.0e-91
 Match length 210
 % identity 77
 NCBI Description (U37060) ascorbate peroxidase [Gossypium hirsutum]

Seq. No. 3222
 Contig ID 2254 2.R1040
 5'-most EST leu701157531.h1
 Method BLASTX
 NCBI GI g1019946
 BLAST score 531
 E value 5.0e-54
 Match length 159
 % identity 73
 NCBI Description (U37060) ascorbate peroxidase [Gossypium hirsutum]

Seq. No. 3223
 Contig ID 2256 1.R1040
 5'-most EST LIB3093-027-Q1-K1-A3
 Method BLASTX
 NCBI GI g4204313
 BLAST score 532
 E value 3.0e-54

Match length 118
 % identity 85
 NCBI Description (AC003027) lcl_prt_seq No definition line found
 [Arabidopsis thaliana]

Seq. No. 3224
 Contig ID 2256_2.R1040
 5'-most EST hyd700727331.h1
 Method BLASTX
 NCBI GI g4204313
 BLAST score 372
 E value 1.0e-35
 Match length 83
 % identity 84
 NCBI Description (AC003027) lcl_prt_seq No definition line found
 [Arabidopsis thaliana]

Seq. No. 3225
 Contig ID 2257_1.R1040
 5'-most EST ssr700556995.h1
 Method BLASTX
 NCBI GI g3548808
 BLAST score 493
 E value 2.0e-49
 Match length 297
 % identity 45
 NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 3226
 Contig ID 2258_1.R1040
 5'-most EST jC-gmle01810093f07d1
 Method BLASTN
 NCBI GI g20721
 BLAST score 150
 E value 1.0e-78
 Match length 290
 % identity 90
 NCBI Description Pea mRNA for ferredoxin-NADP+ reductase

Seq. No. 3227
 Contig ID 2258_2.R1040
 5'-most EST LIB3049-003-Q1-E1-F4
 Method BLASTX
 NCBI GI g1351408
 BLAST score 1781
 E value 0.0e+00
 Match length 467
 % identity 79
 NCBI Description VACUOLAR PROCESSING ENZYME PRECURSOR (VPE)
 >gi_1076563_pir_S51117 cystein proteinase - sweet orange
 >gi_633185_emb_CAA87720_(Z47793) cystein proteinase (by
 similarity) [Citrus sinensis] >gi_1588548_prf_2208463A
 vascular processing protease [Citrus sinensis]

Seq. No. 3228
 Contig ID 2258_3.R1040
 5'-most EST uC-gmflminsoy010h10b1

Method	BLASTN
NCBI GI	g2511696
BLAST score	743
E value	0.0e+00
Match length	1412
% identity	89
NCBI Description	Phaseolus vulgaris Moldavian encoding asparagine-specific endopeptidase precursor (clone cp6b)
Seq. No.	3229
Contig ID	2258_4.R1040
5'-most EST	jC-gmle01810009h12d1
Method	BLASTN
NCBI GI	g551130
BLAST score	437
E value	0.0e+00
Match length	877
% identity	88
NCBI Description	Vicia faba ferredoxin NADP+ reductase precursor (fnr) mRNA, complete cds
Seq. No.	3230
Contig ID	2258_5.R1040
5'-most EST	fde700871556.h1
Method	BLASTN
NCBI GI	g2511696
BLAST score	715
E value	0.0e+00
Match length	1488
% identity	88
NCBI Description	Phaseolus vulgaris Moldavian encoding asparagine-specific endopeptidase precursor (clone cp6b)
Seq. No.	3231
Contig ID	2259_1.R1040
5'-most EST	ssr700554396.h1
Method	BLASTX
NCBI GI	g4539003
BLAST score	203
E value	2.0e-15
Match length	81
% identity	25
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]
Seq. No.	3232
Contig ID	2260_1.R1040
5'-most EST	rlr700898755.h1
Method	BLASTX
NCBI GI	g4544432
BLAST score	227
E value	1.0e-18
Match length	93
% identity	55
NCBI Description	(AC006955) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana]
Seq. No.	3233

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Contig ID 2261_1.R1040
5'-most EST LIB3049-053-Q1-E1-E3

Seq. No. 3234
Contig ID 2262_1.R1040
5'-most EST uC-gmronoir068e07b1

Seq. No. 3235
Contig ID 2262_2.R1040
5'-most EST LIB3170-078-Q1-K1-A7
Method BLASTX
NCBI GI g4049344
BLAST score 158
E value 3.0e-10
Match length 214
% identity 11
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

Seq. No. 3236
Contig ID 2262_3.R1040
5'-most EST uC-gmflminsoy089e10b1

Seq. No. 3237
Contig ID 2264_1.R1040
5'-most EST LIB3138-074-P1-N1-D5

Seq. No. 3238
Contig ID 2268_1.R1040
5'-most EST jC-gmst02400072c10a1
Method BLASTX
NCBI GI g3776005
BLAST score 663
E value 1.0e-69
Match length 156
% identity 87
NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No. 3239
Contig ID 2268_2.R1040
5'-most EST LIB3050-002-Q1-E1-H10
Method BLASTX
NCBI GI g3776005
BLAST score 444
E value 3.0e-44
Match length 94
% identity 93
NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No. 3240
Contig ID 2269_1.R1040
5'-most EST LIB3109-011-Q1-K1-E11
Method BLASTN
NCBI GI g1666229
BLAST score 327
E value 0.0e+00
Match length 655
% identity 87

Method BLASTX
 NCBI GI g1881585
 BLAST score 330
 E value 2.0e-30
 Match length 145
 % identity 52
 NCBI Description (U72489) remorin [Solanum tuberosum]

Seq. No. 3247
 Contig ID 2271_1.R1040
 5'-most EST fC-gmro700848271a1
 Method BLASTX
 NCBI GI g1905785
 BLAST score 895
 E value 2.0e-96
 Match length 347
 % identity 60
 NCBI Description (Y10685) G/HBF-1 [Glycine max]

Seq. No. 3248
 Contig ID 2271_2.R1040
 5'-most EST uC-gmflminsoy020d04b1
 Method BLASTX
 NCBI GI g1905785
 BLAST score 154
 E value 2.0e-15
 Match length 69
 % identity 75
 NCBI Description (Y10685) G/HBF-1 [Glycine max]

Seq. No. 3249
 Contig ID 2272_1.R1040
 5'-most EST fde700870883.h1

Seq. No. 3250
 Contig ID 2277_1.R1040
 5'-most EST LIB3093-058-Q1-K1-E12
 Method BLASTX
 NCBI GI g3075488
 BLAST score 1240
 E value 1.0e-137
 Match length 286
 % identity 82
 NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 3251
 Contig ID 2277_2.R1040
 5'-most EST jC-gmst02400014b12d1
 Method BLASTN
 NCBI GI g3075487
 BLAST score 74
 E value 5.0e-33
 Match length 180
 % identity 79
 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)
 mRNA, complete cds

Seq. No.	3252
Contig ID	2277_3.R1040
5'-most EST	LIB3138-062-Q1-N1-G10
Method	BLASTX
NCBI GI	g2827649
BLAST score	156
E value	3.0e-10
Match length	46
% identity	61
NCBI Description	(AL021637) putative protein [Arabidopsis thaliana]
Seq. No.	3253
Contig ID	2277_4.R1040
5'-most EST	LIB3065-008-Q1-N1-A8
Method	BLASTX
NCBI GI	g3075488
BLAST score	486
E value	8.0e-49
Match length	119
% identity	84
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.	3254
Contig ID	2277_5.R1040
5'-most EST	LIB3093-019-Q1-K2-H3
Method	BLASTN
NCBI GI	g3075487
BLAST score	58
E value	7.0e-24
Match length	86
% identity	92
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds
Seq. No.	3255
Contig ID	2278_1.R1040
5'-most EST	LIB3107-053-Q1-K1-E8
Method	BLASTX
NCBI GI	g2244970
BLAST score	2257
E value	0.0e+00
Match length	585
% identity	69
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana] >gi_2326365_emb_CAA74765_(Y14423) putative cell wall protein [Arabidopsis thaliana]
Seq. No.	3256
Contig ID	2280_1.R1040
5'-most EST	ssr700556839.h1
Method	BLASTX
NCBI GI	g1710807
BLAST score	2464
E value	0.0e+00
Match length	584
% identity	86
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60

NCBI GI g3482919
 BLAST score 900
 E value 4.0e-97
 Match length 241
 % identity 71
 NCBI Description (AC003970) Putative protein kinase [Arabidopsis thaliana]

Seq. No. 3262
 Contig ID 2290_1.R1040
 5'-most EST g5605900
 Method BLASTX
 NCBI GI g2253442
 BLAST score 270
 E value 3.0e-23
 Match length 78
 % identity 56
 NCBI Description (AF007784) LTCOR11 [Lavatera thuringiaca]

Seq. No. 3263
 Contig ID 2290_2.R1040
 5'-most EST LIB3028-023-Q1-B1-A9

Seq. No. 3264
 Contig ID 2290_3.R1040
 5'-most EST jex700904808.h1

Seq. No. 3265
 Contig ID 2290_4.R1040
 5'-most EST crh700851666.h1
 Method BLASTX
 NCBI GI g2253442
 BLAST score 191
 E value 1.0e-14
 Match length 46
 % identity 63
 NCBI Description (AF007784) LTCOR11 [Lavatera thuringiaca]

Seq. No. 3266
 Contig ID 2291_1.R1040
 5'-most EST LIB3049-008-Q1-E1-H2
 Method BLASTX
 NCBI GI g3298548
 BLAST score 340
 E value 6.0e-32
 Match length 138
 % identity 63
 NCBI Description (AC004681) putative spliceosomal protein [Arabidopsis thaliana]

Seq. No. 3267
 Contig ID 2292_1.R1040
 5'-most EST LIB3051-011-Q1-E1-G12

Seq. No. 3268
 Contig ID 2292_2.R1040
 5'-most EST LIB3170-085-Q1-K1-D6

Seq. No. 3269
 Contig ID 2293_1.R1040
 5'-most EST g5175583
 Method BLASTX
 NCBI GI g2078350
 BLAST score 799
 E value 3.0e-85
 Match length 192
 % identity 83
 NCBI Description (U95923) transaldolase [Solanum tuberosum]

Seq. No. 3270
 Contig ID 2293_2.R1040
 5'-most EST LIB3139-031-P1-N1-G9
 Method BLASTX
 NCBI GI g2078350
 BLAST score 1457
 E value 1.0e-162
 Match length 384
 % identity 75
 NCBI Description (U95923) transaldolase [Solanum tuberosum]

Seq. No. 3271
 Contig ID 2293_4.R1040
 5'-most EST uC-gmrominsoy026g11b1
 Method BLASTX
 NCBI GI g2078350
 BLAST score 321
 E value 1.0e-29
 Match length 71
 % identity 83
 NCBI Description (U95923) transaldolase [Solanum tuberosum]

Seq. No. 3272
 Contig ID 2294_1.R1040
 5'-most EST LIB3028-009-Q1-B1-G4
 Method BLASTX
 NCBI GI g1935019
 BLAST score 438
 E value 4.0e-43
 Match length 161
 % identity 56
 NCBI Description (Z93774) sucrose transport protein [Vicia faba]

Seq. No. 3273
 Contig ID 2294_2.R1040
 5'-most EST smc700749544.h1
 Method BLASTX
 NCBI GI g1935019
 BLAST score 473
 E value 2.0e-47
 Match length 112
 % identity 78
 NCBI Description (Z93774) sucrose transport protein [Vicia faba]

Seq. No. 3274
 Contig ID 2294_3.R1040

5'-most EST LIB3093-015-Q1-K1-G9

Seq. No. 3275
 Contig ID 2296_1.R1040
 5'-most EST kl1701214421.h1
 Method BLASTX
 NCBI GI g2245135
 BLAST score 581
 E value 7.0e-60
 Match length 156
 % identity 70
 NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No. 3276
 Contig ID 2297_1.R1040
 5'-most EST LIB3107-025-Q1-K1-G8
 Method BLASTX
 NCBI GI g4433048
 BLAST score 592
 E value 6.0e-61
 Match length 147
 % identity 79
 NCBI Description (D26578) DNA-binding protein [Daucus carota]

Seq. No. 3277
 Contig ID 2297_2.R1040
 5'-most EST uC-gmflminsoy064a03b1
 Method BLASTX
 NCBI GI g4433048
 BLAST score 592
 E value 7.0e-61
 Match length 154
 % identity 78
 NCBI Description (D26578) DNA-binding protein [Daucus carota]

Seq. No. 3278
 Contig ID 2297_5.R1040
 5'-most EST zsg701125668.h1

Seq. No. 3279
 Contig ID 2298_1.R1040
 5'-most EST uC-gmropic094g04b1
 Method BLASTX
 NCBI GI g2827143
 BLAST score 937
 E value 1.0e-101
 Match length 195
 % identity 89
 NCBI Description (AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No. 3280
 Contig ID 2298_2.R1040
 5'-most EST g4292031
 Method BLASTX
 NCBI GI g2827143
 BLAST score 415

E value 1.0e-40
Match length 79
% identity 92
NCBI Description (AF027174) cellulose synthase catalytic subunit
[Arabidopsis thaliana]

Seq. No. 3281
Contig ID 2298_3.R1040
5'-most EST dpv701097183.h1
Method BLASTX
NCBI GI g2827143
BLAST score 2504
E value 0.0e+00
Match length 522
% identity 89
NCBI Description (AF027174) cellulose synthase catalytic subunit
[Arabidopsis thaliana]

Seq. No. 3282
Contig ID 2305_1.R1040
5'-most EST pxt700946213.h1
Method BLASTX
NCBI GI g4185513
BLAST score 589
E value 1.0e-60
Match length 130
% identity 85
NCBI Description (AF102823) actin depolymerizing factor 5 [Arabidopsis
thaliana] >gi_4185517 (AF102825) actin depolymerizing
factor 5 [Arabidopsis thaliana]

Seq. No. 3283
Contig ID 2305_2.R1040
5'-most EST LIB3107-025-Q1-K1-C12
Method BLASTX
NCBI GI g4185513
BLAST score 613
E value 1.0e-63
Match length 143
% identity 83
NCBI Description (AF102823) actin depolymerizing factor 5 [Arabidopsis
thaliana] >gi_4185517 (AF102825) actin depolymerizing
factor 5 [Arabidopsis thaliana]

Seq. No. 3284
Contig ID 2306_1.R1040
5'-most EST LIB3051-042-Q1-K1-H9
Method BLASTX
NCBI GI g2262195
BLAST score 323
E value 1.0e-29
Match length 150
% identity 42
NCBI Description (U64820) josephin MJD1 [Homo sapiens]

Seq. No. 3285
Contig ID 2306_3.R1040

5'-most EST	LIB3051-104-Q1-K1-G1
Method	BLASTX
NCBI GI	g1781299
BLAST score	397
E value	2.0e-38
Match length	151
% identity	57
NCBI Description	(Y09506) transformer-SR ribonucleoprotein [Nicotiana tabacum]
Seq. No.	3286
Contig ID	2306_4.R1040
5'-most EST	g5687810
Method	BLASTX
NCBI GI	g1781299
BLAST score	272
E value	8.0e-28
Match length	110
% identity	66
NCBI Description	(Y09506) transformer-SR ribonucleoprotein [Nicotiana tabacum]
Seq. No.	3287
Contig ID	2307_1.R1040
5'-most EST	ncj700980603.h1
Seq. No.	3288
Contig ID	2309_2.R1040
5'-most EST	uC-gmrominsoy074e05b1
Seq. No.	3289
Contig ID	2310_1.R1040
5'-most EST	jex700908408.h1
Seq. No.	3290
Contig ID	2310_2.R1040
5'-most EST	kl1701202645.h1
Seq. No.	3291
Contig ID	2311_1.R1040
5'-most EST	uC-gmflminsoy061a11b1
Method	BLASTX
NCBI GI	g2511693
BLAST score	2060
E value	0.0e+00
Match length	458
% identity	83
NCBI Description	(Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
Seq. No.	3292
Contig ID	2311_2.R1040
5'-most EST	taw700658011.h1
Method	BLASTN
NCBI GI	g2511692
BLAST score	168
E value	3.0e-89
Match length	454

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% identity 90
NCBI Description Phaseolus vulgaris Moldavian encoding cysteine proteinase precursor (clone cp71)

Seq. No. 3293
Contig ID 2311_3.R1040
5'-most EST zhf700958286.h1
Method BLASTN
NCBI GI g2511692
BLAST score 70
E value 4.0e-31
Match length 209
% identity 86

NCBI Description Phaseolus vulgaris Moldavian encoding cysteine proteinase precursor (clone cp71)

Seq. No. 3294
Contig ID 2311_5.R1040
5'-most EST xpa700793534.h1
Method BLASTN
NCBI GI g2511692
BLAST score 55
E value 4.0e-22
Match length 170
% identity 86

NCBI Description Phaseolus vulgaris Moldavian encoding cysteine proteinase precursor (clone cp71)

Seq. No. 3295
Contig ID 2312_1.R1040
5'-most EST dpv701103305.h1
Method BLASTX
NCBI GI g1350720
BLAST score 452
E value 1.0e-44
Match length 111
% identity 76

NCBI Description 60S RIBOSOMAL PROTEIN L32

Seq. No. 3296
Contig ID 2312_2.R1040
5'-most EST LIB3028-045-Q1-B1-H12
Method BLASTX
NCBI GI g1350720
BLAST score 452
E value 6.0e-45
Match length 111
% identity 76

NCBI Description 60S RIBOSOMAL PROTEIN L32

Seq. No. 3297
Contig ID 2312_3.R1040
5'-most EST LIB3040-060-Q1-E1-E11
Method BLASTX
NCBI GI g1350720
BLAST score 438
E value 3.0e-43

Seq. No. 3307
Contig ID 2316_3.R1040
5'-most EST LIB3039-012-Q1-E1-C9

Seq. No. 3308
Contig ID 2317_1.R1040
5'-most EST uC-gmropic007e02b1
Method BLASTX
NCBI GI g4309738
BLAST score 820
E value 1.0e-87
Match length 297
% identity 58
NCBI Description (AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No. 3309
Contig ID 2317_2.R1040
5'-most EST vwf700673985.h1
Method BLASTX
NCBI GI g4309738
BLAST score 505
E value 5.0e-51
Match length 145
% identity 66
NCBI Description (AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No. 3310
Contig ID 2321_1.R1040
5'-most EST LIB3028-046-Q1-B1-A11
Method BLASTX
NCBI GI g1263160
BLAST score 360
E value 6.0e-34
Match length 251
% identity 12
NCBI Description (X89226) leucine-rich repeat/receptor protein kinase [Oryza sativa]

Seq. No. 3311
Contig ID 2322_1.R1040
5'-most EST asn701130506.h1
Method BLASTN
NCBI GI g1370195
BLAST score 308
E value 1.0e-172
Match length 412
% identity 94
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB8D

Seq. No. 3312
Contig ID 2322_2.R1040
5'-most EST sat701004249.h1
Method BLASTN
NCBI GI g1370195
BLAST score 256
E value 1.0e-142

E value 1.0e-82
 Match length 223
 % identity 68
 NCBI Description (L43510) protein localized in the nucleoli of pea nuclei;
 ORF; putative [Pisum sativum]

Seq. No. 3318
 Contig ID 2328_1.R1040
 5'-most EST g5677260
 Method BLASTX
 NCBI GI g2244910
 BLAST score 316
 E value 6.0e-29
 Match length 105
 % identity 50
 NCBI Description (Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No. 3319
 Contig ID 2329_1.R1040
 5'-most EST LIB3028-045-Q1-B1-F2
 Method BLASTX
 NCBI GI g2832695
 BLAST score 181
 E value 3.0e-13
 Match length 62
 % identity 58
 NCBI Description (AL021713) putative protein [Arabidopsis thaliana]

Seq. No. 3320
 Contig ID 2330_1.R1040
 5'-most EST k11701202518.h1
 Method BLASTX
 NCBI GI g1518855
 BLAST score 211
 E value 2.0e-16
 Match length 72
 % identity 61
 NCBI Description (U65960) HASPP28 [Homo sapiens]

Seq. No. 3321
 Contig ID 2330_2.R1040
 5'-most EST LIB3109-027-Q1-K1-E1
 Method BLASTN
 NCBI GI g3821780
 BLAST score 36
 E value 1.0e-10
 Match length 48
 % identity 65
 NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 3322
 Contig ID 2330_4.R1040
 5'-most EST LIB3051-024-Q1-K1-H6

Seq. No. 3323
 Contig ID 2330_5.R1040
 5'-most EST LIB3040-015-Q1-E1-A2

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NCBI Description Medicago sativa adenosylhomocysteinase mRNA, complete cds

Seq. No. 3334
 Contig ID 2339_9.R1040
 5'-most EST txt700735356.h1
 Method BLASTN
 NCBI GI g170772
 BLAST score 74
 E value 1.0e-33
 Match length 102
 % identity 93

NCBI Description Triticum aestivum S-adenosyl-L-homocysteine hydrolase (SH6.2) mRNA, complete cds

Seq. No. 3335
 Contig ID 2341_1.R1040
 5'-most EST seb700649714.h1

Seq. No. 3336
 Contig ID 2341_2.R1040
 5'-most EST txt700734826.h1

Seq. No. 3337
 Contig ID 2342_1.R1040
 5'-most EST kl1701213196.h1
 Method BLASTX
 NCBI GI g2780365
 BLAST score 229
 E value 8.0e-19
 Match length 90
 % identity 52
 NCBI Description (AB007693) Elongin C [Drosophila melanogaster]

Seq. No. 3338
 Contig ID 2343_1.R1040
 5'-most EST LIB3170-082-Q1-K1-G9
 Method BLASTX
 NCBI GI g1172874
 BLAST score 721
 E value 5.0e-76
 Match length 291
 % identity 57
 NCBI Description DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR
 >gi_479589_pir_S34823 dehydration-induced protein RD22 -
 Arabidopsis thaliana >gi_391608_dbj_BAA01546 (D10703) rd22
 [Arabidopsis thaliana] >gi_447134_prf_1913421A rd22 gene
 [Arabidopsis thaliana]

Seq. No. 3339
 Contig ID 2343_3.R1040
 5'-most EST LIB3170-082-Q1-J1-G9
 Method BLASTX
 NCBI GI g1172874
 BLAST score 300
 E value 3.0e-27
 Match length 70
 % identity 74

BLAST score 379
 E value 1.0e-35
 Match length 352
 % identity 30
 NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]

Seq. No. 3374
 Contig ID 2388_2.R1040
 5'-most EST jC-gmle01810071h10a1

Seq. No. 3375
 Contig ID 2388_3.R1040
 5'-most EST uC-gmrominsoy202c09b1

Seq. No. 3376
 Contig ID 2390_1.R1040
 5'-most EST zzp700830963.h1
 Method BLASTN
 NCBI GI g2980757
 BLAST score 51
 E value 1.0e-19
 Match length 229
 % identity 87
 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No. 3377
 Contig ID 2392_1.R1040
 5'-most EST bth700843551.h1

Seq. No. 3378
 Contig ID 2394_1.R1040
 5'-most EST LIB3039-005-Q1-E1-E2
 Method BLASTX
 NCBI GI g100196
 BLAST score 1174
 E value 1.0e-129
 Match length 249
 % identity 86
 NCBI Description chlorophyll a/b-binding protein (cab-11) - tomato

Seq. No. 3379
 Contig ID 2396_1.R1040
 5'-most EST ncj700983176.h1
 Method BLASTX
 NCBI GI g549060
 BLAST score 1088
 E value 1.0e-136
 Match length 363
 % identity 69
 NCBI Description T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA)
 >gi_631656_pir_S43058 CCTeta protein eta chain - mouse
 >gi_468504_emb_CAA83274_ (Z31399) CCTeta, eta subunit of
 the chaperonin containing TCP-1 (CCT) [Mus musculus]

Seq. No. 3380
 Contig ID 2397_1.R1040

5'-most EST leu701150938.h1

Seq. No. 3381
 Contig ID 2397_2.R1040
 5'-most EST k11701203629.h2
 Method BLASTN
 NCBI GI g3046847
 BLAST score 36
 E value 1.0e-10
 Match length 104
 % identity 84
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]

Seq. No. 3382
 Contig ID 2397_3.R1040
 5'-most EST eep700868680.h1
 Method BLASTN
 NCBI GI g3046847
 BLAST score 36
 E value 1.0e-10
 Match length 104
 % identity 84
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]

Seq. No. 3383
 Contig ID 2400_1.R1040
 5'-most EST LIB3051-054-Q1-K2-B11
 Method BLASTX
 NCBI GI g416564
 BLAST score 631
 E value 9.0e-66
 Match length 203
 % identity 64
 NCBI Description ABCISIC ACID-INDUCIBLE PROTEIN KINASE
 >gi_422013_pir_A46408 abscisic acid-inducible
 serine/threonine protein kinase homolog - wheat (fragment)
 >gi_170664 (M94726) protein kinase [Triticum aestivum]

Seq. No. 3384
 Contig ID 2403_1.R1040
 5'-most EST uC-gmflminsoy045d06b1
 Method BLASTN
 NCBI GI g3449327
 BLAST score 35
 E value 2.0e-09
 Match length 168
 % identity 85
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No. 3385
 Contig ID 2403_2.R1040
 5'-most EST jC-gmst02400007d06a1

Seq. No. 3386

Method	BLASTX
NCBI GI	g3193292
BLAST score	1576
E value	1.0e-176
Match length	371
% identity	84
NCBI Description	(AF069298) similar to ATPases associated with various cellular activities (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana]
Seq. No.	3395
Contig ID	2407_1.R1040
5'-most EST	LIB3028-045-Q1-B1-A1
Method	BLASTX
NCBI GI	g4539351
BLAST score	345
E value	1.0e-32
Match length	139
% identity	47
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]
Seq. No.	3396
Contig ID	2410_1.R1040
5'-most EST	LIB3028-044-Q1-B1-E3
Method	BLASTX
NCBI GI	g115833
BLAST score	1118
E value	1.0e-122
Match length	259
% identity	81
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR (CAB-10A) (LHCP) >gi_100195_pir_S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi_170394 (M32605) a-binding protein [Lycopersicon esculentum]
Seq. No.	3397
Contig ID	2410_2.R1040
5'-most EST	gsv701045116.h1
Method	BLASTX
NCBI GI	g115833
BLAST score	1142
E value	1.0e-125
Match length	256
% identity	81
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR (CAB-10A) (LHCP) >gi_100195_pir_S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi_170394 (M32605) a-binding protein [Lycopersicon esculentum]
Seq. No.	3398
Contig ID	2413_1.R1040
5'-most EST	LIB3055-005-Q1-N1-H2
Method	BLASTX
NCBI GI	g3068705
BLAST score	612
E value	3.0e-63
Match length	245

09684016-101000

polypeptide [Nicotiana tabacum]

Seq. No. 3413
Contig ID 2423_1.R1040
5'-most EST uC-gmflminsoy089a10b1
Method BLASTX
NCBI GI g1402912
BLAST score 646
E value 2.0e-67
Match length 169
% identity 76
NCBI Description (X98317) peroxidase [Arabidopsis thaliana]

Seq. No. 3414
Contig ID 2423_2.R1040
5'-most EST jC-gmfl02220062h05a1
Method BLASTX
NCBI GI g1402912
BLAST score 216
E value 1.0e-26
Match length 88
% identity 73
NCBI Description (X98317) peroxidase [Arabidopsis thaliana]

Seq. No. 3415
Contig ID 2423_3.R1040
5'-most EST LIB3028-001-Q1-B1-H7
Method BLASTX
NCBI GI g1403138
BLAST score 705
E value 5.0e-74
Match length 180
% identity 72
NCBI Description (X98190) peroxidase ATP2a [Arabidopsis thaliana]
>gi_4371288_gb_AAD18146_ (AC006260) putative peroxidase
ATP2a [Arabidopsis thaliana]

Seq. No. 3416
Contig ID 2423_4.R1040
5'-most EST LIB3028-004-Q1-B1-H7
Method BLASTX
NCBI GI g1402912
BLAST score 146
E value 4.0e-09
Match length 33
% identity 79
NCBI Description (X98317) peroxidase [Arabidopsis thaliana]

Seq. No. 3417
Contig ID 2426_1.R1040
5'-most EST uC-gmropic033g08b1
Method BLASTN
NCBI GI g20899
BLAST score 261
E value 1.0e-144
Match length 509
% identity 89

NCBI Description Pea mRNA for Cu/Zn superoxide dismutase II (SOD9)

Seq. No. 3418
Contig ID 2428_1.R1040
5'-most EST wvk700683015.h1
Method BLASTX
NCBI GI g2499614
BLAST score 1423
E value 1.0e-158
Match length 302
% identity 88

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG NTF3 (P43)
>gi_481830_pir_S39559.mitogen-activated protein kinase 3
homolog ntf3 - common tobacco >gi_406751_emb_CAA49592_
(X69971) NTF3 [Nicotiana tabacum]

Seq. No. 3419
Contig ID 2428_2.R1040
5'-most EST LIB3049-045-Q1-E1-H6
Method BLASTX
NCBI GI g2499612
BLAST score 187
E value 2.0e-18
Match length 55
% identity 89

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 1 (PMEK1)
>gi_1076650_pir_S52989.mitogen-activated,
extracellular-regulated protein kinase 1 (EC 2.7.1.-) -
garden petunia >gi_603871_emb_CAA58466_ (X83440) MAP/ERK
kinase 1 [Petunia x hybrida]

Seq. No. 3420
Contig ID 2429_1.R1040
5'-most EST LIB3106-056-Q1-K1-H1

Seq. No. 3421
Contig ID 2429_2.R1040
5'-most EST g5688463
Method BLASTX
NCBI GI g1582580
BLAST score 1759
E value 0.0e+00
Match length 364
% identity 90

NCBI Description caffeic acid O-methyltransferase [Stylosanthes humilis]

Seq. No. 3422
Contig ID 2429_3.R1040
5'-most EST LIB3139-024-P1-N1-A2
Method BLASTN
NCBI GI g4468045
BLAST score 76
E value 1.0e-34
Match length 156
% identity 87

NCBI Description V.planifolia mRNA for methyltransferase

NCBI GI g3434973
 BLAST score 251
 E value 5.0e-21
 Match length 66
 % identity 73
 NCBI Description (AB008106) ethylene responsive element binding factor 4
 [Arabidopsis thaliana]

Seq. No. 3445
 Contig ID 2450_5.R1040
 5'-most EST wrg700790552.h2
 Method BLASTN
 NCBI GI g4099920
 BLAST score 63
 E value 2.0e-26
 Match length 143
 % identity 90
 NCBI Description Stylosanthes hamata EREBP-3 homolog mRNA, complete cds

Seq. No. 3446
 Contig ID 2450_6.R1040
 5'-most EST LIB3170-031-Q1-K1-A12
 Method BLASTX
 NCBI GI g643469
 BLAST score 264
 E value 1.0e-22
 Match length 71
 % identity 72
 NCBI Description (U19886) unknown [Lycopersicon esculentum]

Seq. No. 3447
 Contig ID 2450_10.R1040
 5'-most EST jC-gmst02400057b12d1

Seq. No. 3448
 Contig ID 2450_11.R1040
 5'-most EST jC-gmle01810042e11a1
 Method BLASTX
 NCBI GI g4099921
 BLAST score 287
 E value 1.0e-25
 Match length 108
 % identity 54
 NCBI Description (U91982) EREBP-3 homolog [Stylosanthes hamata]

Seq. No. 3449
 Contig ID 2450_12.R1040
 5'-most EST epx701107465.h1

Seq. No. 3450
 Contig ID 2450_14.R1040
 5'-most EST dpv701101450.h1
 Method BLASTN
 NCBI GI g3434972
 BLAST score 57
 E value 2.0e-23
 Match length 101

% identity 89
NCBI Description Arabidopsis thaliana AtERF-4 mRNA for ethylene responsive element binding factor 4, complete cds

Seq. No. 3451
Contig ID 2453 1.R1040
5'-most EST LIB3030-006-Q1-B1-D8
Method BLASTX
NCBI GI g4105097
BLAST score 281
E value 4.0e-41
Match length 110
% identity 80
NCBI Description (AF043255) MADS box protein 26 [Cucumis sativus]

Seq. No. 3452
Contig ID 2454 1.R1040
5'-most EST LIB3109-010-Q1-K1-E1
Method BLASTX
NCBI GI g2570047
BLAST score 339
E value 5.0e-31
Match length 164
% identity 43
NCBI Description (Y09234) MSTK2S kinase-like protein [Mus musculus]

Seq. No. 3453
Contig ID 2457 1.R1040
5'-most EST LIB3030-008-Q1-B1-E2
Method BLASTX
NCBI GI g3386614
BLAST score 415
E value 1.0e-40
Match length 115
% identity 40
NCBI Description (AC004665) putative transcription factor SF3 [Arabidopsis thaliana]

Seq. No. 3454
Contig ID 2458 1.R1040
5'-most EST LIB3028-044-Q1-B1-B11
Method BLASTX
NCBI GI g3123059
BLAST score 185
E value 5.0e-13
Match length 180
% identity 31
NCBI Description HYPOTHETICAL PROTEIN KIAA0253 >gi_1665773_dbj_BAA13383_ (D87442) KIAA0253 [Homo sapiens]

Seq. No. 3455
Contig ID 2459 1.R1040
5'-most EST LIB3028-043-Q1-B1-H5
Method BLASTX
NCBI GI g2264373
BLAST score 335
E value 4.0e-31

Match length 169
 % identity 43
 NCBI Description (AC002354) putative NAM/no apical meristem protein
 [Arabidopsis thaliana]

Seq. No. 3456
 Contig ID 2461_1.R1040
 5'-most EST jC-gmle01810068f07a1
 Method BLASTX
 NCBI GI g1749474
 BLAST score 151
 E value 2.0e-09
 Match length 96
 % identity 40
 NCBI Description (D89133) similar to Saccharomyces cerevisiae Lph16p,
 GENBANK Accession Number U43503 [Schizosaccharomyces pombe]

Seq. No. 3457
 Contig ID 2462_1.R1040
 5'-most EST leu701151985.h1
 Method BLASTX
 NCBI GI g3747111
 BLAST score 627
 E value 3.0e-65
 Match length 211
 % identity 55
 NCBI Description (AF095641) MTN3 homolog [Arabidopsis thaliana]

Seq. No. 3458
 Contig ID 2462_2.R1040
 5'-most EST epX701105770.h1
 Method BLASTN
 NCBI GI g11565
 BLAST score 308
 E value 1.0e-173
 Match length 316
 % identity 99
 NCBI Description Soybean chloroplast psb A gene coding for photosystem II
 thylakoid membrane protein

Seq. No. 3459
 Contig ID 2465_1.R1040
 5'-most EST bth700845088.h1
 Method BLASTX
 NCBI GI g2792297
 BLAST score 334
 E value 8.0e-31
 Match length 66
 % identity 83
 NCBI Description (AF039183) GAST-like gene product [Fragaria x ananassa]

Seq. No. 3460
 Contig ID 2465_2.R1040
 5'-most EST LIB3093-015-Q1-K1-A3
 Method BLASTX
 NCBI GI g2792297
 BLAST score 334

E value 5.0e-31
Match length 66
% identity 83
NCBI Description (AF039183) GAST-like gene product [Fragaria x ananassa]

Seq. No. 3461
Contig ID 2465_3.R1040
5'-most EST LIB3107-060-Q1-K1-G3
Method BLASTX
NCBI GI g2792297
BLAST score 342
E value 8.0e-32
Match length 66
% identity 86
NCBI Description (AF039183) GAST-like gene product [Fragaria x ananassa]

Seq. No. 3462
Contig ID 2466_1.R1040
5'-most EST jsh701067168.h1
Method BLASTX
NCBI GI g4572679
BLAST score 322
E value 2.0e-29
Match length 69
% identity 87
NCBI Description (AC006954) RSZp22 splicing factor; contains RNA recognition motif [Arabidopsis thaliana]

Seq. No. 3463
Contig ID 2466_2.R1040
5'-most EST LIB3051-005-Q1-E1-D11
Method BLASTX
NCBI GI g4572679
BLAST score 406
E value 2.0e-39
Match length 104
% identity 76
NCBI Description (AC006954) RSZp22 splicing factor; contains RNA recognition motif [Arabidopsis thaliana]

Seq. No. 3464
Contig ID 2466_3.R1040
5'-most EST jC-gmfl02220115e04a1

Seq. No. 3465
Contig ID 2466_4.R1040
5'-most EST jC-gmst02400026d01a1
Method BLASTX
NCBI GI g4572679
BLAST score 278
E value 1.0e-24
Match length 60
% identity 87
NCBI Description (AC006954) RSZp22 splicing factor; contains RNA recognition motif [Arabidopsis thaliana]

Seq. No. 3466

Contig ID 2466 5.R1040
5'-most EST LIB3106-040-Q1-K1-B2

Seq. No. 3467
Contig ID 2467 1.R1040
5'-most EST LIB3109-028-Q1-K1-F3
Method BLASTX
NCBI GI g3128228
BLAST score 871
E value 9.0e-94
Match length 178
% identity 90
NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No. 3468
Contig ID 2467 2.R1040
5'-most EST LIB3028-043-Q1-B1-G5
Method BLASTX
NCBI GI g3128228
BLAST score 601
E value 1.0e-62
Match length 123
% identity 91
NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No. 3469
Contig ID 2469 1.R1040
5'-most EST leu701146773.h1
Method BLASTX
NCBI GI g4220524
BLAST score 185
E value 2.0e-13
Match length 68
% identity 54
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 3470
Contig ID 2469 2.R1040
5'-most EST kl1701203514.h2

Seq. No. 3471
Contig ID 2469 3.R1040
5'-most EST pxt700942179.h1

Seq. No. 3472
Contig ID 2472 1.R1040
5'-most EST LIB3028-043-Q1-B1-H1
Method BLASTX
NCBI GI g4538897
BLAST score 461
E value 4.0e-46
Match length 134
% identity 63

Contig ID 2488_4.R1040
5'-most EST jC-gmro02800038a07d1

Seq. No. 3490
Contig ID 2488_6.R1040
5'-most EST eep700865123.h1
Method BLASTX
NCBI GI g4220481
BLAST score 242
E value 2.0e-20
Match length 85
% identity 55
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 3491
Contig ID 2488_8.R1040
5'-most EST pcp700992848.h1

Seq. No. 3492
Contig ID 2489_1.R1040
5'-most EST LIB3170-007-Q1-K1-E9

Seq. No. 3493
Contig ID 2490_1.R1040
5'-most EST LIB3028-043-Q1-B1-F7
Method BLASTX
NCBI GI g1353018
BLAST score 196
E value 2.0e-14
Match length 157
% identity 31
NCBI Description HYPOTHETICAL 34.4 KD PROTEIN IN IDS2-MPI2 INTERGENIC REGION
>gi_1077841_pir_S55168 hypothetical protein YJL145w -
yeast (Saccharomyces cerevisiae) >gi_854552_emb_CAA60810_
(X87371) ORF10 [Saccharomyces cerevisiae]
>gi_1015557_emb_CAA89440_ (Z49420) ORF YJL145w
[Saccharomyces cerevisiae]

Seq. No. 3494
Contig ID 2491_1.R1040
5'-most EST uC-gmrominsoy119a01b1
Method BLASTX
NCBI GI g1684851
BLAST score 326
E value 3.0e-30
Match length 117
% identity 62
NCBI Description (U77935) DnaJ-like protein [Phaseolus vulgaris]

Seq. No. 3495
Contig ID 2492_1.R1040
5'-most EST gsv701055713.h1

Seq. No. 3496
Contig ID 2492_2.R1040
5'-most EST LIB3106-072-P1-K1-B6

>gi_4559389_gb_AAD23049.1_AC006526_14 (AC006526) unknown
protein [Arabidopsis thaliana]

Seq. No. 3503
Contig ID 2501_1.R1040
5'-most EST LIB3028-043-Q1-B1-D7
Method BLASTX
NCBI GI g4006922
BLAST score 158
E value 1.0e-10
Match length 35
% identity 77
NCBI Description (Z99708) cytochrome P450 like protein [Arabidopsis
thaliana]

Seq. No. 3504
Contig ID 2503_1.R1040
5'-most EST uC-gmrominsoyl35g07b1
Method BLASTX
NCBI GI g2462826
BLAST score 759
E value 1.0e-109
Match length 477
% identity 45
NCBI Description (AF000657) unknown protein [Arabidopsis thaliana]

Seq. No. 3505
Contig ID 2503_2.R1040
5'-most EST zhf700956794.h1
Method BLASTX
NCBI GI g2462826
BLAST score 240
E value 3.0e-20
Match length 99
% identity 45
NCBI Description (AF000657) unknown protein [Arabidopsis thaliana]

Seq. No. 3506
Contig ID 2504_1.R1040
5'-most EST LIB3039-018-Q1-E1-E6
Method BLASTX
NCBI GI g3241945
BLAST score 438
E value 4.0e-43
Match length 146
% identity 55
NCBI Description (AC004625) unknown protein [Arabidopsis thaliana]

Seq. No. 3507
Contig ID 2505_1.R1040
5'-most EST uC-gmflminsoy053h03b1
Method BLASTX
NCBI GI g2935523
BLAST score 142
E value 1.0e-08
Match length 74
% identity 43

0363416 301000

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Seq. No.          3509
Contig ID         2508_1.R1040
5'-most EST      zhf700963215.h1
Method            BLASTX
NCBI GI           g2252871
BLAST score       162
E value           2.0e-23
Match length      134
% identity        48
NCBI Description  (AF013294) No definition line found [Arabidopsis thaliana]
```

```
Seq. No.          3510
Contig ID         2510_1.R1040
5'-most EST      LIB3170-036-Q1-K2-A6
Method            BLASTX
NCBI GI           g2895866
BLAST score       399
E value           1.0e-38
Match length      154
% identity        59
NCBI Description  (AF045770) methylmalonate semi-aldehyde dehydrogenase
                  [Orvza sativa]
```

Seq. No.	3511
Contig ID	2510_2.R1040
5'-most EST	LIB3092-048-O1-K1-F8

```
Seq. No.          3512
Contig ID         2511_1.R1040
5'-most EST      LIB3138-006-Q1-N1-C7
Method            BLASTX
NCBI GI           g2529683
BLAST score       426
E value           9.0e-42
Match length      186
% identity        48
NCBI Description  (AC002535) unknown protein [Arabidopsis thaliana]
```

Seq. No.	3513
Contig ID	2512_1.R1040
5'-most EST	LIB3049-046-O1-E1-H9

BLAST score 281
 E value 1.0e-156
 Match length 782
 % identity 84
 NCBI Description C.arietinum mRNA for cysteine proteinase

Seq. No. 3526
 Contig ID 2528_2.R1040
 5'-most EST LIB3093-045-Q1-K1-B2
 Method BLASTN
 NCBI GI g3820639
 BLAST score 101
 E value 5.0e-49
 Match length 312
 % identity 86
 NCBI Description C.arietinum mRNA for cysteine proteinase

Seq. No. 3527
 Contig ID 2528_3.R1040
 5'-most EST LIB3092-058-Q1-K1-B11
 Method BLASTN
 NCBI GI g3820639
 BLAST score 203
 E value 1.0e-110
 Match length 632
 % identity 84
 NCBI Description C.arietinum mRNA for cysteine proteinase

Seq. No. 3528
 Contig ID 2528_4.R1040
 5'-most EST g5510260
 Method BLASTN
 NCBI GI g3820639
 BLAST score 169
 E value 6.0e-90
 Match length 404
 % identity 86
 NCBI Description C.arietinum mRNA for cysteine proteinase

Seq. No. 3529
 Contig ID 2528_5.R1040
 5'-most EST jC-gmfl02220070g10a1
 Method BLASTX
 NCBI GI g1134882
 BLAST score 226
 E value 2.0e-18
 Match length 94
 % identity 49
 NCBI Description (Z68291) cysteine protease [Pisum sativum]

Seq. No. 3530
 Contig ID 2529_1.R1040
 5'-most EST LIB3107-062-Q1-K1-D8
 Method BLASTN
 NCBI GI g1370145
 BLAST score 386
 E value 0.0e+00

Method BLASTX
 NCBI GI g128592
 BLAST score 425
 E value 8.0e-42
 Match length 126
 % identity 63
 NCBI Description POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR
 >gi_82190_pir_S22495 pollen-specific protein precursor -
 common tobacco >gi_19902_emb_CAA43454_ (X61146) pollen
 specific protein [Nicotiana tabacum]

Seq. No. 3550
 Contig ID 2544_1.R1040
 5'-most EST ujr700646514.h1

Seq. No. 3551
 Contig ID 2544_4.R1040
 5'-most EST hrw701063009.h1

Seq. No. 3552
 Contig ID 2545_1.R1040
 5'-most EST sat701014436.h1
 Method BLASTX
 NCBI GI g2160156
 BLAST score 606
 E value 1.0e-62
 Match length 214
 % identity 56
 NCBI Description (AC000132) Strong similarity to S. pombe leucyl-tRNA
 synthetase (gb_Z73100). [Arabidopsis thaliana]

Seq. No. 3553
 Contig ID 2547_1.R1040
 5'-most EST LIB3107-061-Q1-K1-H1

Seq. No. 3554
 Contig ID 2547_2.R1040
 5'-most EST pcp700995149.h1

Seq. No. 3555
 Contig ID 2548_1.R1040
 5'-most EST uC-gmropic074b05b1
 Method BLASTX
 NCBI GI g2506277
 BLAST score 2497
 E value 0.0e+00
 Match length 543
 % identity 93
 NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60
 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi_806808
 (U21139) chaperonin precursor [Pisum sativum]

Seq. No. 3556
 Contig ID 2548_2.R1040
 5'-most EST LIB3106-005-Q1-K1-F7
 Method BLASTN
 NCBI GI g2746720

Seq. No. 3567
 Contig ID 2556_2.R1040
 5'-most EST LIB3109-037-Q1-K1-E4
 Method BLASTN
 NCBI GI g2656025
 BLAST score 42
 E value 3.0e-14
 Match length 58
 % identity 93
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCD7

Seq. No. 3568
 Contig ID 2556_3.R1040
 5'-most EST kmv700737795.h1
 Method BLASTX
 NCBI GI g3894172
 BLAST score 171
 E value 3.0e-12
 Match length 56
 % identity 55
 NCBI Description (AC005312) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No. 3569
 Contig ID 2556_5.R1040
 5'-most EST uC-gmrominsoy121d12b1
 Method BLASTN
 NCBI GI g2656025
 BLAST score 39
 E value 1.0e-12
 Match length 51
 % identity 94
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCD7

Seq. No. 3570
 Contig ID 2556_6.R1040
 5'-most EST LIB3109-018-Q1-K1-H8
 Method BLASTX
 NCBI GI g3482924
 BLAST score 191
 E value 6.0e-24
 Match length 117
 % identity 53
 NCBI Description (AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi_1143445 [Arabidopsis thaliana]

Seq. No. 3571
 Contig ID 2556_7.R1040
 5'-most EST ssr700560974.h1
 Method BLASTX
 NCBI GI g3482925
 BLAST score 125
 E value 2.0e-13
 Match length 92

Seq. No. 3583
 Contig ID 2567_3.R1040
 5'-most EST jC-gmro02800029f04d1
 Method BLASTX
 NCBI GI g1743354
 BLAST score 353
 E value 1.0e-33
 Match length 71
 % identity 90
 NCBI Description (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No. 3584
 Contig ID 2567_5.R1040
 5'-most EST zsg701126328.h1
 Method BLASTX
 NCBI GI g1421730
 BLAST score 418
 E value 5.0e-41
 Match length 86
 % identity 88
 NCBI Description (U43082) RF2 [Zea mays]

Seq. No. 3585
 Contig ID 2569_1.R1040
 5'-most EST LIB3028-042-Q1-B1-E8
 Method BLASTX
 NCBI GI g2459445
 BLAST score 218
 E value 1.0e-17
 Match length 96
 % identity 26
 NCBI Description (AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No. 3586
 Contig ID 2570_1.R1040
 5'-most EST dpv701101023.h1
 Method BLASTX
 NCBI GI g2959767
 BLAST score 1002
 E value 1.0e-109
 Match length 261
 % identity 75
 NCBI Description (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292
 (AC005309) glutathione-conjugate transporter AtMRP4
 [Arabidopsis thaliana]

Seq. No. 3587
 Contig ID 2572_1.R1040
 5'-most EST LIB3028-042-Q1-B1-B7

Seq. No. 3588
 Contig ID 2574_1.R1040
 5'-most EST LIB3028-042-Q1-B1-C1
 Method BLASTX
 NCBI GI g4490330

E value 0.0e+00
 Match length 611
 % identity 91
 NCBI Description L.japonicus mRNA for small GTP-binding protein, RAC1

Seq. No. 3611
 Contig ID 2598 2.R1040
 5'-most EST g4286070
 Method BLASTN
 NCBI GI g1370199
 BLAST score 196
 E value 1.0e-106
 Match length 276
 % identity 93
 NCBI Description L.japonicus mRNA for small GTP-binding protein, RAC1

Seq. No. 3612
 Contig ID 2599 1.R1040
 5'-most EST g4395750
 Method BLASTX
 NCBI GI g3882309
 BLAST score 310
 E value 3.0e-28
 Match length 186
 % identity 34
 NCBI Description (AB018337) KIAA0794 protein [Homo sapiens]

Seq. No. 3613
 Contig ID 2609 1.R1040
 5'-most EST jC-gmst02400027h09a1
 Method BLASTN
 NCBI GI g684941
 BLAST score 352
 E value 0.0e+00
 Match length 716
 % identity 87
 NCBI Description Medicago sativa S-adenosyl-L-methionine:trans-caffeoyl-CoA 3-O-methyltransferase (CCOMT) mRNA, complete cds

Seq. No. 3614
 Contig ID 2609 2.R1040
 5'-most EST jC-gmst02400031b03d1
 Method BLASTN
 NCBI GI g857577
 BLAST score 141
 E value 3.0e-73
 Match length 313
 % identity 86
 NCBI Description Populus tremuloides caffeoyl-CoA 3-O-methyltransferase mRNA, complete cds

Seq. No. 3615
 Contig ID 2609 3.R1040
 5'-most EST fua701042628.h1
 Method BLASTN
 NCBI GI g2465011
 BLAST score 96

Seq. No. 3658
 Contig ID 2663_1.R1040
 5'-most EST LIB3028-040-Q1-B1-H3

Seq. No. 3659
 Contig ID 2664_1.R1040
 5'-most EST fde700874478.h1
 Method BLASTX
 NCBI GI g1922240
 BLAST score 143
 E value 1.0e-08
 Match length 28
 % identity 82
 NCBI Description (Y10083) hypothetical protein [Arabidopsis thaliana]

Seq. No. 3660
 Contig ID 2669_1.R1040
 5'-most EST LIB3049-034-Q1-E1-F6
 Method BLASTX
 NCBI GI g4454263
 BLAST score 152
 E value 2.0e-09
 Match length 94
 % identity 38
 NCBI Description (Y18046) FGFR1 oncogene partner (FOP) [Homo sapiens]

Seq. No. 3661
 Contig ID 2669_2.R1040
 5'-most EST vzy700755346.h1
 Method BLASTX
 NCBI GI g4454263
 BLAST score 153
 E value 5.0e-10
 Match length 94
 % identity 38
 NCBI Description (Y18046) FGFR1 oncogene partner (FOP) [Homo sapiens]

Seq. No. 3662
 Contig ID 2669_3.R1040
 5'-most EST eep700864394.h1

Seq. No. 3663
 Contig ID 2672_1.R1040
 5'-most EST uC-gmflminsoy029c04b1
 Method BLASTX
 NCBI GI g2578444
 BLAST score 275
 E value 1.0e-23
 Match length 89
 % identity 61
 NCBI Description (X67427) ptxA [Pisum sativum]

Seq. No. 3664
 Contig ID 2672_2.R1040
 5'-most EST jC-gmst02400061d09d1

Seq. No.	3679
Contig ID	2683_1.R1040
5'-most EST	jC-qmf102220091c10d1

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Seq. No.          3680
Contig ID         2686_1.R1040
5'-most EST      txt700736173.h1
Method            BLASTX
NCBI GI           g3182981
BLAST score       2770
E value           0.0e+00
Match length      567
% identity        89
NCBI Description  CELL ELONGATION PROTEIN DIMINUTO >gi_1695692_dbj_BAA13096_
                  (D86494) diminuto [Pisum sativum]
```

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Seq. No.          3681
Contig ID         2690_1.R1040
5'-most EST      crh700855489.h1
Method            BLASTX
NCBI GI           g3510538
BLAST score       403
E value           4.0e-39
Match length      125
% identity        60
NCBI Description  (U93167) expansin [Prunus armeniaca]
```

Seq. No.	3682
Contig ID	2693_1.R1040
5'-most EST	LIB3028-040-O1-B1-F5

Seq. No.	3683
Contig ID	2693_2.R1040
5'-most EST	LIB3055-011-O1-N1-D11

```
Seq. No.          3684
Contig ID         2694_1.R1040
5'-most EST      uC-gmropic011g06b1
Method            BLASTX
NCBI GI           g2351378
BLAST score       367
E value           1.0e-34
Match length      173
% identity        53
NCBI Description  (U54558) translation initiation factor eIF3 p66 subunit
                  [Homo sapiens] >gi_4200328_emb_CAA18440_ (AL022313)
                  EIF3-P66 [Homo sapiens]
                  >gi_4503523_ref NP_003744.1 pEIF3S7 UNKNOWN
```

```
Seq. No.          3685
Contig ID         2695_1.R1040
5'-most EST      vzy700752220.h1
Method            BLASTX
NCBI GI           g3402282
BLAST score       184
```

E value 2.0e-28
 Match length 112
 % identity 54
 NCBI Description (AJ000997) proline-rich protein [Solanum tuberosum]

Seq. No. 3686
 Contig ID 2699_1.R1040
 5'-most EST bth700845695.h1
 Method BLASTX
 NCBI GI g4512651
 BLAST score 1083
 E value 1.0e-118
 Match length 410
 % identity 49
 NCBI Description (AC007048) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No. 3687
 Contig ID 2699_2.R1040
 5'-most EST fC-gmfl700908904a1

Seq. No. 3688
 Contig ID 2699_3.R1040
 5'-most EST jC-gmfl02220063e05d1
 Method BLASTX
 NCBI GI g4512651
 BLAST score 263
 E value 1.0e-22
 Match length 121
 % identity 39
 NCBI Description (AC007048) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No. 3689
 Contig ID 2699_4.R1040
 5'-most EST jC-gmfl02220148b08a1
 Method BLASTX
 NCBI GI g4512651
 BLAST score 203
 E value 7.0e-16
 Match length 111
 % identity 35
 NCBI Description (AC007048) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No. 3690
 Contig ID 2699_5.R1040
 5'-most EST pcp700990102.h1

Seq. No. 3691
 Contig ID 2700_1.R1040
 5'-most EST LIB3028-040-Q1-B1-E5

Seq. No. 3692
 Contig ID 2701_2.R1040
 5'-most EST LIB3028-040-Q1-B1-E6
 Method BLASTX

NCBI GI g4558548
 BLAST score 188
 E value 6.0e-14
 Match length 55
 % identity 64
 NCBI Description (AC007138) putative RNaseP-associated protein [Arabidopsis thaliana]

Seq. No. 3693
 Contig ID 2701_3.R1040
 5'-most EST ejt700606219.h1
 Method BLASTX
 NCBI GI g4558548
 BLAST score 314
 E value 2.0e-34
 Match length 152
 % identity 48
 NCBI Description (AC007138) putative RNaseP-associated protein [Arabidopsis thaliana]

Seq. No. 3694
 Contig ID 2703_1.R1040
 5'-most EST LIB3107-025-Q1-K1-A8

Seq. No. 3695
 Contig ID 2704_1.R1040
 5'-most EST uC-gmropic062g06b1
 Method BLASTX
 NCBI GI g4103243
 BLAST score 460
 E value 1.0e-48
 Match length 185
 % identity 59
 NCBI Description (AF022368) BIPOSTO [Arabidopsis thaliana]

Seq. No. 3696
 Contig ID 2706_1.R1040
 5'-most EST zhf700962987.h1
 Method BLASTX
 NCBI GI g4056489
 BLAST score 429
 E value 5.0e-42
 Match length 222
 % identity 42
 NCBI Description (AC005896) putative white protein [Arabidopsis thaliana]

Seq. No. 3697
 Contig ID 2708_1.R1040
 5'-most EST zpv700763310.h1
 Method BLASTX
 NCBI GI g3873710
 BLAST score 353
 E value 5.0e-33
 Match length 113
 % identity 56
 NCBI Description (Z73102) predicted using Genefinder; similar to Zinc finger, C2H2 type; cDNA EST EMBL:M89161 comes from this

gene; cDNA EST EMBL:T01394 comes from this gene; cDNA EST EMBL:T02192 comes from this gene; cDNA EST EMBL:D71409 comes

Seq. No. 3698
 Contig ID 2708 2.R1040
 5'-most EST LIB3093-031-Q1-K1-B12
 Method BLASTN
 NCBI GI g4191760
 BLAST score 54
 E value 1.0e-21
 Match length 134
 % identity 85
 NCBI Description Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence [Arabidopsis thaliana]

Seq. No. 3699
 Contig ID 2709 1.R1040
 5'-most EST g5057680
 Method BLASTX
 NCBI GI g3033380
 BLAST score 1159
 E value 1.0e-127
 Match length 285
 % identity 76
 NCBI Description (AC004238) putative coatomer epsilon subunit [Arabidopsis thaliana]

Seq. No. 3700
 Contig ID 2709 2.R1040
 5'-most EST gsv701045190.h1
 Method BLASTX
 NCBI GI g3033380
 BLAST score 286
 E value 1.0e-25
 Match length 83
 % identity 67
 NCBI Description (AC004238) putative coatomer epsilon subunit [Arabidopsis thaliana]

Seq. No. 3701
 Contig ID 2709 3.R1040
 5'-most EST sat701008044.h1
 Method BLASTX
 NCBI GI g3033380
 BLAST score 203
 E value 5.0e-16
 Match length 45
 % identity 82
 NCBI Description (AC004238) putative coatomer epsilon subunit [Arabidopsis thaliana]

Seq. No. 3702
 Contig ID 2709 4.R1040
 5'-most EST zhf700961443.h1

Seq. No. 3703

Contig ID 2710_1.R1040
5'-most EST wvk700681157.h2

Seq. No. 3704
Contig ID 2711_1.R1040
5'-most EST uC-gmflminsoy054f05b1
Method BLASTX
NCBI GI g4101589
BLAST score 629
E value 2.0e-65
Match length 238
% identity 52
NCBI Description (AF005050) aspartyl aminopeptidase [Homo sapiens]

Seq. No. 3705
Contig ID 2712_1.R1040
5'-most EST LIB3093-044-Q1-K1-D4
Method BLASTX
NCBI GI g2462746
BLAST score 1864
E value 0.0e+00
Match length 423
% identity 84
NCBI Description (AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No. 3706
Contig ID 2712_2.R1040
5'-most EST zhf700959649.h1
Method BLASTX
NCBI GI g2462746
BLAST score 355
E value 9.0e-34
Match length 88
% identity 77
NCBI Description (AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No. 3707
Contig ID 2712_4.R1040
5'-most EST LIB3106-025-Q1-K1-G7
Method BLASTX
NCBI GI g2462746
BLAST score 150
E value 6.0e-10
Match length 37
% identity 81
NCBI Description (AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No. 3708
Contig ID 2712_6.R1040
5'-most EST wrg700791527.h1
Method BLASTX
NCBI GI g2462746
BLAST score 253
E value 5.0e-22

BLAST score	214
E value	6.0e-17
Match length	61
% identity	62
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]
Seq. No.	3719
Contig ID	2728_1.R1040
5'-most EST	LIB3049-015-Q1-E1-A2
Method	BLASTX
NCBI GI	g2827710
BLAST score	214
E value	3.0e-17
Match length	99
% identity	45
NCBI Description	(AL021684) lysosomal Pro-X carboxypeptidase - like protein [Arabidopsis thaliana]
Seq. No.	3720
Contig ID	2732_1.R1040
5'-most EST	LIB3028-035-Q1-B1-F7
Seq. No.	3721
Contig ID	2733_1.R1040
5'-most EST	LIB3109-014-Q1-K1-D2
Method	BLASTX
NCBI GI	g3044214
BLAST score	1125
E value	1.0e-123
Match length	271
% identity	80
NCBI Description	(AF057044) acyl-CoA oxidase [Arabidopsis thaliana]
Seq. No.	3722
Contig ID	2733_2.R1040
5'-most EST	uC-gmrominsoyl89c09b1
Method	BLASTX
NCBI GI	g2245030
BLAST score	260
E value	4.0e-24
Match length	141
% identity	68
NCBI Description	(Z97341) apetala2 domain TINY homolog [Arabidopsis thaliana]
Seq. No.	3723
Contig ID	2736_1.R1040
5'-most EST	pcp700995727.h1
Method	BLASTX
NCBI GI	g3335359
BLAST score	1989
E value	0.0e+00
Match length	489
% identity	77
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]
Seq. No.	3724

Seq. No.	3737
Contig ID	2754_3.R1040
5'-most EST	seb700651223.h1

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Seq. No.          3739
Contig ID         2755_2.R1040
5'-most EST      zhff700953477.h1
Method            BLASTX
NCBI GI           g3236248
BLAST score       324
E value           5.0e-30
Match length      95
% identity        72
NCBI Description  (AC004684) unknown protein [Arabidopsis thaliana]
```

Seq. No.	3741
Contig ID	2760 1.R1040

NCBI GI	g1706955
BLAST score	81
E value	1.0e-37
Match length	157
% identity	88
NCBI Description	Gossypium hirsutum cellulose synthase (celA1) mRNA, complete cds
Seq. No.	3748
Contig ID	2768_1.R1040
5'-most EST	LIB3028-039-Q1-B1-F10
Method	BLASTX
NCBI GI	g2500036
BLAST score	141
E value	1.0e-08
Match length	31
% identity	74
NCBI Description	DIHYDROOROTASE PRECURSOR (DHOASE) >gi_2121273 (AF000146) dihydroorotase [Arabidopsis thaliana] >gi_3292818_emb_CAA19808_ (AL031018) dihydroorotase [Arabidopsis thaliana]
Seq. No.	3749
Contig ID	2769_1.R1040
5'-most EST	jC-gmfl02220053a03a1
Method	BLASTX
NCBI GI	g2388689
BLAST score	359
E value	1.0e-101
Match length	319
% identity	66
NCBI Description	(AF016633) GH1 protein [Glycine max]
Seq. No.	3750
Contig ID	2769_2.R1040
5'-most EST	zhf700958581.h1
Method	BLASTX
NCBI GI	g2388689
BLAST score	974
E value	1.0e-105
Match length	324
% identity	64
NCBI Description	(AF016633) GH1 protein [Glycine max]
Seq. No.	3751
Contig ID	2769_4.R1040
5'-most EST	jC-gmfl02220065e10a1
Method	BLASTX
NCBI GI	g2388689
BLAST score	154
E value	4.0e-10
Match length	77
% identity	47
NCBI Description	(AF016633) GH1 protein [Glycine max]
Seq. No.	3752
Contig ID	2772_1.R1040

Seq. No. 3764
 Contig ID 2807_1.R1040
 5'-most EST LIB3109-047-Q1-K1-D2
 Method BLASTN
 NCBI GI g4519195
 BLAST score 35
 E value 6.0e-10
 Match length 43
 % identity 95
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No. 3765
 Contig ID 2809_1.R1040
 5'-most EST LIB3056-006-Q1-N1-A4
 Method BLASTX
 NCBI GI g3367524
 BLAST score 403
 E value 6.0e-39
 Match length 193
 % identity 56
 NCBI Description (AC004392) F8K4.12 [Arabidopsis thaliana]

Seq. No. 3766
 Contig ID 2809_2.R1040
 5'-most EST LIB3051-009-Q1-E1-A10

Seq. No. 3767
 Contig ID 2810_1.R1040
 5'-most EST wvk700681381.h2

Seq. No. 3768
 Contig ID 2811_1.R1040
 5'-most EST LIB3028-039-Q1-B1-G12
 Method BLASTX
 NCBI GI g1766046
 BLAST score 738
 E value 2.0e-78
 Match length 153
 % identity 90
 NCBI Description (U81993) NAD+ dependent isocitrate dehydrogenase subunit 1 [Arabidopsis thaliana]

Seq. No. 3769
 Contig ID 2812_1.R1040
 5'-most EST LIB3039-034-Q1-E1-D5
 Method BLASTX
 NCBI GI g3004565
 BLAST score 333
 E value 1.0e-30
 Match length 123
 % identity 58
 NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 3770
 Contig ID 2822_1.R1040
 5'-most EST LIB3028-039-Q1-B1-D8

Method BLASTX
 NCBI GI g2651310
 BLAST score 193
 E value 6.0e-26
 Match length 152
 % identity 39
 NCBI Description (AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]

Seq. No. 3771
 Contig ID 2825_1.R1040
 5'-most EST k11701207614.h1
 Method BLASTX
 NCBI GI g2827637
 BLAST score 370
 E value 3.0e-35
 Match length 107
 % identity 63
 NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 3772
 Contig ID 2828_1.R1040
 5'-most EST gsv701054363.h1

Seq. No. 3773
 Contig ID 2828_2.R1040
 5'-most EST LIB3072-017-Q1-E1-C2

Seq. No. 3774
 Contig ID 2829_1.R1040
 5'-most EST jC-gmst02400018f02a1
 Method BLASTX
 NCBI GI g2244876
 BLAST score 1168
 E value 1.0e-128
 Match length 286
 % identity 74
 NCBI Description (Z97338) hypothetical protein [Arabidopsis thaliana]

Seq. No. 3775
 Contig ID 2831_1.R1040
 5'-most EST leu701152319.h1
 Method BLASTX
 NCBI GI g2642443
 BLAST score 826
 E value 2.0e-88
 Match length 371
 % identity 44
 NCBI Description (AC002391) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 3776
 Contig ID 2832_1.R1040
 5'-most EST fC-gmle7000742258f1
 Method BLASTX
 NCBI GI g1706822
 BLAST score 365
 E value 1.0e-34

Match length 98
 % identity 65
 NCBI Description FLAVONOL SYNTHASE (FLS) >gi_421946_pir_S33510 flavonol
 synthase - garden petunia >gi_311658_emb_CAA80264_ (Z22543)
 flavonol synthase [Petunia x hybrida]

Seq. No. 3777
 Contig ID 2832_2.R1040
 5'-most EST LIB3028-039-Q1-B1-A6
 Method BLASTX
 NCBI GI g1706822
 BLAST score 934
 E value 1.0e-101
 Match length 265
 % identity 65
 NCBI Description FLAVONOL SYNTHASE (FLS) >gi_421946_pir_S33510 flavonol
 synthase - garden petunia >gi_311658_emb_CAA80264_ (Z22543)
 flavonol synthase [Petunia x hybrida]

Seq. No. 3778
 Contig ID 2837_1.R1040
 5'-most EST asn701134785.h2
 Method BLASTX
 NCBI GI g3892051
 BLAST score 1126
 E value 1.0e-123
 Match length 251
 % identity 84
 NCBI Description (AC002330) predicted NADH dehydrogenase 24 kD subunit
 [Arabidopsis thaliana]

Seq. No. 3779
 Contig ID 2840_1.R1040
 5'-most EST uc-gmrominsoy035c05b1
 Method BLASTX
 NCBI GI g2924792
 BLAST score 880
 E value 1.0e-94
 Match length 221
 % identity 76
 NCBI Description (AC002334) similar to synaptobrevin [Arabidopsis thaliana]

Seq. No. 3780
 Contig ID 2841_1.R1040
 5'-most EST zhf700958558.h1
 Method BLASTX
 NCBI GI g3150411
 BLAST score 1011
 E value 1.0e-110
 Match length 384
 % identity 55
 NCBI Description (AC004165) hookless1-like protein [Arabidopsis thaliana]

Seq. No. 3781
 Contig ID 2842_1.R1040
 5'-most EST zzp700831646.h1
 Method BLASTN

Contig ID	2848_1.R1040
5'-most EST	kmv700743979.h1
Method	BLASTX
NCBI GI	g2244866
BLAST score	912
E value	2.0e-98
Match length	249
% identity	68
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.	3788
Contig ID	2849_1.R1040
5'-most EST	jC-gmro02800031c11a1
Method	BLASTX
NCBI GI	g2660670
BLAST score	1056
E value	1.0e-115
Match length	282
% identity	73
NCBI Description	(AC002342) putative Cu ²⁺ -transporting ATPase [Arabidopsis thaliana]
Seq. No.	3789
Contig ID	2851_1.R1040
5'-most EST	LIB3056-008-Q1-N1-A11
Method	BLASTX
NCBI GI	g2464865
BLAST score	1848
E value	0.0e+00
Match length	516
% identity	66
NCBI Description	(Z99707) pectinesterase like protein [Arabidopsis thaliana]
Seq. No.	3790
Contig ID	2851_2.R1040
5'-most EST	LIB3107-059-Q1-K1-D7
Method	BLASTX
NCBI GI	g2464865
BLAST score	372
E value	2.0e-35
Match length	104
% identity	64
NCBI Description	(Z99707) pectinesterase like protein [Arabidopsis thaliana]
Seq. No.	3791
Contig ID	2851_3.R1040
5'-most EST	gsv701051641.h1
Method	BLASTX
NCBI GI	g2464865
BLAST score	274
E value	2.0e-24
Match length	66
% identity	73
NCBI Description	(Z99707) pectinesterase like protein [Arabidopsis thaliana]
Seq. No.	3792
Contig ID	2851_4.R1040

098016 10100

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Seq. No.          3799
Contig ID         2858 1.R1040
5'-most EST      LIB3106-033-Q1-K1-E2
Method            BLASTX
NCBI GI           g2558512
BLAST score       159
E value           2.0e-10
Match length      91
% identity        41
NCBI Description  (AJ002020)  proton pu
```

Seq. No.	3801
Contig ID	2861_2.R1040
5'-most EST	jC-qmle01810093a10d1

```
Seq. No.          3803
Contig ID         2861 4.R1040
5'-most EST      LIB3028-038-Q1-B1-E5
Method           BLASTX
NCBI GI          g2827536
BLAST score       184
E value          2.0e-13
Match length      45
% identity        62
NCBI Description  (AL021633) hypothetical protein [Arabidopsis thaliana]
```

761

% identity 54
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 3824
Contig ID 2895_2.R1040
5'-most EST LIB3040-061-Q1-E11-E4
Method BLASTX
NCBI GI g4454032
BLAST score 257
E value 3.0e-22
Match length 89
% identity 56
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 3825
Contig ID 2897_1.R1040
5'-most EST LIB3051-040-Q1-K1-F12
Method BLASTX
NCBI GI g2921823
BLAST score 327
E value 6.0e-30
Match length 144
% identity 55
NCBI Description (AF046934) shoot-forming PKSF1 [Paulownia kawakamii]

Seq. No. 3826
Contig ID 2897_2.R1040
5'-most EST LIB3028-038-Q1-B1-B5
Method BLASTX
NCBI GI g2246376
BLAST score 171
E value 4.0e-12
Match length 62
% identity 68
NCBI Description (Z86093) b-Zip DNA binding protein [Arabidopsis thaliana]

Seq. No. 3827
Contig ID 2898_1.R1040
5'-most EST jex700905254.h1
Method BLASTX
NCBI GI g2961384
BLAST score 383
E value 1.0e-36
Match length 140
% identity 54
NCBI Description (AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]

Seq. No. 3828
Contig ID 2898_2.R1040
5'-most EST LIB3028-038-Q1-B1-B6
Method BLASTX
NCBI GI g2961384
BLAST score 238
E value 7.0e-20
Match length 86
% identity 50

NCBI Description (AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]

Seq. No. 3829
Contig ID 2899_1.R1040
5'-most EST LIB3170-002-Q1-K1-A5
Method BLASTN
NCBI GI g498907
BLAST score 170
E value 2.0e-90
Match length 382
& identity 88

NCBI Description Pisum sativum ribosomal protein L34 homolog (RPL34) mRNA, complete cds

Seq. No. 3830
Contig ID 2900_1.R1040
5'-most EST uC-gmflminsoy002d01b1
Method BLASTX
NCBI GI g1177320
BLAST score 487
E value 1.0e-48
Match length 176
& identity 53

NCBI Description (X89891) EFA27 for EF hand, abscisic acid, 27kD [Oryza sativa]

Seq. No. 3831
Contig ID 2900_3.R1040
5'-most EST LIB3051-048-Q1-K1-D5
Method BLASTX
NCBI GI g2270994
BLAST score 121
E value 1.0e-13
Match length 57
& identity 63

NCBI Description (AF004809) Ca²⁺-binding EF hand protein [Glycine max]

Seq. No. 3832
Contig ID 2901_1.R1040
5'-most EST LIB3093-022-Q1-K1-G7

Seq. No. 3833
Contig ID 2901_2.R1040
5'-most EST LIB3049-006-Q1-E1-E10
Method BLASTX
NCBI GI g114420
BLAST score 2306
E value 0.0e+00
Match length 513
& identity 89

NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
>gi_100882_pir_S11491 H⁺-transporting ATP synthase (EC 3.6.1.34) beta chain, mitochondrial - maize
>gi_22173_emb_CAA38140_(X54233) ATPase F1 subunit protein [Zea mays] >gi_897618_(M36087) F-1-ATPase subunit 2 [Zea mays]

BLAST score 731
 E value 2.0e-77
 Match length 151
 % identity 95
 NCBI Description 40S RIBOSOMAL PROTEIN S13 >gi_480095_pir_S36423 ribosomal protein S13.e - garden pea >gi_396639_emb_CAA80974_ (Z25509) ribosomal protein S13 [Pisum sativum]

Seq. No. 3852
 Contig ID 2920_2.R1040
 5'-most EST LIB3138-033-Q1-N1-B6
 Method BLASTX
 NCBI GI g3450842
 BLAST score 415
 E value 2.0e-40
 Match length 212
 % identity 45
 NCBI Description (AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No. 3853
 Contig ID 2920_3.R1040
 5'-most EST LIB3094-002-Q1-K1-A7
 Method BLASTX
 NCBI GI g1173198
 BLAST score 723
 E value 2.0e-76
 Match length 151
 % identity 93
 NCBI Description 40S RIBOSOMAL PROTEIN S13 >gi_480095_pir_S36423 ribosomal protein S13.e - garden pea >gi_396639_emb_CAA80974_ (Z25509) ribosomal protein S13 [Pisum sativum]

Seq. No. 3854
 Contig ID 2920_5.R1040
 5'-most EST 2DC-01-Q1-E1-E7
 Method BLASTN
 NCBI GI g3193311
 BLAST score 43
 E value 7.0e-15
 Match length 71
 % identity 90
 NCBI Description Arabidopsis thaliana BAC F6N15

Seq. No. 3855
 Contig ID 2920_8.R1040
 5'-most EST taw700657103.h1

Seq. No. 3856
 Contig ID 2923_1.R1040
 5'-most EST ncj700976784.h1
 Method BLASTX
 NCBI GI g3046700
 BLAST score 337
 E value 1.0e-31
 Match length 91
 % identity 70

NCBI Description (AJ005261) cytidine deaminase [Arabidopsis thaliana]
>gi_3093276_emb_CAA06671_ (AJ005687) cytidine deaminase
[Arabidopsis thaliana] >gi_4191787 (AC005917) putative
cytidine deaminase [Arabidopsis thaliana]

Seq. No. 3857
Contig ID 2926_1.R1040
5'-most EST kl1701204486.h2

Seq. No. 3858
Contig ID 2926_2.R1040
5'-most EST LIB3028-037-Q1-B1-G1

Seq. No. 3859
Contig ID 2929_1.R1040
5'-most EST jC-gmfl02220063f08a1
Method BLASTX
NCBI GI g3775993
BLAST score 1425
E value 0.0e+00
Match length 424
% identity 80
NCBI Description (AJ010460) RNA helicase [Arabidopsis thaliana]

Seq. No. 3860
Contig ID 2929_2.R1040
5'-most EST uC-gmrominsoy122f10b1

Seq. No. 3861
Contig ID 2929_3.R1040
5'-most EST LIB3051-090-Q1-K1-F5

Seq. No. 3862
Contig ID 2929_4.R1040
5'-most EST LIB3051-084-Q1-K1-C9

Seq. No. 3863
Contig ID 2930_1.R1040
5'-most EST LIB3040-061-Q1-E1-A11
Method BLASTN
NCBI GI g20761
BLAST score 58
E value 2.0e-23
Match length 225
% identity 84
NCBI Description Pea mRNA for H1 histone

Seq. No. 3864
Contig ID 2930_2.R1040
5'-most EST LIB3049-056-Q1-E1-G12
Method BLASTN
NCBI GI g20761
BLAST score 64
E value 6.0e-27
Match length 232
% identity 87
NCBI Description Pea mRNA for H1 histone

Seq. No. 3871
 Contig ID 2945_1.R1040
 5'-most EST uC-gmflminsoy099g11b1

Seq. No. 3872
 Contig ID 2946_1.R1040
 5'-most EST LIB3109-005-Q1-K1-C3
 Method BLASTX
 NCBI GI g2832686
 BLAST score 214
 E value 4.0e-17
 Match length 69
 % identity 65
 NCBI Description (AL021712) putative protein [Arabidopsis thaliana]

Seq. No. 3873
 Contig ID 2947_1.R1040
 5'-most EST uC-gmrominsoy263h01b1
 Method BLASTX
 NCBI GI g4063746
 BLAST score 700
 E value 2.0e-73
 Match length 506
 % identity 33
 NCBI Description (AC005851) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 3874
 Contig ID 2947_2.R1040
 5'-most EST uC-gmrominsoy048a04b1

Seq. No. 3875
 Contig ID 2947_3.R1040
 5'-most EST uC-gmrominsoy165e07b1
 Method BLASTX
 NCBI GI g4455155
 BLAST score 350
 E value 4.0e-33
 Match length 115
 % identity 65
 NCBI Description (AL022023) EF-1 alpha - like protein (fragment) [Arabidopsis thaliana]

Seq. No. 3876
 Contig ID 2948_1.R1040
 5'-most EST pmv700893325.h1

Seq. No. 3877
 Contig ID 2948_2.R1040
 5'-most EST jC-gmle01810052g12a1

Seq. No. 3878
 Contig ID 2950_1.R1040
 5'-most EST zhf700963838.h1

Seq. No. 3879
 Contig ID 2950_2.R1040
 5'-most EST jC-gmle01810033d04a2

030601000

Seq. No.	3882
Contig ID	2950_6.R1040
5'-most EST	LIB3051-109-Q1-K1-A2

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Seq. No.          3884
Contig ID         2951_2.R1040
5'-most EST      fC-gmse700654980f1
Method            BLASTX
NCBI GI           g4510342
BLAST score       516
E value           2.0e-52
Match length      133
% identity        73
NCBI Description  (AC006921) putative serine/threonine protein kinase
                  [Arabidopsis thaliana]
```

```
Seq. No.          3885
Contig ID         2951 3.R1040
5'-most EST      LIB3051-091-Q1-K1-E6
Method            BLASTX
NCBI GI           g4510342
BLAST score       355
E value           1.0e-33
Match length      104
% identity        66
NCBI Description  (AC006921) putative serine/threonine protein kinase
                  [Arabidopsis thaliana]
```

774

Contig ID 2983_3.R1040
 5'-most EST uC-gmropic020b03b1
 Method BLASTN
 NCBI GI g2582799
 BLAST score 194
 E value 1.0e-105
 Match length 417
 % identity 88
 NCBI Description M.sativa mRNA for protein phosphatase 2C

Seq. No. 3911
 Contig ID 2983_4.R1040
 5'-most EST LIB3139-095-P1-N1-G11
 Method BLASTN
 NCBI GI g2582799
 BLAST score 113
 E value 1.0e-56
 Match length 266
 % identity 88
 NCBI Description M.sativa mRNA for protein phosphatase 2C

Seq. No. 3912
 Contig ID 2983_5.R1040
 5'-most EST wrq700786175.h2
 Method BLASTN
 NCBI GI g2582799
 BLAST score 43
 E value 6.0e-15
 Match length 67
 % identity 91
 NCBI Description M.sativa mRNA for protein phosphatase 2C

Seq. No. 3913
 Contig ID 2983_6.R1040
 5'-most EST uC-gmrominsoy208a02b1

Seq. No. 3914
 Contig ID 2984_1.R1040
 5'-most EST LIB3065-004-Q1-N1-H9

Seq. No. 3915
 Contig ID 2988_1.R1040
 5'-most EST LIB3028-036-Q1-B1-G8

Seq. No. 3916
 Contig ID 2989_1.R1040
 5'-most EST LIB3170-042-Q1-J1-B12
 Method BLASTX
 NCBI GI g1279640
 BLAST score 666
 E value 6.0e-70
 Match length 153
 % identity 80
 NCBI Description (X92204) NAM [Petunia x hybrida]

Seq. No. 3917
 Contig ID 2989_2.R1040

5'-most EST	k11701211357.h1
Method	BLASTX
NCBI GI	g1944132
BLAST score	558
E value	3.0e-57
Match length	162
% identity	68
NCBI Description	(AB002560) CUC2 [Arabidopsis thaliana]
Seq. No.	3918
Contig ID	2992_1.R1040
5'-most EST	LIB3167-029-P1-K1-G2
Method	BLASTX
NCBI GI	g3282505
BLAST score	196
E value	8.0e-15
Match length	139
% identity	35
NCBI Description	(AF020786) polyphenol oxidase precursor [Prunus armeniaca]
Seq. No.	3919
Contig ID	2993_1.R1040
5'-most EST	jC-gmf102220139a10a1
Method	BLASTX
NCBI GI	g4314378
BLAST score	451
E value	1.0e-44
Match length	231
% identity	43
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]
Seq. No.	3920
Contig ID	2998_1.R1040
5'-most EST	vzy700752164.h1
Method	BLASTX
NCBI GI	g1531758
BLAST score	751
E value	6.0e-80
Match length	182
% identity	79
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]
Seq. No.	3921
Contig ID	2999_1.R1040
5'-most EST	pxt700944601.h1
Method	BLASTX
NCBI GI	g1518059
BLAST score	287
E value	2.0e-25
Match length	121
% identity	45
NCBI Description	(U65650) blue-copper binding protein III [Arabidopsis thaliana] >gi_3395770 (AF039404) uclacyanin 3 [Arabidopsis thaliana]
Seq. No.	3922

NCBI Description (AF081202) villin 2 [Arabidopsis thaliana]

Seq. No. 3928
 Contig ID 3021_1.R1040
 5'-most EST LIB3106-113-Q1-K1-E8
 Method BLASTX
 NCBI GI g4510381
 BLAST score 343
 E value 1.0e-31
 Match length 123
 % identity 61

NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 3929
 Contig ID 3022_1.R1040
 5'-most EST LIB3107-013-Q1-K1-G9
 Method BLASTX
 NCBI GI g3913518
 BLAST score 563
 E value 2.0e-65
 Match length 196
 % identity 70

NCBI Description 3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE
 (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE)
 (DPNPASE) >gi_1103921 (U40433) 3'(2'),5'-bisphosphate
 nucleotidase [Arabidopsis thaliana]

Seq. No. 3930
 Contig ID 3022_2.R1040
 5'-most EST wrg700790744.h1
 Method BLASTX
 NCBI GI g3913518
 BLAST score 291
 E value 4.0e-26
 Match length 91
 % identity 66

NCBI Description 3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE
 (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE)
 (DPNPASE) >gi_1103921 (U40433) 3'(2'),5'-bisphosphate
 nucleotidase [Arabidopsis thaliana]

Seq. No. 3931
 Contig ID 3027_1.R1040
 5'-most EST bth700848545.h1
 Method BLASTX
 NCBI GI g3128218
 BLAST score 617
 E value 5.0e-64
 Match length 204
 % identity 64

NCBI Description (AC004077) putative end13 protein [Arabidopsis thaliana]

Seq. No. 3932
 Contig ID 3030_1.R1040
 5'-most EST LIB3167-013-P1-K1-D5
 Method BLASTX
 NCBI GI g4325341

Seq. No. 3939
 Contig ID 3037_1.R1040
 5'-most EST ep^x701108588.h1
 Method BLASTX
 NCBI GI g4006871
 BLAST score 700
 E value 2.0e-73
 Match length 355
 % identity 47
 NCBI Description (Z99707) patatin-like protein [Arabidopsis thaliana]

Seq. No. 3940
 Contig ID 3041_1.R1040
 5'-most EST jC-gmfl02220140b12d1
 Method BLASTX
 NCBI GI g1483228
 BLAST score 142
 E value 6.0e-11
 Match length 52
 % identity 77
 NCBI Description (X99653) MADS3 protein [Betula pendula]

Seq. No. 3941
 Contig ID 3041_2.R1040
 5'-most EST LIB3109-022-Q1-K1-G8
 Method BLASTX
 NCBI GI g1483228
 BLAST score 237
 E value 7.0e-20
 Match length 78
 % identity 63
 NCBI Description (X99653) MADS3 protein [Betula pendula]

Seq. No. 3942
 Contig ID 3043_1.R1040
 5'-most EST jC-gmfl02220127a03a1

Seq. No. 3943
 Contig ID 3047_1.R1040
 5'-most EST k11701206723.h1
 Method BLASTX
 NCBI GI g2501497
 BLAST score 466
 E value 1.0e-48
 Match length 258
 % identity 40
 NCBI Description FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE) (ANTHOCYANIN RHAMNOSYL TRANSFERASE)

Seq. No. 3944
 Contig ID 3048_1.R1040
 5'-most EST pcp700994804.h1

Seq. No. 3945
 Contig ID 3048_2.R1040
 5'-most EST vzy700756210.h1

Method BLASTX
 NCBI GI g4249382
 BLAST score 656
 E value 1.0e-68
 Match length 175
 % identity 77
 NCBI Description (AC005966) Strong similarity to gi_3337350 F13P17.3
 putative permease from Arabidopsis thaliana BAC
 gb_AC004481. [Arabidopsis thaliana]

Seq. No. 3952
 Contig ID 3052_4.R1040
 5'-most EST asn701131917.h1
 Method BLASTX
 NCBI GI g4249382
 BLAST score 302
 E value 2.0e-27
 Match length 72
 % identity 75
 NCBI Description (AC005966) Strong similarity to gi_3337350 F13P17.3
 putative permease from Arabidopsis thaliana BAC
 gb_AC004481. [Arabidopsis thaliana]

Seq. No. 3953
 Contig ID 3052_5.R1040
 5'-most EST uC-gmropic089b11b1
 Method BLASTX
 NCBI GI g4249382
 BLAST score 476
 E value 8.0e-48
 Match length 113
 % identity 81
 NCBI Description (AC005966) Strong similarity to gi_3337350 F13P17.3
 putative permease from Arabidopsis thaliana BAC
 gb_AC004481. [Arabidopsis thaliana]

Seq. No. 3954
 Contig ID 3052_6.R1040
 5'-most EST LIB3139-089-P1-N1-F8
 Method BLASTX
 NCBI GI g4249382
 BLAST score 283
 E value 2.0e-25
 Match length 70
 % identity 81
 NCBI Description (AC005966) Strong similarity to gi_3337350 F13P17.3
 putative permease from Arabidopsis thaliana BAC
 gb_AC004481. [Arabidopsis thaliana]

Seq. No. 3955
 Contig ID 3052_8.R1040
 5'-most EST bth700849121.h1
 Method BLASTN
 NCBI GI g4519191
 BLAST score 41
 E value 7.0e-14
 Match length 105

% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9P8, complete sequence
Seq. No.	3956
Contig ID	3052_9.R1040
5'-most EST	eep700869859.h1
Method	BLASTX
NCBI GI	g4249382
BLAST score	321
E value	7.0e-30
Match length	71
% identity	87
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]
Seq. No.	3957
Contig ID	3052_10.R1040
5'-most EST	uC-gmropic104b03b1
Seq. No.	3958
Contig ID	3052_11.R1040
5'-most EST	sat701008109.h1
Seq. No.	3959
Contig ID	3054_1.R1040
5'-most EST	LIB3028-036-Q1-B1-A11
Seq. No.	3960
Contig ID	3056_1.R1040
5'-most EST	LIB3028-028-Q1-B1-D7
Method	BLASTX
NCBI GI	g1209756
BLAST score	694
E value	4.0e-73
Match length	162
% identity	84
NCBI Description	(U43629) integral membrane protein [Beta vulgaris]
Seq. No.	3961
Contig ID	3060_1.R1040
5'-most EST	LIB3092-020-Q1-K1-A9
Seq. No.	3962
Contig ID	3061_1.R1040
5'-most EST	leu701148824.h1
Method	BLASTN
NCBI GI	g4406531
BLAST score	346
E value	0.0e+00
Match length	977
% identity	85
NCBI Description	Vigna radiata NADPH-protochlorophyllide oxidoreductase mRNA, chloroplast gene encoding chloroplast protein, complete cds

E value 9.0e-95
 Match length 307
 % identity 57
 NCBI Description (AB015643) Polygalacturonase-inhibiting protein [Citrus sp. cv. sannumphung]

Seq. No. 3968
 Contig ID 3069_1.R1040
 5'-most EST LIB3040-047-Q1-E1-C9
 Method BLASTX
 NCBI GI g4467119
 BLAST score 1303
 E value 1.0e-144
 Match length 261
 % identity 90
 NCBI Description (AL035538) Histone deacetylase [Arabidopsis thaliana]

Seq. No. 3969
 Contig ID 3070_1.R1040
 5'-most EST LIB3106-095-Q1-K1-D9

Seq. No. 3970
 Contig ID 3071_1.R1040
 5'-most EST LIB3051-094-Q1-K1-C4
 Method BLASTX
 NCBI GI g2275196
 BLAST score 693
 E value 5.0e-73
 Match length 171
 % identity 78
 NCBI Description (AC002337) water stress-induced protein, WSI76 isolog [Arabidopsis thaliana]

Seq. No. 3971
 Contig ID 3071_2.R1040
 5'-most EST LIB3028-004-Q1-B1-E5
 Method BLASTX
 NCBI GI g2275196
 BLAST score 150
 E value 4.0e-13
 Match length 67
 % identity 61
 NCBI Description (AC002337) water stress-induced protein, WSI76 isolog [Arabidopsis thaliana]

Seq. No. 3972
 Contig ID 3072_1.R1040
 5'-most EST uC-gmflminsoy026a05b1
 Method BLASTX
 NCBI GI g2244993
 BLAST score 318
 E value 5.0e-29
 Match length 115
 % identity 52
 NCBI Description (Z97341) similarity to AMP-activated protein kinase beta [Arabidopsis thaliana]

Seq. No. 3973
 Contig ID 3075_1.R1040
 5'-most EST LIB3107-025-Q1-K1-E10
 Method BLASTX
 NCBI GI g3033397
 BLAST score 281
 E value 5.0e-25
 Match length 72
 % identity 76
 NCBI Description (AC004238) unknown protein [Arabidopsis thaliana]

Seq. No. 3974
 Contig ID 3075_2.R1040
 5'-most EST LIB3106-096-Q1-K1-B2
 Method BLASTX
 NCBI GI g3033397
 BLAST score 252
 E value 1.0e-21
 Match length 60
 % identity 80
 NCBI Description (AC004238) unknown protein [Arabidopsis thaliana]

Seq. No. 3975
 Contig ID 3076_1.R1040
 5'-most EST jC-gmro02910063c10a1

Seq. No. 3976
 Contig ID 3076_2.R1040
 5'-most EST wvk700686545.h1

Seq. No. 3977
 Contig ID 3077_1.R1040
 5'-most EST leu701154357.h1
 Method BLASTN
 NCBI GI g3290208
 BLAST score 126
 E value 3.0e-64
 Match length 230
 % identity 89
 NCBI Description Malus domestica MADS-box protein 1 mRNA, complete cds

Seq. No. 3978
 Contig ID 3077_2.R1040
 5'-most EST leu701151545.h1
 Method BLASTN
 NCBI GI g3646333
 BLAST score 91
 E value 2.0e-43
 Match length 189
 % identity 90
 NCBI Description Malus domestica mRNA for MADS box protein MdMADS8

Seq. No. 3979
 Contig ID 3078_1.R1040
 5'-most EST LIB3028-035-Q1-B1-E11
 Method BLASTX
 NCBI GI g3068717

Seq. No. 3989
 Contig ID 3093_1.R1040
 5'-most EST pcp700995355.h1
 Method BLASTX
 NCBI GI g2500036
 BLAST score 801
 E value 4.0e-87
 Match length 186
 % identity 81
 NCBI Description DIHYDROOROTASE PRECURSOR (DHOASE) >gi_2121273 (AF000146)
 dihydroorotase [Arabidopsis thaliana]
 >gi_3292818_emb_CAA19808_ (AL031018) dihydroorotase
 [Arabidopsis thaliana]

Seq. No. 3990
 Contig ID 3094_1.R1040
 5'-most EST gsv701045588.h1
 Method BLASTN
 NCBI GI g1041244
 BLAST score 268
 E value 1.0e-149
 Match length 657
 % identity 87
 NCBI Description A.glutinosa mRNA for enolase

Seq. No. 3991
 Contig ID 3094_2.R1040
 5'-most EST vwf700674352.h1
 Method BLASTX
 NCBI GI g3023713
 BLAST score 466
 E value 2.0e-55
 Match length 147
 % identity 67
 NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
 (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372
 (U09450) enolase [Oryza sativa]

Seq. No. 3992
 Contig ID 3094_3.R1040
 5'-most EST g4293723
 Method BLASTN
 NCBI GI g1041244
 BLAST score 142
 E value 6.0e-74
 Match length 375
 % identity 87
 NCBI Description A.glutinosa mRNA for enolase

Seq. No. 3993
 Contig ID 3094_6.R1040
 5'-most EST kmv700741338.h1
 Method BLASTX
 NCBI GI g3912997
 BLAST score 147
 E value 2.0e-09
 Match length 37

Contig ID 3102_1.R1040
 5'-most EST LIB3028-023-Q1-B1-E2
 Method BLASTX
 NCBI GI g2244964
 BLAST score 743
 E value 1.0e-78
 Match length 233
 % identity 61
 NCBI Description (Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 4003
 Contig ID 3104_1.R1040
 5'-most EST LIB3093-030-Q1-K1-E2
 Method BLASTX
 NCBI GI g4185141
 BLAST score 1794
 E value 0.0e+00
 Match length 655
 % identity 59
 NCBI Description (AC005724) putative calmodulin-binding protein [Arabidopsis thaliana]

Seq. No. 4004
 Contig ID 3104_2.R1040
 5'-most EST vzy700754865.h1
 Method BLASTX
 NCBI GI g4185141
 BLAST score 214
 E value 5.0e-17
 Match length 64
 % identity 92
 NCBI Description (AC005724) putative calmodulin-binding protein [Arabidopsis thaliana]

Seq. No. 4005
 Contig ID 3104_5.R1040
 5'-most EST epX701104351.h1
 Method BLASTN
 NCBI GI g1698547
 BLAST score 38
 E value 5.0e-12
 Match length 86
 % identity 86
 NCBI Description Nicotiana tabacum calmodulin-binding protein (TCB60) mRNA, complete cds

Seq. No. 4006
 Contig ID 3107_1.R1040
 5'-most EST 2DC-01-Q1-B1-D7
 Method BLASTX
 NCBI GI g418399
 BLAST score 257
 E value 7.0e-22
 Match length 110
 % identity 51
 NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT)
 >gi_320705_pir_S30826 hypothetical protein YEL051w - yeast

E value 3.0e-79
 Match length 149
 % identity 92
 NCBI Description B2 PROTEIN >gi_322726_pir_S32124 B2 protein - carrot
 >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus
 carota]

Seq. No. 4068
 Contig ID 3166_3.R1040
 5'-most EST jC-gmro02910054h09d1

Seq. No. 4069
 Contig ID 3166_4.R1040
 5'-most EST LIB3092-034-Q1-K1-G1
 Method BLASTX
 NCBI GI g584825
 BLAST score 196
 E value 9.0e-15
 Match length 75
 % identity 81
 NCBI Description B2 PROTEIN >gi_322726_pir_S32124 B2 protein - carrot
 >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus
 carota]

Seq. No. 4070
 Contig ID 3166_5.R1040
 5'-most EST ncj700980819.h1

Seq. No. 4071
 Contig ID 3166_6.R1040
 5'-most EST jC-gmro02910075c03d1

Seq. No. 4072
 Contig ID 3167_1.R1040
 5'-most EST fC-gmst700888545a4
 Method BLASTN
 NCBI GI g440592
 BLAST score 513
 E value 0.0e+00
 Match length 785
 % identity 82
 NCBI Description V.faba mRNA (VfAGPC) for ADP-glucose pyrophosphorylase

Seq. No. 4073
 Contig ID 3168_1.R1040
 5'-most EST ncj700981229.h1
 Method BLASTN
 NCBI GI g2565339
 BLAST score 133
 E value 3.0e-68
 Match length 460
 % identity 88
 NCBI Description Lupinus luteus ribosomal protein S14 (rps14) mRNA, complete
 cds

Seq. No. 4074
 Contig ID 3168_2.R1040

5'-most EST sat701004906.h1

Seq. No. 4097
 Contig ID 3191_1.R1040
 5'-most EST jC-gmle01810087a10d1
 Method BLASTX
 NCBI GI g2245092
 BLAST score 195
 E value 6.0e-15
 Match length 136
 % identity 34
 NCBI Description (Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No. 4098
 Contig ID 3193_1.R1040
 5'-most EST LIB3053-003-Q1-N1-B6

Seq. No. 4099
 Contig ID 3196_1.R1040
 5'-most EST LIB3028-034-Q1-B1-C10
 Method BLASTX
 NCBI GI g1123105
 BLAST score 142
 E value 8.0e-09
 Match length 111
 % identity 33
 NCBI Description (U42438) similar to *S. cerevisiae* longevity-assurance protein 1 (SP:P38703) [Caenorhabditis elegans]

Seq. No. 4100
 Contig ID 3198_1.R1040
 5'-most EST LIB3040-009-Q1-E1-E5
 Method BLASTN
 NCBI GI g499692
 BLAST score 148
 E value 4.0e-77
 Match length 343
 % identity 87
 NCBI Description Vicia faba cyclophilin mRNA, complete cds

Seq. No. 4101
 Contig ID 3200_1.R1040
 5'-most EST LIB3028-033-Q1-B1-F12
 Method BLASTX
 NCBI GI g2642157
 BLAST score 1285
 E value 1.0e-142
 Match length 286
 % identity 78
 NCBI Description (AC003000) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 4102
 Contig ID 3201_1.R1040
 5'-most EST fua701042634.h1
 Method BLASTX
 NCBI GI g2498892
 BLAST score 434

5'-most EST pmv700894463.h1
 Method BLASTX
 NCBI GI g1777443
 BLAST score 228
 E value 1.0e-18
 Match length 48
 % identity 83
 NCBI Description (U28422) CCA1 [Arabidopsis thaliana] >gi_3510263 (AC005310)
 DNA-binding protein CCA1 [Arabidopsis thaliana] >gi_4090569
 (U79156) CCA1 [Arabidopsis thaliana]

Seq. No. 4122
 Contig ID 3217_9.R1040
 5'-most EST ncj700977410.h1

Seq. No. 4123
 Contig ID 3217_12.R1040
 5'-most EST LIB3138-130-Q1-N1-D2
 Method BLASTN
 NCBI GI g3281845
 BLAST score 43
 E value 6.0e-15
 Match length 83
 % identity 88
 NCBI Description Arabidopsis thaliana mRNA for LATE ELONGATED HYPOCOTYL MYB
 transcription factor

Seq. No. 4124
 Contig ID 3217_16.R1040
 5'-most EST zhf700953467.h1

Seq. No. 4125
 Contig ID 3217_17.R1040
 5'-most EST wvk700683912.h1

Seq. No. 4126
 Contig ID 3219_1.R1040
 5'-most EST jC-gmst02400015f08a1
 Method BLASTX
 NCBI GI g1706082
 BLAST score 836
 E value 2.0e-89
 Match length 313
 % identity 53
 NCBI Description SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3)
 >gi_629787_pir_S44191 serine-type carboxypeptidase (EC
 3.4.16.1) II-3 - barley >gi_619350_bbs_153536
 CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley,
 cv. Alexis, aleurone, Peptide, 516 aa]
 >gi_474392_emb_CAA55478_ (X78877) serine carboxylase II-3
 [Hordeum vulgare]

Seq. No. 4127
 Contig ID 3220_1.R1040
 5'-most EST LIB3073-009-Q1-K1-C11
 Method BLASTX
 NCBI GI g4544418

BLAST score 401
 E value 9.0e-39
 Match length 145
 % identity 56
 NCBI Description (AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No. 4128
 Contig ID 3221_1.R1040
 5'-most EST uC-gmrominsoy103f05b1
 Method BLASTX
 NCBI GI g2980770
 BLAST score 1519
 E value 1.0e-169
 Match length 430
 % identity 69
 NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 4129
 Contig ID 3221_2.R1040
 5'-most EST fC-gmro7000750362r1
 Method BLASTX
 NCBI GI g2980770
 BLAST score 339
 E value 2.0e-31
 Match length 94
 % identity 69
 NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 4130
 Contig ID 3221_3.R1040
 5'-most EST uC-gmrominsoy117f06b1
 Method BLASTX
 NCBI GI g2980770
 BLAST score 190
 E value 3.0e-14
 Match length 77
 % identity 56
 NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 4131
 Contig ID 3223_1.R1040
 5'-most EST jC-gmfl02220141g06a1
 Method BLASTX
 NCBI GI g2232354
 BLAST score 439
 E value 2.0e-43
 Match length 159
 % identity 53
 NCBI Description (AF006081) UDPG glucosyltransferase [Solanum berthaultii]

Seq. No. 4132
 Contig ID 3224_1.R1040
 5'-most EST uC-gmrominsoy136g03b1

Seq. No. 4133
 Contig ID 3224_2.R1040
 5'-most EST dpv701102995.h1

E value 1.0e-101
 Match length 218
 % identity 82
 NCBI Description (X95269) LRR protein [*Lycopersicon esculentum*]

 Seq. No. 4142
 Contig ID 3230 2.R1040
 5'-most EST zzp700834740.h1

 Seq. No. 4143
 Contig ID 3232 1.R1040
 5'-most EST wrg700790475.h2
 Method BLASTX
 NCBI GI g1655637
 BLAST score 380
 E value 9.0e-80
 Match length 188
 % identity 80
 NCBI Description (Z54179) orf [*Mus musculus*]

 Seq. No. 4144
 Contig ID 3232 2.R1040
 5'-most EST jsh701067294.h1

 Seq. No. 4145
 Contig ID 3232 4.R1040
 5'-most EST LIB3028-015-Q1-B1-G5
 Method BLASTX
 NCBI GI g1655637
 BLAST score 428
 E value 3.0e-42
 Match length 100
 % identity 81
 NCBI Description (Z54179) orf [*Mus musculus*]

 Seq. No. 4146
 Contig ID 3233 1.R1040
 5'-most EST crh700855064.h1
 Method BLASTX
 NCBI GI g2980770
 BLAST score 485
 E value 1.0e-48
 Match length 155
 % identity 66
 NCBI Description (AL022198) putative protein kinase [*Arabidopsis thaliana*]

 Seq. No. 4147
 Contig ID 3233 2.R1040
 5'-most EST jC-gmle01810016b03d1
 Method BLASTX
 NCBI GI g2980770
 BLAST score 304
 E value 2.0e-27
 Match length 83
 % identity 70
 NCBI Description (AL022198) putative protein kinase [*Arabidopsis thaliana*]

Seq. No. 4148
 Contig ID 3235_1.R1040
 5'-most EST LIB3028-032-Q1-B1-H10

Seq. No. 4149
 Contig ID 3237_1.R1040
 5'-most EST wrg700790785.h1
 Method BLASTX
 NCBI GI g3746791
 BLAST score 279
 E value 2.0e-24
 Match length 186
 % identity 32
 NCBI Description (AF081788) putative spliceosome associated protein [Homo sapiens] >gi_3985930_dbj_BAA34863_ (AB020623) DAM1 [Homo sapiens]

Seq. No. 4150
 Contig ID 3238_1.R1040
 5'-most EST jC-gmfl02220084a05a1
 Method BLASTX
 NCBI GI g3844596
 BLAST score 369
 E value 7.0e-35
 Match length 153
 % identity 47
 NCBI Description (U28941) contains similarity to human copine I (GB:U83246) [Caenorhabditis elegans]

Seq. No. 4151
 Contig ID 3238_2.R1040
 5'-most EST LIB3028-032-Q1-B1-H4
 Method BLASTX
 NCBI GI g1176658
 BLAST score 399
 E value 1.0e-38
 Match length 158
 % identity 54
 NCBI Description HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II >gi_726363 (U23168) No definition line found [Caenorhabditis elegans]

Seq. No. 4152
 Contig ID 3238_3.R1040
 5'-most EST uC-gmrominsoyl08d01b1
 Method BLASTX
 NCBI GI g3844596
 BLAST score 185
 E value 1.0e-13
 Match length 67
 % identity 54
 NCBI Description (U28941) contains similarity to human copine I (GB:U83246) [Caenorhabditis elegans]

Seq. No. 4153
 Contig ID 3238_4.R1040
 5'-most EST jex700904237.h1

Seq. No. 4154
 Contig ID 3239_1.R1040
 5'-most EST LIB3040-022-Q1-E1-F10
 Method BLASTN
 NCBI GI g498895
 BLAST score 120
 E value 1.0e-60
 Match length 392
 % identity 83
 NCBI Description Pisum sativum histone H2A homolog mRNA, complete cds

Seq. No. 4155
 Contig ID 3239_2.R1040
 5'-most EST uC-gmflminsoy058d06b1
 Method BLASTN
 NCBI GI g498895
 BLAST score 116
 E value 2.0e-58
 Match length 368
 % identity 83
 NCBI Description Pisum sativum histone H2A homolog mRNA, complete cds

Seq. No. 4156
 Contig ID 3239_3.R1040
 5'-most EST LIB3106-110-Q1-K1-B8
 Method BLASTN
 NCBI GI g498895
 BLAST score 117
 E value 9.0e-59
 Match length 385
 % identity 83
 NCBI Description Pisum sativum histone H2A homolog mRNA, complete cds

Seq. No. 4157
 Contig ID 3239_4.R1040
 5'-most EST uC-gmropic062d07b1
 Method BLASTN
 NCBI GI g498895
 BLAST score 113
 E value 2.0e-56
 Match length 385
 % identity 82
 NCBI Description Pisum sativum histone H2A homolog mRNA, complete cds

Seq. No. 4158
 Contig ID 3239_5.R1040
 5'-most EST zvj700605109.h2
 Method BLASTN
 NCBI GI g498895
 BLAST score 103
 E value 1.0e-50
 Match length 323
 % identity 83
 NCBI Description Pisum sativum histone H2A homolog mRNA, complete cds

Seq. No. 4159

Contig ID 3240_1.R1040
 5'-most EST jC-gmfl02220138h05a1
 Method BLASTX
 NCBI GI g3158476
 BLAST score 1185
 E value 1.0e-130
 Match length 286
 % identity 80
 NCBI Description (AF067185) aquaporin 2 [Samanea saman]

Seq. No. 4160
 Contig ID 3240_2.R1040
 5'-most EST g4298424
 Method BLASTN
 NCBI GI g1402832
 BLAST score 98
 E value 2.0e-47
 Match length 290
 % identity 83
 NCBI Description Beta vulgaris plasma membrane major intrinsic protein 1 mRNA, complete cds

Seq. No. 4161
 Contig ID 3240_5.R1040
 5'-most EST g4313924
 Method BLASTX
 NCBI GI g1657948
 BLAST score 348
 E value 1.0e-32
 Match length 153
 % identity 58
 NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]

Seq. No. 4162
 Contig ID 3240_9.R1040
 5'-most EST pxt700943836.h1

Seq. No. 4163
 Contig ID 3241_1.R1040
 5'-most EST sat701012981.h1
 Method BLASTX
 NCBI GI g3776578
 BLAST score 382
 E value 2.0e-36
 Match length 136
 % identity 50
 NCBI Description (AC005388) ESTs gb_F13915 and gb_F13916 come from this gene. [Arabidopsis thaliana]

Seq. No. 4164
 Contig ID 3243_1.R1040
 5'-most EST uaw700665294.h1
 Method BLASTX
 NCBI GI g3252807
 BLAST score 364
 E value 1.0e-34
 Match length 184

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Seq. No. 4212
 Contig ID 3292_1.R1040
 5'-most EST leu701148679.h1
 Method BLASTX
 NCBI GI g2062167
 BLAST score 1341
 E value 1.0e-148
 Match length 321
 % identity 78
 NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No. 4213
 Contig ID 3292_2.R1040
 5'-most EST LIB3107-013-Q1-K1-B11
 Method BLASTX
 NCBI GI g2062167
 BLAST score 300
 E value 6.0e-27
 Match length 68
 % identity 82
 NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No. 4214
 Contig ID 3293_1.R1040
 5'-most EST wrg700786729.h2
 Method BLASTN
 NCBI GI g603218
 BLAST score 183
 E value 3.0e-98
 Match length 457
 % identity 85
 NCBI Description Medicago sativa glucose-6-phosphate dehydrogenase mRNA, complete cds

Seq. No. 4215
 Contig ID 3296_1.R1040
 5'-most EST leu701153364.h1
 Method BLASTX
 NCBI GI g2760326
 BLAST score 582
 E value 6.0e-60
 Match length 261
 % identity 48
 NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana]

Seq. No. 4216
 Contig ID 3297_1.R1040
 5'-most EST LIB3028-032-Q1-B1-D3
 Method BLASTX
 NCBI GI g2239262
 BLAST score 444
 E value 7.0e-44
 Match length 207
 % identity 43

0-968-0161-1

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Seq. No.          4224
Contig ID         3315_3.R1040
5'-most EST      hrw701058023.h1
Method            BLASTX
NCBI GI           g462013
BLAST score       229
E value           4.0e-19
Match length      52
% identity        88
NCBI Description  ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)
                  >gi_542022_pir_S39558 HSP90 homolog - Madagascar
                  periwinkle >gi_348696 (L14594) heat shock protein 90
                  [Catharanthus roseus]
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Seq. No.          4226
Contig ID         3319_1.R1040
5'-most EST      jC-gmle01810060g11a1
Method            BLASTX
NCBI GI           g3763926
BLAST score       302
E value           7.0e-27
Match length      313
% identity        35
NCBI Description  (AC004450) unknown protein [Arabidopsis thaliana]
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BLAST score 820
 E value 8.0e-88
 Match length 197
 % identity 74
 NCBI Description (AF017150) betaine aldehyde dehydrogenase [Amaranthus hypochondriacus]

Seq. No. 4239
 Contig ID 3330_4.R1040
 5'-most EST bth700844477.h1
 Method BLASTX
 NCBI GI g1169286
 BLAST score 143
 E value 3.0e-09
 Match length 35
 % identity 71
 NCBI Description BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (BADH)
 >gi_1085671_pir_S49205 betaine-aldehyde dehydrogenase (EC 1.2.1.8) precursor - Atriplex hortensis
 >gi_510574_emb_CAA49425_(X69770) betaine-aldehyde dehydrogenase [Atriplex hortensis]

Seq. No. 4240
 Contig ID 3331_1.R1040
 5'-most EST uaw700665055.h1
 Method BLASTX
 NCBI GI g4539322
 BLAST score 241
 E value 9.0e-32
 Match length 111
 % identity 62
 NCBI Description (AL035679) putative protein [Arabidopsis thaliana]

Seq. No. 4241
 Contig ID 3333_1.R1040
 5'-most EST wrg700790526.h2
 Method BLASTX
 NCBI GI g3193316
 BLAST score 642
 E value 3.0e-95
 Match length 284
 % identity 65
 NCBI Description (AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No. 4242
 Contig ID 3335_1.R1040
 5'-most EST LIB3074-039-Q1-K1-C6
 Method BLASTX
 NCBI GI g1653488
 BLAST score 173
 E value 3.0e-12
 Match length 79
 % identity 42
 NCBI Description (D90914) hypothetical protein [Synechocystis sp.]

Seq. No. 4243

Contig ID 3335_2.R1040
5'-most EST leu701146566.h1

Seq. No. 4244
Contig ID 3336_1.R1040
5'-most EST LIB3028-031-Q1-B1-E5
Method BLASTX
NCBI GI g4337025
BLAST score 590
E value 8.0e-61
Match length 192
% identity 59
NCBI Description (AF123253) AIM1 protein [Arabidopsis thaliana]

Seq. No. 4245
Contig ID 3336_2.R1040
5'-most EST jC-gmf102220054c05d1
Method BLASTX
NCBI GI g4337025
BLAST score 296
E value 1.0e-26
Match length 82
% identity 71
NCBI Description (AF123253) AIM1 protein [Arabidopsis thaliana]

Seq. No. 4246
Contig ID 3340_1.R1040
5'-most EST leu701156583.h1
Method BLASTN
NCBI GI g2961299
BLAST score 266
E value 1.0e-147
Match length 474
% identity 89
NCBI Description Cicer arietinum mRNA for ribosomal protein L24

Seq. No. 4247
Contig ID 3340_2.R1040
5'-most EST LIB3073-016-Q1-K1-B3
Method BLASTN
NCBI GI g2961299
BLAST score 202
E value 1.0e-109
Match length 485
% identity 85
NCBI Description Cicer arietinum mRNA for ribosomal protein L24

Seq. No. 4248
Contig ID 3341_1.R1040
5'-most EST taw700659875.h1

Seq. No. 4249
Contig ID 3343_1.R1040
5'-most EST jsh701066525.h1

Seq. No. 4250
Contig ID 3346_1.R1040

0607010

Seq. No.	4252
Contig ID	3347_2.R1040
5'-most EST	uC-qmflminsoy032e12b1

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Seq. No.          4254
Contig ID         3351_2.R1040
5'-most EST      leu701151416.h1
Method            BLASTX
NCBI GI           g3850580
BLAST score       254
E value           8.0e-22
Match length      102
% identity        54
NCBI Description  (AC005278) Strong similarity to gb_D14550 extracellular
                  dermal glycoprotein (EDGP) precursor from Daucus carota.
                  ESTs gb_84105 and gb_AI100071 come from this gene.
                  [Arabidopsis thaliana]
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Seq. No.          4255
Contig ID         3354_1.R1040
5'-most EST      leu701153022.h1
Method            BLASTX
NCBI GI           g3894186
BLAST score       861
E value           2.0e-92
Match length      260
% identity        63
NCBI Description  (AC005662) putative embryo-abundant protein [Arabidopsis
                  thaliana]
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Seq. No.	4258
Contig ID	3361_1.R1040
5'-most EST	hrw701059490.h1

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Seq. No.          4260
Contig ID         3362_1.R1040
5'-most EST      leu701155858.h1
Method            BLASTX
NCBI GI           g3421104
BLAST score       1252
E value           1.0e-138
Match length      268
% identity        88
```

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Seq. No.          4261
Contig ID         3362_2.R1040
5'-most EST      leu701152736.h1
Method            BLASTX
NCBI GI           g3421104
BLAST score       887
E value           1.0e-95
Match length      195
% identity        86
```

Seq. No.	4262
Contig ID	3362_3.R1040
5'-most EST	LIB3170-053-Q1-K1-F10
Method	BLASTX
NCBI GI	g3421104
BLAST score	721
E value	2.0e-76
Match length	148
% identity	91

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Seq. No. 4263
 Contig ID 3362_4.R1040
 5'-most EST LIB3065-005-Q1-N1-F8
 Method BLASTX
 NCBI GI g3421104
 BLAST score 435
 E value 5.0e-43
 Match length 107
 % identity 75
 NCBI Description (AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis thaliana]

Seq. No. 4264
 Contig ID 3362_5.R1040
 5'-most EST jC-gmro02910037b10a1
 Method BLASTX
 NCBI GI g3421104
 BLAST score 522
 E value 3.0e-66
 Match length 141
 % identity 91
 NCBI Description (AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis thaliana]

Seq. No. 4265
 Contig ID 3363_1.R1040
 5'-most EST leu701156343.h1

Seq. No. 4266
 Contig ID 3364_1.R1040
 5'-most EST rca701001508.h1
 Method BLASTX
 NCBI GI g2194137
 BLAST score 291
 E value 2.0e-25
 Match length 89
 % identity 63
 NCBI Description (AC002062) ESTs gb_R29947,gb_H76702 come from this gene. [Arabidopsis thaliana]

Seq. No. 4267
 Contig ID 3364_2.R1040
 5'-most EST LIB3107-032-Q1-K1-G12
 Method BLASTX
 NCBI GI g2194137
 BLAST score 350
 E value 6.0e-33
 Match length 131
 % identity 59
 NCBI Description (AC002062) ESTs gb_R29947,gb_H76702 come from this gene. [Arabidopsis thaliana]

Seq. No. 4268
 Contig ID 3364_3.R1040
 5'-most EST wrg700785911.h2

Seq. No. 4269

09084012-101000

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Seq. No.          4271
Contig ID         3371_1.R1040
5'-most EST      zzp700836229.h1
Method            BLASTX
NCBI GI           g1707642
BLAST score       1420
E value           1.0e-158
Match length      571
% identity        48
NCBI Description  (Y07748) TMK [Oryza sativa]
```

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Seq. No.          4273
Contig ID         3377_1.R1040
5'-most EST      LIB3051-010-Q1-E1-B11
Method            BLASTX
NCBI GI          g1685005
BLAST score       395
E value          4.0e-38
Match length      208
% identity        39
NCBI Description  (U32644) immediate-early salicylate-induced
                  glucosyltransferase [Nicotiana tabacum]

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Seq. No.          4274
Contig ID         3378_1.R1040
5'-most EST      LIB3039-044-Q1-E1-E9
Method            BLASTX
NCBI GI           g416662
BLAST score       216
E value           5.0e-17
Match length      173
% identity        40
NCBI Description  21 KD SEED PROTEIN PRECURSOR >gi_99954_pir_S16252 trypsin
                  inhibitor homolog - soybean >gi_21909_emb_CAA39860_
                  (X56509) 21 kDa seed protein [Theobroma cacao]
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Seq. No.	4277
Contig ID	3386_1.R1040
5'-most EST	LIB3028-031-Q1-B1-C2

Seq. No.	4279
Contig ID	3390_1.R1040
5'-most EST	zsq701122962.h1

Seq. No.	4281
Contig ID	3394_2.R1040
5'-most EST	LIB3170-058-Q1-K1-F5

Seq. No.	4283
Contig ID	3398_2.R1040
5'-most EST	qsv701046010.h1

840

Contig ID 3399_1.R1040
 5'-most EST uC-gmflminsoy093c05b1
 Method BLASTX
 NCBI GI g2664214
 BLAST score 1307
 E value 1.0e-144
 Match length 633
 % identity 47
 NCBI Description (AJ222646) G2484-1 [Arabidopsis thaliana]

Seq. No. 4285
 Contig ID 3399_5.R1040
 5'-most EST taw700654495.h1
 Method BLASTX
 NCBI GI g2664214
 BLAST score 293
 E value 4.0e-26
 Match length 233
 % identity 34
 NCBI Description (AJ222646) G2484-1 [Arabidopsis thaliana]

Seq. No. 4286
 Contig ID 3400_1.R1040
 5'-most EST LIB3107-022-Q1-K1-E8
 Method BLASTN
 NCBI GI g2605886
 BLAST score 75
 E value 1.0e-33
 Match length 225
 % identity 87
 NCBI Description Pisum sativum dormancy-associated protein (DRM1) mRNA, complete cds

Seq. No. 4287
 Contig ID 3400_2.R1040
 5'-most EST jC-gmro02910046d03a1
 Method BLASTN
 NCBI GI g2995991
 BLAST score 52
 E value 3.0e-20
 Match length 68
 % identity 94
 NCBI Description Arabidopsis thaliana dormancy-associated protein (DRM1) gene, complete cds

Seq. No. 4288
 Contig ID 3400_4.R1040
 5'-most EST LIB3049-013-Q1-E1-G7
 Method BLASTN
 NCBI GI g2605886
 BLAST score 56
 E value 2.0e-22
 Match length 172
 % identity 88
 NCBI Description Pisum sativum dormancy-associated protein (DRM1) mRNA, complete cds

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Method BLASTX
NCBI GI g4164408
BLAST score 218
E value 2.0e-17
Match length 66
% identity 50
NCBI Description (AJ132228) amino acid carrier [Ricinus communis]

Seq. No. 4300
Contig ID 3409_3.R1040
5'-most EST jC-gmfl02220088d03a1
Method BLASTX
NCBI GI g4164408
BLAST score 149
E value 1.0e-09
Match length 46
% identity 65
NCBI Description (AJ132228) amino acid carrier [Ricinus communis]

Seq. No. 4301
Contig ID 3409_4.R1040
5'-most EST pcp700991253.h1

Seq. No. 4302
Contig ID 3410_1.R1040
5'-most EST uC-gmrominsoy279b04b1
Method BLASTX
NCBI GI g3281853
BLAST score 1167
E value 1.0e-128
Match length 259
% identity 92
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 4303
Contig ID 3410_2.R1040
5'-most EST hyd700730125.h1
Method BLASTX
NCBI GI g3281853
BLAST score 318
E value 4.0e-29
Match length 62
% identity 97
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 4304
Contig ID 3410_3.R1040
5'-most EST jC-gmst02400069e07a1

Seq. No. 4305
Contig ID 3410_7.R1040
5'-most EST kmv700738573.h1

Seq. No. 4306
Contig ID 3410_8.R1040
5'-most EST pmv700889945.h1

Method BLASTX
 NCBI GI g4467128
 BLAST score 635
 E value 4.0e-66
 Match length 242
 % identity 49
 NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 4316
 Contig ID 3431_1.R1040
 5'-most EST LIB3139-004-P1-N1-B5

Seq. No. 4317
 Contig ID 3432_1.R1040
 5'-most EST uC-gmflminsoy031b04b1
 Method BLASTX
 NCBI GI g2497753
 BLAST score 327
 E value 5.0e-30
 Match length 114
 % identity 54
 NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
 >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein
 [Prunus dulcis]

Seq. No. 4318
 Contig ID 3433_1.R1040
 5'-most EST LIB3106-006-Q1-K2-F9
 Method BLASTX
 NCBI GI g3660471
 BLAST score 2865
 E value 0.0e+00
 Match length 630
 % identity 85
 NCBI Description (AJ001809) succinate dehydrogenase flavoprotein alpha
 subunit [Arabidopsis thaliana]

Seq. No. 4319
 Contig ID 3433_3.R1040
 5'-most EST LIB3138-061-Q1-N1-H5
 Method BLASTX
 NCBI GI g3660471
 BLAST score 304
 E value 2.0e-27
 Match length 108
 % identity 56
 NCBI Description (AJ001809) succinate dehydrogenase flavoprotein alpha
 subunit [Arabidopsis thaliana]

Seq. No. 4320
 Contig ID 3437_1.R1040
 5'-most EST LIB3028-030-Q1-B1-E9

Seq. No. 4321
 Contig ID 3439_1.R1040
 5'-most EST trc700563801.h1
 Method BLASTX

BLAST score	855
E value	6.0e-92
Match length	204
% identity	79
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]
Seq. No.	4329
Contig ID	3444_2.R1040
5'-most EST	LIB3170-004-Q1-K1-D9
Method	BLASTX
NCBI GI	g2982318
BLAST score	536
E value	2.0e-54
Match length	182
% identity	61
NCBI Description	(AF051244) probable 60S ribosomal protein L15 [Picea mariana]
Seq. No.	4330
Contig ID	3444_3.R1040
5'-most EST	jC-gmro02910067a02a1
Method	BLASTX
NCBI GI	g3122673
BLAST score	664
E value	1.0e-85
Match length	203
% identity	78
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]
Seq. No.	4331
Contig ID	3444_4.R1040
5'-most EST	LIB3106-107-Q1-K1-E7
Method	BLASTX
NCBI GI	g3122673
BLAST score	830
E value	5.0e-89
Match length	204
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]
Seq. No.	4332
Contig ID	3444_5.R1040
5'-most EST	LIB3138-070-P1-N1-D1
Method	BLASTX
NCBI GI	g3122673
BLAST score	267
E value	4.0e-23
Match length	55
% identity	91
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]
Seq. No.	4333
Contig ID	3444_6.R1040

BLAST score 45
E value 8.0e-16
Match length 89
% identity 93
NCBI Description Cicer arietinum mRNA for unidentified protein

Seq. No. 4346
Contig ID 3467_4.R1040
5'-most EST uC-gmropic016g06b1

Seq. No. 4347
Contig ID 3468_1.R1040
5'-most EST g4313544
Method BLASTX
NCBI GI g548437
BLAST score 164
E value 4.0e-11
Match length 103
% identity 40
NCBI Description OSH1 PROTEIN >gi_1078479_pir_S53463 SWH1 protein (version 1) - yeast (Saccharomyces cerevisiae) >gi_456143 (L28920) Oshlp [Saccharomyces cerevisiae]

Seq. No. 4348
Contig ID 3469_1.R1040
5'-most EST LIB3030-003-Q1-B1-H5

Seq. No. 4349
Contig ID 3472_1.R1040
5'-most EST jC-gmro02910039g08a1
Method BLASTX
NCBI GI g2245378
BLAST score 1106
E value 1.0e-121
Match length 545
% identity 54
NCBI Description (U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No. 4350
Contig ID 3472_2.R1040
5'-most EST jC-gmro02910046h09d1

Seq. No. 4351
Contig ID 3476_1.R1040
5'-most EST LIB3028-029-Q1-B1-G4
Method BLASTX
NCBI GI g3193298
BLAST score 312
E value 2.0e-28
Match length 120
% identity 48
NCBI Description (AF069298) T14P8.17 gene product [Arabidopsis thaliana]

Seq. No. 4352
Contig ID 3476_2.R1040
5'-most EST epx701104722.h1

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5'-most EST uC-gmflminsoy055h11b1
 Method BLASTX
 NCBI GI g3004549
 BLAST score 597
 E value 2.0e-61
 Match length 278
 % identity 44
 NCBI Description (AC003673) unknown protein [Arabidopsis thaliana]
 >gi_4185152 (AC005724) unknown protein [Arabidopsis thaliana]

Seq. No. 4365
 Contig ID 3494_3.R1040
 5'-most EST uC-gmropic019g05b1
 Method BLASTX
 NCBI GI g3004549
 BLAST score 187
 E value 5.0e-14
 Match length 56
 % identity 64
 NCBI Description (AC003673) unknown protein [Arabidopsis thaliana]
 >gi_4185152 (AC005724) unknown protein [Arabidopsis thaliana]

Seq. No. 4366
 Contig ID 3494_5.R1040
 5'-most EST dpv701099759.h1
 Method BLASTX
 NCBI GI g3004549
 BLAST score 149
 E value 3.0e-18
 Match length 73
 % identity 68
 NCBI Description (AC003673) unknown protein [Arabidopsis thaliana]
 >gi_4185152 (AC005724) unknown protein [Arabidopsis thaliana]

Seq. No. 4367
 Contig ID 3495_1.R1040
 5'-most EST zhf700956320.h1
 Method BLASTX
 NCBI GI g3559805
 BLAST score 473
 E value 3.0e-47
 Match length 97
 % identity 85
 NCBI Description (AJ006787) putative phytochelatase [Arabidopsis thaliana]

Seq. No. 4368
 Contig ID 3496_1.R1040
 5'-most EST LIB3139-113-P1-N1-E11
 Method BLASTX
 NCBI GI g2459443
 BLAST score 736
 E value 5.0e-78
 Match length 210

BLAST score 285
E value 3.0e-25
Match length 196
% identity 3
NCBI Description (AF071172) HERC2 [Homo sapiens]

Seq. No. 4374
Contig ID 3500_1.R1040
5'-most EST jC-gmfl02220065e10d1

Seq. No. 4375
Contig ID 3502_1.R1040
5'-most EST ncj700981882.h1
Method BLASTX
NCBI GI g131187
BLAST score 732
E value 2.0e-77
Match length 220
% identity 67
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR
(LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)
>gi_72681_pir_F1SP3 photosystem I chain III precursor -
spinach >gi_21303_emb_CAA31523_(X13133) PSI subunit IV
preprotein (AA -77 to 154) [Spinacia oleracea]
>gi_226166_prf_1413236A photosystem I reaction center IV
[Spinacia oleracea]

Seq. No. 4376
Contig ID 3506_1.R1040
5'-most EST LIB3028-029-Q1-B1-C7

Seq. No. 4377
Contig ID 3508_1.R1040
5'-most EST zhf700965192.h1
Method BLASTX
NCBI GI g2253583
BLAST score 172
E value 3.0e-12
Match length 82
% identity 51
NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No. 4378
Contig ID 3514_1.R1040
5'-most EST uC-gmflminsoy053c08b1
Method BLASTX
NCBI GI g886130
BLAST score 561
E value 2.0e-80
Match length 327
% identity 47
NCBI Description (U28148) putative pectinesterase [Medicago sativa]

Seq. No. 4379
Contig ID 3514_2.R1040
5'-most EST LIB3028-029-Q1-B1-D4

Seq. No. 4380
 Contig ID 3515_1.R1040
 5'-most EST leu701151350.h1
 Method BLASTN
 NCBI GI g3264758
 BLAST score 116
 E value 2.0e-58
 Match length 360
 % identity 83
 NCBI Description Prunus armeniaca 40S ribosomal protein S8 (RPS8) mRNA, complete cds

Seq. No. 4381
 Contig ID 3517_2.R1040
 5'-most EST LIB3139-056-P1-N1-B1

Seq. No. 4382
 Contig ID 3518_1.R1040
 5'-most EST jC-gmro02910022g03a1
 Method BLASTX
 NCBI GI g3075392
 BLAST score 179
 E value 5.0e-16
 Match length 71
 % identity 66
 NCBI Description (AC004484) putative steroid dehydrogenase [Arabidopsis thaliana]

Seq. No. 4383
 Contig ID 3522_1.R1040
 5'-most EST LIB3056-010-Q1-N1-A1
 Method BLASTX
 NCBI GI g3834310
 BLAST score 716
 E value 1.0e-75
 Match length 141
 % identity 99
 NCBI Description (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]

Seq. No. 4384
 Contig ID 3522_2.R1040
 5'-most EST LIB3056-004-Q1-N1-A12
 Method BLASTX
 NCBI GI g3834310
 BLAST score 712
 E value 4.0e-75
 Match length 141
 % identity 99
 NCBI Description (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]

Seq. No. 4385

Contig ID 3522 3.R1040
 5'-most EST pxt700943960.h1
 Method BLASTX
 NCBI GI g3834310
 BLAST score 240
 E value 8.0e-30
 Match length 71
 % identity 89
 NCBI Description (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]

Seq. No. 4386
 Contig ID 3524 1.R1040
 5'-most EST LIB3028-029-Q1-B1-B12

Seq. No. 4387
 Contig ID 3527 1.R1040
 5'-most EST V4R-02-Q1-B1-D2
 Method BLASTX
 NCBI GI g3702631
 BLAST score 350
 E value 7.0e-33
 Match length 214
 % identity 36
 NCBI Description (AL031824) protein transport protein sec23 homolog [Schizosaccharomyces pombe]

Seq. No. 4388
 Contig ID 3529 1.R1040
 5'-most EST jex700903469.h1

Seq. No. 4389
 Contig ID 3530 1.R1040
 5'-most EST jC-gmle01810020e10d1

Seq. No. 4390
 Contig ID 3530 2.R1040
 5'-most EST LIB3092-004-Q1-K1-A3

Seq. No. 4391
 Contig ID 3531 1.R1040
 5'-most EST crh700855207.h1
 Method BLASTX
 NCBI GI g3757523
 BLAST score 247
 E value 1.0e-20
 Match length 61
 % identity 74
 NCBI Description (AC005167) putative transportin [Arabidopsis thaliana]

Seq. No. 4392
 Contig ID 3531 2.R1040
 5'-most EST ncj700981843.h1
 Method BLASTX
 NCBI GI g3757523

BLAST score 345
 E value 2.0e-36
 Match length 104
 % identity 73
 NCBI Description (AC005167) putative transportin [Arabidopsis thaliana]

Seq. No. 4393
 Contig ID 3533_1.R1040
 5'-most EST LIB3138-119-Q1-N1-G1
 Method BLASTX
 NCBI GI g2598589
 BLAST score 426
 E value 8.0e-42
 Match length 143
 % identity 58
 NCBI Description (Y15367) MtN19 [Medicago truncatula]

Seq. No. 4394
 Contig ID 3533_2.R1040
 5'-most EST LIB3051-087-Q1-K1-F1
 Method BLASTX
 NCBI GI g2598589
 BLAST score 359
 E value 4.0e-34
 Match length 134
 % identity 51
 NCBI Description (Y15367) MtN19 [Medicago truncatula]

Seq. No. 4395
 Contig ID 3533_3.R1040
 5'-most EST LIB3051-062-Q1-K1-H4
 Method BLASTX
 NCBI GI g2598589
 BLAST score 220
 E value 8.0e-18
 Match length 75
 % identity 51
 NCBI Description (Y15367) MtN19 [Medicago truncatula]

Seq. No. 4396
 Contig ID 3536_1.R1040
 5'-most EST LIB3051-077-Q1-K1-D11
 Method BLASTN
 NCBI GI g20355
 BLAST score 49
 E value 2.0e-18
 Match length 125
 % identity 85
 NCBI Description Rice rgpl mRNA for a ras-related GTP-binding protein

Seq. No. 4397
 Contig ID 3537_1.R1040
 5'-most EST jC-gmle01810080e09d1
 Method BLASTX
 NCBI GI g2739382
 BLAST score 396
 E value 3.0e-38

Match length 233
 % identity 42
 NCBI Description (AC002505) myosin heavy chain-like protein [Arabidopsis thaliana]

Seq. No. 4398
 Contig ID 3538_1.R1040
 5'-most EST uaw700660890.h1
 Method BLASTX
 NCBI GI g1256509
 BLAST score 546
 E value 1.0e-105
 Match length 220
 % identity 81
 NCBI Description (X92943) pectate lyase [Musa acuminata]

Seq. No. 4399
 Contig ID 3538_2.R1040
 5'-most EST LIB3028-029-Q1-B1-A9
 Method BLASTX
 NCBI GI g2463509
 BLAST score 975
 E value 1.0e-106
 Match length 226
 % identity 77
 NCBI Description (Y09541) pectate lyase [Zinnia elegans]

Seq. No. 4400
 Contig ID 3539_1.R1040
 5'-most EST pxt700945309.h1
 Method BLASTX
 NCBI GI g2880043
 BLAST score 942
 E value 1.0e-102
 Match length 272
 % identity 65
 NCBI Description (AC002340) putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]

Seq. No. 4401
 Contig ID 3539_2.R1040
 5'-most EST bth700843808.h1

Seq. No. 4402
 Contig ID 3542_1.R1040
 5'-most EST zsg701125459.h1

Seq. No. 4403
 Contig ID 3543_1.R1040
 5'-most EST LIB3028-028-Q1-B1-H8
 Method BLASTX
 NCBI GI g4263781
 BLAST score 346
 E value 2.0e-32
 Match length 191
 % identity 41
 NCBI Description (AC006068) putative membrane transport protein [Arabidopsis

thaliana]

Seq. No. 4404
 Contig ID 3545_1.R1040
 5'-most EST bth700843502.h1
 Method BLASTX
 NCBI GI g100535
 BLAST score 313
 E value 2.0e-28
 Match length 79
 % identity 78
 NCBI Description hypothetical protein - swollen duckweed
 >gi_1929057_emb_CAA32236_ (X14075) longest ORF (1) [Lemna
 gibba]

Seq. No. 4405
 Contig ID 3546_1.R1040
 5'-most EST LIB3051-065-Q1-K1-E9
 Method BLASTX
 NCBI GI g481762
 BLAST score 249
 E value 3.0e-21
 Match length 135
 % identity 35
 NCBI Description beta-adaptin 1 - fruit fly (*Drosophila melanogaster*)
 >gi_434902_emb_CAA53509_ (X75910) beta-adaptin *Drosophila* 1
 [*Drosophila melanogaster*]

Seq. No. 4406
 Contig ID 3547_1.R1040
 5'-most EST jC-gmst02400046a06a1
 Method BLASTX
 NCBI GI g2339978
 BLAST score 1270
 E value 1.0e-150
 Match length 357
 % identity 75
 NCBI Description (Y11336) RGA1 protein [*Arabidopsis thaliana*]

Seq. No. 4407
 Contig ID 3547_2.R1040
 5'-most EST vzy700751203.h1
 Method BLASTX
 NCBI GI g2569938
 BLAST score 217
 E value 3.0e-17
 Match length 47
 % identity 85
 NCBI Description (Y15193) GAI [*Arabidopsis thaliana*]

Seq. No. 4408
 Contig ID 3549_1.R1040
 5'-most EST trc700563015.h1

Seq. No. 4409
 Contig ID 3552_1.R1040
 5'-most EST LIB3107-080-Q1-K1-D10

Seq. No. 4415
 Contig ID 3558_5.R1040
 5'-most EST jC-gmro02910032f01a1
 Method BLASTX
 NCBI GI g4335745
 BLAST score 221
 E value 2.0e-25
 Match length 162
 % identity 41
 NCBI Description (AC006284) putative hydrolase (contains an
 esterase/lipase/thioesterase active site serine domain
 (prosite: PS50187) [Arabidopsis thaliana]

Seq. No. 4416
 Contig ID 3558_8.R1040
 5'-most EST leu701149426.h1
 Method BLASTX
 NCBI GI g4115367
 BLAST score 167
 E value 1.0e-11
 Match length 82
 % identity 43
 NCBI Description (AC005957) unknown protein [Arabidopsis thaliana]

Seq. No. 4417
 Contig ID 3561_1.R1040
 5'-most EST uC-gmropic108f06b1
 Method BLASTX
 NCBI GI g1149595
 BLAST score 207
 E value 3.0e-16
 Match length 141
 % identity 35
 NCBI Description (Z49860) 1-acyl-sn-glycerol-3-phosphate acyltransferase
 [Brassica napus]

Seq. No. 4418
 Contig ID 3562_1.R1040
 5'-most EST LIB3028-028-Q1-B1-G5
 Method BLASTX
 NCBI GI g4140691
 BLAST score 350
 E value 6.0e-33
 Match length 148
 % identity 53
 NCBI Description (AF101972) zeatin O-glucosyltransferase [Phaseolus lunatus]

Seq. No. 4419
 Contig ID 3564_1.R1040
 5'-most EST zsg701123081.h1
 Method BLASTX
 NCBI GI g3298540
 BLAST score 985
 E value 1.0e-107
 Match length 239
 % identity 79

Contig ID 3575_1.R1040
 5'-most EST LIB3049-011-Q1-E1-F7
 Method BLASTX
 NCBI GI g2289003
 BLAST score 1619
 E value 0.0e+00
 Match length 496
 % identity 65
 NCBI Description (AC002335) membrane transporter D1 isolog [Arabidopsis thaliana]

Seq. No. 4428
 Contig ID 3575_2.R1040
 5'-most EST jC-gmle01810086b11d1

Seq. No. 4429
 Contig ID 3579_1.R1040
 5'-most EST LIB3167-077-P1-K2-E5
 Method BLASTX
 NCBI GI g2582665
 BLAST score 1377
 E value 1.0e-153
 Match length 336
 % identity 82
 NCBI Description (Z82983) thi [Citrus sinensis]

Seq. No. 4430
 Contig ID 3579_2.R1040
 5'-most EST ncj700979158.h1
 Method BLASTX
 NCBI GI g3212869
 BLAST score 704
 E value 2.0e-74
 Match length 160
 % identity 82
 NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 4431
 Contig ID 3579_3.R1040
 5'-most EST jC-gmst02400052h01d1
 Method BLASTN
 NCBI GI g1289203
 BLAST score 93
 E value 1.0e-44
 Match length 213
 % identity 86
 NCBI Description A.glutinosa mRNA for thiazole biosynthetic enzyme

Seq. No. 4432
 Contig ID 3579_4.R1040
 5'-most EST jC-gmro02910034h10d1
 Method BLASTX
 NCBI GI g3212869
 BLAST score 2167
 E value 0.0e+00
 Match length 487
 % identity 82

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 4433
 Contig ID 3579_5.R1040
 5'-most EST LIB3106-114-Q1-K1-B9
 Method BLASTN
 NCBI GI g596077
 BLAST score 63
 E value 8.0e-27
 Match length 159
 % identity 86
 NCBI Description Zea mays thiamine biosynthetic enzyme (thi1-1) mRNA, complete cds

Seq. No. 4434
 Contig ID 3579_7.R1040
 5'-most EST LIB3106-077-P1-K1-E6
 Method BLASTX
 NCBI GI g2582665
 BLAST score 216
 E value 5.0e-17
 Match length 115
 % identity 65
 NCBI Description (Z82983) thi [Citrus sinensis]

Seq. No. 4435
 Contig ID 3579_11.R1040
 5'-most EST jC-gmst02400043c02a1
 Method BLASTX
 NCBI GI g3212869
 BLAST score 334
 E value 3.0e-31
 Match length 73
 % identity 81
 NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 4436
 Contig ID 3581_1.R1040
 5'-most EST epx701109079.h1
 Method BLASTX
 NCBI GI g1617270
 BLAST score 2744
 E value 0.0e+00
 Match length 659
 % identity 76
 NCBI Description (X94624) acyl-CoA synthetase [Brassica napus]

Seq. No. 4437
 Contig ID 3582_1.R1040
 5'-most EST LIB3170-026-Q1-K1-B2
 Method BLASTX
 NCBI GI g2511594
 BLAST score 1026
 E value 1.0e-112
 Match length 233
 % identity 85
 NCBI Description (Y13694) multicatalytic endopeptidase complex, proteasome

E value 9.0e-39
 Match length 115
 % identity 66
 NCBI Description (AC004165) putative Fe(II) transport protein [Arabidopsis thaliana] >gi_3420044 (AC004680) putative Fe(II) transport protein [Arabidopsis thaliana]

Seq. No. 4448
 Contig ID 3598_1.R1040
 5'-most EST leu701150063.h1
 Method BLASTX
 NCBI GI g4335734
 BLAST score 458
 E value 1.0e-45
 Match length 151
 % identity 41
 NCBI Description (AC006248) putative calmodulin [Arabidopsis thaliana]

Seq. No. 4449
 Contig ID 3602_1.R1040
 5'-most EST LIB3093-006-Q1-K1-F8
 Method BLASTX
 NCBI GI g2497538
 BLAST score 220
 E value 1.0e-17
 Match length 92
 % identity 55
 NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632) pyruvate kinase [Glycine max]

Seq. No. 4450
 Contig ID 3602_2.R1040
 5'-most EST LIB3051-013-Q1-E1-C8
 Method BLASTX
 NCBI GI g2497543
 BLAST score 204
 E value 6.0e-16
 Match length 70
 % identity 61
 NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir_S41379 pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_(Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No. 4451
 Contig ID 3604_1.R1040
 5'-most EST epx701105730.h1

Seq. No. 4452
 Contig ID 3608_1.R1040
 5'-most EST uC-gmropic113g01b1
 Method BLASTX
 NCBI GI g135861
 BLAST score 137
 E value 1.0e-10
 Match length 160
 % identity 36
 NCBI Description INTERFERON-RELATED PROTEIN PC4 (TPA INDUCED SEQUENCE 7)

Seq. No. 4464
Contig ID 3628_2.R1040
5'-most EST bth700845465.h1

Seq. No. 4465
Contig ID 3628_3.R1040
5'-most EST bth700849368.h1

Seq. No. 4466
Contig ID 3629_1.R1040
5'-most EST LIB3028-028-Q1-B1-A3

Seq. No. 4467
Contig ID 3631_1.R1040
5'-most EST ncj700987071.h1
Method BLASTX
NCBI GI g3850587
BLAST score 509
E value 3.0e-51
Match length 221
% identity 56
NCBI Description (AC005278) Strong similarity to gi_2244780 hypothetical protein from Arabidopsis thaliana chromosome 4 contig gb_Z97335. [Arabidopsis thaliana]

Seq. No. 4468
Contig ID 3631_2.R1040
5'-most EST k11701214264.h1
Method BLASTX
NCBI GI g2244779
BLAST score 373
E value 1.0e-35
Match length 130
% identity 58
NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 4469
Contig ID 3631_3.R1040
5'-most EST LIB3028-028-Q1-B1-A4
Method BLASTX
NCBI GI g2244780
BLAST score 174
E value 2.0e-12
Match length 67
% identity 54
NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 4470
Contig ID 3635_1.R1040
5'-most EST g5678054
Method BLASTX
NCBI GI g3108053
BLAST score 1536
E value 1.0e-171
Match length 324
% identity 92
NCBI Description (AF056326) myo-inositol 1-phosphate synthase; INO1 [Zea

SECRET

```
Seq. No.          4472
Contig ID         3635_3.R1040
5'-most EST      LIB3055-012-Q1-N1-H8
Method            BLASTN
NCBI GI           g602564
BLAST score       102
E value           5.0e-50
Match length      310
% identity        83
NCBI Description  C.paradisi (Macf) INO1 gene
```

```
Seq. No.          4473
Contig ID         3635_4.R1040
5'-most EST      jC-gmst02400014d06a1
Method            BLASTN
NCBI GI           g602564
BLAST score       167
E value           8.0e-89
Match length      431
% identity        85
NCBI Description  C.paradisi (Macf) INO1 gene
```

```
Seq. No.          4474
Contig ID         3635_5.R1040
5'-most EST      uC-gmflminsoy059b08b1
Method            BLASTX
NCBI GI           g1170567
BLAST score       595
E value           1.0e-61
Match length      124
% identity        89
NCBI Description  MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)
                  >gi_1085960_pir_S52648 INO1 protein - Citrus paradisi
                  >qi_602565_emb_CAA83565 (Z32632) INO1 [Citrus x paradisi]
```

```
Seq. No.          4475
Contig ID         3635_6.R1040
5'-most EST      LIB3107-036-Q1-K1-G12
Method            BLASTN
NCBI GI           g602564
BLAST score       105
E value           7.0e-52
Match length      282
% identity        84
```

SECRET

```
Seq. No.          4477
Contig ID         3635_9.R1040
5'-most EST      jC-gmro02910004c10a1
Method            BLASTX
NCBI GI           g4567202
BLAST score       294
E value           8.0e-35
Match length      127
% identity        93
NCBI Description  (AC007168) putative myo-inositol 1-phosphate synthase
                  [Arabidopsis thaliana]
```

```
Seq. No.          4479
Contig ID         3637 1.R1040
5'-most EST      LIB3040-008-Q1-E1-H2
Method           BLASTX
NCBI GI          g3913416
BLAST score      872
E value          9.0e-94
Match length     231
% identity       71
NCBI Description  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                  (SAMDC) >gi_2129920_pir_S68990 adenosylmethionine
                  decarboxylase (EC 4.1.1.50) - Madagascar periwinkle
                  >gi_758695 (U12573) S-adenosyl-L-methionine decarboxylase
                  proenzyme [Catharanthus roseus] >gi_1094441_prf_2106177A
                  Met(S-adenosyl) decarboxylase [Catharanthus roseus]
```

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Seq. No.	4508
Contig ID	3671_1.R1040
5'-most EST	LIB3028-027-Q1-B2-B11

```
Seq. No.          4509
Contig ID         3672 1.R1040
5'-most EST      LIB3039-026-Q1-E1-C4
Method            BLASTX
NCBI GI           g2582665
BLAST score       1284
E value           1.0e-142
Match length      282
% identity        88
NCBI Description   (Z82983) thi [Citrus sinensis]
```

Seq. No.	4511
Contig ID	3674_1.R1040
5'-most EST	pcp700994538.h2

```
Seq. No.          4512
Contig ID         3676_1.R1040
5'-most EST      hrw701060639.h1
Method            BLASTX
NCBI GI           g3063467
BLAST score       467
E value           2.0e-46
Match length      126
% identity        73
NCBI Description  (AC003981) F22013.29 [Arabidopsis thaliana]
```

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Seq. No. 4523
 Contig ID 3712_3.R1040
 5'-most EST LIB3073-026-Q1-K1-D8
 Method BLASTN
 NCBI GI g2565428
 BLAST score 46
 E value 9.0e-17
 Match length 106
 % identity 86
 NCBI Description Onobrychis viciifolia glycine-rich protein mRNA, complete cds

Seq. No. 4524
 Contig ID 3715_1.R1040
 5'-most EST g5753666
 Method BLASTN
 NCBI GI g408793
 BLAST score 472
 E value 0.0e+00
 Match length 613
 % identity 96
 NCBI Description Glycine soja chloroplast 3-omega faty acid desaturase (Fad3) mRNA, complete cds

Seq. No. 4525
 Contig ID 3715_2.R1040
 5'-most EST leu701149421.h1
 Method BLASTN
 NCBI GI g408793
 BLAST score 375
 E value 0.0e+00
 Match length 379
 % identity 100
 NCBI Description Glycine soja chloroplast 3-omega faty acid desaturase (Fad3) mRNA, complete cds

Seq. No. 4526
 Contig ID 3716_1.R1040
 5'-most EST jC-gmfl02220061a1a1
 Method BLASTX
 NCBI GI g1709449
 BLAST score 1754
 E value 0.0e+00
 Match length 396
 % identity 85
 NCBI Description PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT PRECURSOR (PDHE1-A) >gi_1263302 (U51918) pyruvate dehydrogenase E1 alpha subunit [Pisum sativum]

Seq. No. 4527
 Contig ID 3716_2.R1040
 5'-most EST LIB3170-041-Q1-K1-C9
 Method BLASTX
 NCBI GI g1709449
 BLAST score 1118
 E value 1.0e-175
 Match length 370

% identity 83
NCBI Description PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT
PRECURSOR (PDHE1-A) >gi_1263302 (U51918) pyruvate
dehydrogenase E1 alpha subunit [Pisum sativum]

Seq. No. 4528
Contig ID 3716_3.R1040
5'-most EST fC-gmse700756337a2
Method BLASTN
NCBI GI g3851004
BLAST score 106
E value 2.0e-52
Match length 194
% identity 89
NCBI Description Zea mays pyruvate dehydrogenase E1 alpha subunit RNA,
nuclear gene encoding mitochondrial protein, complete cds

Seq. No. 4529
Contig ID 3716_6.R1040
5'-most EST uC-gmropic041f09b1

Seq. No. 4530
Contig ID 3721_1.R1040
5'-most EST jC-gmle01810094c05a1
Method BLASTX
NCBI GI g4455246
BLAST score 691
E value 1.0e-72
Match length 238
% identity 58
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 4531
Contig ID 3721_2.R1040
5'-most EST LIB3138-031-Q1-N1-D2
Method BLASTX
NCBI GI g4455246
BLAST score 334
E value 3.0e-31
Match length 95
% identity 69
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 4532
Contig ID 3721_3.R1040
5'-most EST fua701043571.h1
Method BLASTX
NCBI GI g4455246
BLAST score 191
E value 9.0e-15
Match length 62
% identity 75
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 4533
Contig ID 3723_1.R1040
5'-most EST jex700906481.h1

09684016_101000

Seq. No. 4568
 Contig ID 3753_5.R1040
 5'-most EST zzp700834785.h1
 Method BLASTX
 NCBI GI g3319355
 BLAST score 250
 E value 2.0e-21
 Match length 55
 % identity 85
 NCBI Description (AF077407) similar to chaperonin containing TCP-1 complex gamma chain [Arabidopsis thaliana]

Seq. No. 4569
 Contig ID 3753_6.R1040
 5'-most EST uxk700669084.h1

Seq. No. 4570
 Contig ID 3754_1.R1040
 5'-most EST LIB3051-037-Q1-K1-H10
 Method BLASTX
 NCBI GI g2623158
 BLAST score 165
 E value 3.0e-11
 Match length 110
 % identity 31
 NCBI Description (AF030177) N-acetylglucosaminyl transferase component Gpi1 [Homo sapiens] >gi_2911142_dbj_BAA24948_ (AB003723) GPI1 [Homo sapiens]

Seq. No. 4571
 Contig ID 3755_1.R1040
 5'-most EST LIB3028-026-Q1-B1-D10
 Method BLASTX
 NCBI GI g1168314
 BLAST score 357
 E value 2.0e-33
 Match length 235
 % identity 18
 NCBI Description REGULATOR OF ACETYL-COA SYNTHETASE ACTIVITY >gi_1084627_pir_S57116 probable carrier protein ACR1 - yeast (Saccharomyces cerevisiae) >gi_1015794_emb_CAA89624_ (Z49595) ORF YJR095w [Saccharomyces cerevisiae]

Seq. No. 4572
 Contig ID 3756_1.R1040
 5'-most EST LIB3028-026-Q1-B1-D12

Seq. No. 4573
 Contig ID 3758_1.R1040
 5'-most EST uC-gmflminsoyl19b08b1
 Method BLASTX
 NCBI GI g4220527
 BLAST score 943
 E value 1.0e-102
 Match length 342
 % identity 56

% identity 77
 NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]

Seq. No. 4579
 Contig ID 3771_2.R1040
 5'-most EST LIB3092-032-Q1-K1-F8
 Method BLASTX
 NCBI GI g2459429
 BLAST score 580
 E value 7.0e-60
 Match length 147
 % identity 74
 NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]

Seq. No. 4580
 Contig ID 3772_1.R1040
 5'-most EST LIB3093-037-Q1-K1-E4
 Method BLASTX
 NCBI GI g3790587
 BLAST score 996
 E value 1.0e-108
 Match length 347
 % identity 61
 NCBI Description (AF079182) RING-H2 finger protein RHF2a [Arabidopsis thaliana]

Seq. No. 4581
 Contig ID 3772_2.R1040
 5'-most EST rca700997363.h1
 Method BLASTX
 NCBI GI g3790587
 BLAST score 360
 E value 5.0e-34
 Match length 74
 % identity 88
 NCBI Description (AF079182) RING-H2 finger protein RHF2a [Arabidopsis thaliana]

Seq. No. 4582
 Contig ID 3777_1.R1040
 5'-most EST zhf700953648.h1
 Method BLASTX
 NCBI GI g3877358
 BLAST score 188
 E value 6.0e-14
 Match length 85
 % identity 28
 NCBI Description (Z66520) similar to RBB3 like protein; cDNA EST EMBL:C08891 comes from this gene; cDNA EST EMBL:C09371 comes from this gene; cDNA EST yk468f10.5 comes from this gene [Caenorhabditis elegans]

Seq. No. 4583
 Contig ID 3778_1.R1040
 5'-most EST smc700745972.h1
 Method BLASTX
 NCBI GI g2443751

BLAST score 1368
 E value 1.0e-162
 Match length 351
 % identity 84
 NCBI Description (AF020303) fumarase [Arabidopsis thaliana] >gi_2529676
 (AC002535) putative fumarase [Arabidopsis thaliana]

Seq. No. 4584
 Contig ID 3778_2.R1040
 5'-most EST asn701138372.h1
 Method BLASTX
 NCBI GI g2443751
 BLAST score 292
 E value 3.0e-26
 Match length 60
 % identity 92
 NCBI Description (AF020303) fumarase [Arabidopsis thaliana] >gi_2529676
 (AC002535) putative fumarase [Arabidopsis thaliana]

Seq. No. 4585
 Contig ID 3778_3.R1040
 5'-most EST leu701157217.h1
 Method BLASTX
 NCBI GI g2443751
 BLAST score 146
 E value 2.0e-09
 Match length 61
 % identity 54
 NCBI Description (AF020303) fumarase [Arabidopsis thaliana] >gi_2529676
 (AC002535) putative fumarase [Arabidopsis thaliana]

Seq. No. 4586
 Contig ID 3779_1.R1040
 5'-most EST ep701108935.h1
 Method BLASTX
 NCBI GI g1076534
 BLAST score 1833
 E value 0.0e+00
 Match length 433
 % identity 81
 NCBI Description monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - garden
 pea >gi_497120 (U06461) monodehydroascorbate reductase
 [Pisum sativum]

Seq. No. 4587
 Contig ID 3784_1.R1040
 5'-most EST LIB3093-032-Q1-K1-C6
 Method BLASTX
 NCBI GI g2245378
 BLAST score 819
 E value 3.0e-87
 Match length 398
 % identity 56
 NCBI Description (U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No. 4588
 Contig ID 3786_1.R1040

5'-most EST LIB3028-026-Q1-B1-A10
 Method BLASTX
 NCBI GI g586021
 BLAST score 218
 E value 2.0e-17
 Match length 96
 % identity 45
 NCBI Description PROBABLE PEPTIDYL-TRNA HYDROLASE (PTH) (STAGE V SPORULATION PROTEIN C) >gi_2127242_pir_S66083 stage V sporulation protein - *Bacillus subtilis* >gi_467442_dbj_BAA05288_ (D26185) stage V sporulation [*Bacillus subtilis*] >gi_2632320_emb_CAB11829_ (Z99104) thermosensitive mutant blocks spore coat formation (stage V sporulation) [*Bacillus subtilis*]

Seq. No. 4589
 Contig ID 3787_1.R1040
 5'-most EST LIB3028-026-Q1-B1-A11

Seq. No. 4590
 Contig ID 3789_1.R1040
 5'-most EST jex700908228.h1
 Method BLASTX
 NCBI GI g3256770
 BLAST score 306
 E value 3.0e-27
 Match length 314
 % identity 31
 NCBI Description (AP000002) 318aa long hypothetical UDP-glucose 4-epimerase [*Pyrococcus horikoshii*]

Seq. No. 4591
 Contig ID 3789_3.R1040
 5'-most EST trc700567883.h1

Seq. No. 4592
 Contig ID 3789_4.R1040
 5'-most EST ncj700987768.h1

Seq. No. 4593
 Contig ID 3789_6.R1040
 5'-most EST uC-gmronoir031f04b1

Seq. No. 4594
 Contig ID 3794_1.R1040
 5'-most EST LIB3028-025-Q1-B1-H11
 Method BLASTX
 NCBI GI g3461817
 BLAST score 287
 E value 7.0e-26
 Match length 66
 % identity 80
 NCBI Description (AC004138) unknown protein [*Arabidopsis thaliana*]

Seq. No. 4595
 Contig ID 3795_1.R1040
 5'-most EST uC-gmflminsoy057d10b1

Method BLASTN
 NCBI GI g556421
 BLAST score 45
 E value 1.0e-15
 Match length 247
 % identity 89
 NCBI Description Stylosanthes humilis cinnamyl alcohol dehydrogenase (CAD1) mRNA, complete cds

Seq. No. 4596
 Contig ID 3795_2.R1040
 5'-most EST LIB3028-025-Q1-B1-F5
 Method BLASTX
 NCBI GI g4056499
 BLAST score 149
 E value 2.0e-09
 Match length 44
 % identity 66
 NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 4597
 Contig ID 3798_1.R1040
 5'-most EST ncj700983420.h1

Seq. No. 4598
 Contig ID 3798_2.R1040
 5'-most EST ncj700978215.h1

Seq. No. 4599
 Contig ID 3803_1.R1040
 5'-most EST hyd700726639.h1
 Method BLASTX
 NCBI GI g4539383
 BLAST score 535
 E value 1.0e-54
 Match length 189
 % identity 54
 NCBI Description (AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No. 4600
 Contig ID 3806_1.R1040
 5'-most EST leu701153143.h1
 Method BLASTX
 NCBI GI g4115377
 BLAST score 664
 E value 2.0e-72
 Match length 292
 % identity 45
 NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 4601
 Contig ID 3806_2.R1040
 5'-most EST jC-gmst02400046c12d1

Seq. No. 4602
 Contig ID 3808_1.R1040

5'-most EST zzp700831734.h1
 Method BLASTX
 NCBI GI g3341697
 BLAST score 290
 E value 3.0e-53
 Match length 143
 % identity 77
 NCBI Description (AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No. 4603
 Contig ID 3809_1.R1040
 5'-most EST eep700867020.h1
 Method BLASTX
 NCBI GI g3386597
 BLAST score 222
 E value 7.0e-18
 Match length 77
 % identity 61
 NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
 >gi_3702347 (AC005397) putative permease [Arabidopsis thaliana]

Seq. No. 4604
 Contig ID 3809_2.R1040
 5'-most EST xpa700793883.h1

Seq. No. 4605
 Contig ID 3810_1.R1040
 5'-most EST pxt700946473.h1
 Method BLASTX
 NCBI GI g3461835
 BLAST score 1325
 E value 1.0e-146
 Match length 408
 % identity 64
 NCBI Description (AC005315) putative protein kinase [Arabidopsis thaliana]
 >gi_3927840 (AC005727) putative protein kinase [Arabidopsis thaliana]

Seq. No. 4606
 Contig ID 3810_3.R1040
 5'-most EST taw700657682.h1

Seq. No. 4607
 Contig ID 3812_1.R1040
 5'-most EST sat701013536.h1
 Method BLASTX
 NCBI GI g3123515
 BLAST score 713
 E value 3.0e-75
 Match length 146
 % identity 92
 NCBI Description (Y08761) Mago Nashi-like protein [Euphorbia lagascae]

Seq. No. 4608
 Contig ID 3812_2.R1040
 5'-most EST ncj700977319.h1

E value 8.0e-39
 Match length 140
 % identity 65
 NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 4620
 Contig ID 3824_1.R1040
 5'-most EST kl1701205335.h1
 Method BLASTN
 NCBI GI g287561
 BLAST score 181
 E value 3.0e-97
 Match length 325
 % identity 89
 NCBI Description Vigna radiata auxin-regulated mRNA

Seq. No. 4621
 Contig ID 3826_1.R1040
 5'-most EST uC-gmropic036b10b1
 Method BLASTX
 NCBI GI g3395432
 BLAST score 1841
 E value 0.0e+00
 Match length 450
 % identity 76
 NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 4622
 Contig ID 3826_2.R1040
 5'-most EST 2DC-01-Q1-E1-E1
 Method BLASTX
 NCBI GI g3915826
 BLAST score 1124
 E value 1.0e-123
 Match length 294
 % identity 72
 NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 4623
 Contig ID 3826_3.R1040
 5'-most EST fC-gmse700654972d1
 Method BLASTX
 NCBI GI g3395432
 BLAST score 278
 E value 1.0e-24
 Match length 65
 % identity 77
 NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 4624
 Contig ID 3826_4.R1040
 5'-most EST jC-gmst02400017g01d1
 Method BLASTX
 NCBI GI g3914771
 BLAST score 422
 E value 2.0e-41
 Match length 101

% identity 78
NCBI Description 60S RIBOSOMAL PROTEIN L5 >gi_1881380_dbj_BAA19415_ (AB001583) ribosomal protein L5 [Solanum melongena]

Seq. No. 4625
Contig ID 3826_5.R1040
5'-most EST g5753460
Method BLASTX
NCBI GI g3915826
BLAST score 575
E value 3.0e-59
Match length 140
% identity 74
NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 4626
Contig ID 3826_6.R1040
5'-most EST LIB3094-047-Q1-K1-D3
Method BLASTX
NCBI GI g3915826
BLAST score 534
E value 1.0e-54
Match length 121
% identity 82
NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 4627
Contig ID 3826_8.R1040
5'-most EST uC-gmrominsoyl21e11b1
Method BLASTN
NCBI GI g1183936
BLAST score 64
E value 2.0e-27
Match length 119
% identity 89
NCBI Description P.sativum 5S rRNA gene

Seq. No. 4628
Contig ID 3826_12.R1040
5'-most EST awf700841854.h1
Method BLASTX
NCBI GI g3914771
BLAST score 185
E value 1.0e-13
Match length 42
% identity 86
NCBI Description 60S RIBOSOMAL PROTEIN L5 >gi_1881380_dbj_BAA19415_ (AB001583) ribosomal protein L5 [Solanum melongena]

Seq. No. 4629
Contig ID 3826_13.R1040
5'-most EST jex700908485.h1
Method BLASTX
NCBI GI g3395432
BLAST score 332
E value 7.0e-31
Match length 106

Match length 361
 % identity 84
 NCBI Description Cicer arietinum mRNA for plantacyanin

Seq. No. 4637
 Contig ID 3844 1.R1040
 5'-most EST LIB3170-079-Q1-K1-C7
 Method BLASTX
 NCBI GI g4220461
 BLAST score 147
 E value 3.0e-09
 Match length 73
 % identity 45
 NCBI Description (AC006216) ESTs gb_T75642 and gb_AA650997 come from this gene. [Arabidopsis thaliana]

Seq. No. 4638
 Contig ID 3845 1.R1040
 5'-most EST LIB3170-023-Q1-K1-F9

Seq. No. 4639
 Contig ID 3845 2.R1040
 5'-most EST LIB3039-032-Q1-E1-F2

Seq. No. 4640
 Contig ID 3846 1.R1040
 5'-most EST 6HA-02-Q1-E1-A7

Seq. No. 4641
 Contig ID 3848 1.R1040
 5'-most EST LIB3050-024-Q1-K1-C6
 Method BLASTX
 NCBI GI g2500341
 BLAST score 165
 E value 5.0e-11
 Match length 38
 % identity 74
 NCBI Description 50S RIBOSOMAL PROTEIN L36 >gi_1652406_dbj_BAA17328_ (D90905) 50S ribosomal protein L36 [Synechocystis sp.]

Seq. No. 4642
 Contig ID 3849 1.R1040
 5'-most EST kmv700740822.h1

Seq. No. 4643
 Contig ID 3854 1.R1040
 5'-most EST uC-gmrominsoy241g01b1

Seq. No. 4644
 Contig ID 3854 2.R1040
 5'-most EST LIB3052-002-Q1-B1-C2
 Method BLASTX
 NCBI GI g4572675
 BLAST score 203
 E value 1.0e-15
 Match length 146
 % identity 42

NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]

Seq. No. 4645
Contig ID 3854_3.R1040
5'-most EST LIB3053-003-Q1-N1-D3

Seq. No. 4646
Contig ID 3855_1.R1040
5'-most EST zhf700956406.h1
Method BLASTX
NCBI GI g3776581
BLAST score 368
E value 5.0e-35
Match length 84
% identity 75
NCBI Description (AC005388) Similar to Beta integral membrane protein homolog gb_U43629 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 4647
Contig ID 3855_2.R1040
5'-most EST LIB3028-025-Q1-B1-B5
Method BLASTX
NCBI GI g3776581
BLAST score 187
E value 5.0e-14
Match length 46
% identity 74
NCBI Description (AC005388) Similar to Beta integral membrane protein homolog gb_U43629 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 4648
Contig ID 3857_1.R1040
5'-most EST uC-gmflminsoy002b11b1

Seq. No. 4649
Contig ID 3857_2.R1040
5'-most EST zhf700963527.h1

Seq. No. 4650
Contig ID 3858_1.R1040
5'-most EST uC-gmropic039f10b1
Method BLASTX
NCBI GI g2809262
BLAST score 698
E value 3.0e-73
Match length 349
% identity 44
NCBI Description (AC002560) F21B7.31 [Arabidopsis thaliana]

Seq. No. 4651
Contig ID 3858_2.R1040
5'-most EST LIB3170-053-Q1-K1-F9
Method BLASTX
NCBI GI g3201632
BLAST score 218
E value 9.0e-28
Match length 150


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% identity      79
NCBI Description (AF062915) putative transcription factor [Arabidopsis
thaliana]

Seq. No.        4661
Contig ID       3868_1.R1040
5'-most EST     seb700653512.h1
Method          BLASTX
NCBI GI         g2842486
BLAST score     357
E value         1.0e-33
Match length    131
% identity      58
NCBI Description (AL021749) putative protein [Arabidopsis thaliana]

Seq. No.        4662
Contig ID       3868_2.R1040
5'-most EST     g4293429

Seq. No.        4663
Contig ID       3868_3.R1040
5'-most EST     uC-gmronoir064a11b1

Seq. No.        4664
Contig ID       3872_1.R1040
5'-most EST     jex700909729.h1
Method          BLASTX
NCBI GI         g1171161
BLAST score     654
E value         1.0e-68
Match length    175
% identity      69
NCBI Description (U41472) pectate lyase homolog [Medicago sativa]

Seq. No.        4665
Contig ID       3876_1.R1040
5'-most EST     jex700904814.h1
Method          BLASTX
NCBI GI         g1171579
BLAST score     1857
E value         0.0e+00
Match length    478
% identity      73
NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum]

Seq. No.        4666
Contig ID       3879_1.R1040
5'-most EST     jex700905393.h1
Method          BLASTX
NCBI GI         g2895576
BLAST score     557
E value         1.0e-56
Match length    433
% identity      29
NCBI Description (AF041337) vacuolar proton pump subunit SFD beta isoform
[Bos taurus]

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Seq. No. 4676
Contig ID 3900_2.R1040
5'-most EST LIB3028-021-Q1-B1-G11

Seq. No. 4677
Contig ID 3900_3.R1040
5'-most EST gsv701045626.h1

Seq. No. 4678
Contig ID 3902_1.R1040
5'-most EST LIB3028-024-Q1-B1-D12
Method BLASTX
NCBI GI g2960120
BLAST score 563
E value 1.0e-57
Match length 248
% identity 47
NCBI Description (AL022121) glpK [Mycobacterium tuberculosis]

Seq. No. 4679
Contig ID 3904_1.R1040
5'-most EST gsv701051707.h1
Method BLASTX
NCBI GI g2688828
BLAST score 290
E value 5.0e-26
Match length 121
% identity 50
NCBI Description (U97530) ethylene-forming-enzyme-like dioxygenase [Prunus armeniaca]

Seq. No. 4680
Contig ID 3906_1.R1040
5'-most EST LIB3073-006-Q1-K1-E7
Method BLASTN
NCBI GI g2982267
BLAST score 150
E value 2.0e-78
Match length 422
% identity 84
NCBI Description Picea mariana probable 40S ribosomal protein S15 (Sb23) mRNA, complete cds

Seq. No. 4681
Contig ID 3906_2.R1040
5'-most EST LIB3093-027-Q1-K1-B3
Method BLASTN
NCBI GI g2982267
BLAST score 178
E value 4.0e-95
Match length 422
% identity 86
NCBI Description Picea mariana probable 40S ribosomal protein S15 (Sb23) mRNA, complete cds

Seq. No. 4682

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
HELICASE >gi_1402875_emb_CAA66825_ (X98130) RNA helicase
[Arabidopsis thaliana] >gi_1495271_emb_CAA66613_ (X97970)
RNA helicase [Arabidopsis thaliana]

Seq. No. 4687
Contig ID 3916_1.R1040
5'-most EST jC-gmro02800031h12d1

Seq. No. 4688
Contig ID 3917_1.R1040
5'-most EST LIB3028-024-Q1-B1-B3
Method BLASTX
NCBI GI g4056495
BLAST score 176
E value 1.0e-12
Match length 88
% identity 51
NCBI Description (AC005896) putative TKRP125 [Arabidopsis thaliana]

Seq. No. 4689
Contig ID 3918_1.R1040
5'-most EST LIB3028-024-Q1-B1-B4
Method BLASTX
NCBI GI g2829910
BLAST score 1025
E value 1.0e-112
Match length 295
% identity 40
NCBI Description (AC002291) Unknown protein, contains regulator of
chromosome condensation motifs [Arabidopsis thaliana]

Seq. No. 4690
Contig ID 3921_1.R1040
5'-most EST zzp700833785.h1
Method BLASTX
NCBI GI g3881976
BLAST score 530
E value 5.0e-54
Match length 155
% identity 63
NCBI Description (AJ012409) hypothetical protein [Homo sapiens]

Seq. No. 4691
Contig ID 3922_1.R1040
5'-most EST LIB3049-042-Q1-E1-H3
Method BLASTX
NCBI GI g1353516
BLAST score 2150
E value 0.0e+00
Match length 501
% identity 81
NCBI Description (U38651) sugar transporter [Medicago truncatula]

Seq. No. 4692
Contig ID 3922_2.R1040
5'-most EST g4282909

Method BLASTN
 NCBI GI g169717
 BLAST score 54
 E value 2.0e-21
 Match length 110
 % identity 87
 NCBI Description Ricinus communis (clone PST293) sugar carrier protein (RCSTC) mRNA, complete CDS

Seq. No. 4693
 Contig ID 3922_3.R1040
 5'-most EST uC-gmrominsoy258d01b1
 Method BLASTX
 NCBI GI g3915039
 BLAST score 270
 E value 2.0e-23
 Match length 60
 % identity 90
 NCBI Description SUGAR CARRIER PROTEIN C >gi_169718 (L08196) sugar carrier protein [Ricinus communis]

Seq. No. 4694
 Contig ID 3922_4.R1040
 5'-most EST fC-gmse7000755922r1
 Method BLASTX
 NCBI GI g1083942
 BLAST score 651
 E value 6.0e-68
 Match length 254
 % identity 48
 NCBI Description rubber particle cytochrome P450 - guayule >gi_791093_emb_CAA55025_ (X78166) rubber particle protein [Parthenium argentatum]

Seq. No. 4695
 Contig ID 3922_5.R1040
 5'-most EST uC-gmrominsoy140g06b1
 Method BLASTX
 NCBI GI g1353516
 BLAST score 431
 E value 2.0e-42
 Match length 120
 % identity 72
 NCBI Description (U38651) sugar transporter [Medicago truncatula]

Seq. No. 4696
 Contig ID 3922_6.R1040
 5'-most EST zhf700959335.h1

Seq. No. 4697
 Contig ID 3922_8.R1040
 5'-most EST uC-gmronoir024d11b1
 Method BLASTN
 NCBI GI g1353515
 BLAST score 63
 E value 5.0e-27
 Match length 123

NCBI Description amino acid permease AAP3 - Arabidopsis thaliana

Seq. No. 4705
Contig ID 3937_1.R1040
5'-most EST hyd700730315.h1
Method BLASTN
NCBI GI g20872
BLAST score 217
E value 1.0e-118
Match length 525
% identity 85
NCBI Description Pea mRNA for plastid ribosomal protein CL24

Seq. No. 4706
Contig ID 3940_1.R1040
5'-most EST LIB3170-042-Q1-K1-A6
Method BLASTX
NCBI GI g285741
BLAST score 1512
E value 1.0e-168
Match length 422
% identity 70
NCBI Description (D14550) EDGP precursor [Daucus carota]

Seq. No. 4707
Contig ID 3941_1.R1040
5'-most EST fua701042582.h1
Method BLASTN
NCBI GI g1620908
BLAST score 239
E value 1.0e-131
Match length 523
% identity 86
NCBI Description Carrot mRNA for DcARF1, complete cds

Seq. No. 4708
Contig ID 3941_2.R1040
5'-most EST LIB3109-035-Q1-K1-D6
Method BLASTN
NCBI GI g1620908
BLAST score 235
E value 1.0e-129
Match length 531
% identity 86
NCBI Description Carrot mRNA for DcARF1, complete cds

Seq. No. 4709
Contig ID 3941_3.R1040
5'-most EST LIB3106-060-Q1-K1-G9
Method BLASTX
NCBI GI g2281102
BLAST score 213
E value 1.0e-16
Match length 93
% identity 71
NCBI Description (AC002333) SF16 isolog [Arabidopsis thaliana]

5'-most EST LIB3087-012-Q1-K1-A5
 Method BLASTN
 NCBI GI g1184986
 BLAST score 76
 E value 2.0e-34
 Match length 160
 % identity 87
 NCBI Description Nicotiana tabacum GTP-binding protein NTGB1 mRNA, partial cds

Seq. No. 4717
 Contig ID 3942_1.R1040
 5'-most EST LIB3040-008-Q1-E1-G9
 Method BLASTN
 NCBI GI g170919
 BLAST score 122
 E value 8.0e-62
 Match length 322
 % identity 85
 NCBI Description C.maltosa ribosomal protein L41 (LEL41) gene, complete cds

Seq. No. 4718
 Contig ID 3943_1.R1040
 5'-most EST pmv700895034.h1

Seq. No. 4719
 Contig ID 3944_1.R1040
 5'-most EST pmv700893947.h1
 Method BLASTX
 NCBI GI g3894194
 BLAST score 479
 E value 7.0e-48
 Match length 158
 % identity 56
 NCBI Description (AC005662) putative strictosidine synthase [Arabidopsis thaliana]

Seq. No. 4720
 Contig ID 3945_1.R1040
 5'-most EST LIB3039-042-Q1-E1-C11

Seq. No. 4721
 Contig ID 3945_2.R1040
 5'-most EST smc700747713.h1

Seq. No. 4722
 Contig ID 3946_1.R1040
 5'-most EST LIB3049-002-Q1-E1-D7
 Method BLASTX
 NCBI GI g3283893
 BLAST score 143
 E value 8.0e-12
 Match length 87
 % identity 43
 NCBI Description (AF070626) unknown [Homo sapiens]

Seq. No. 4723

NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
(PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
>gi_1438075 (L33686) phospholipase D [Ricinus communis]

Seq. No. 4730
Contig ID 3951_2.R1040
5'-most EST LIB3051-105-Q1-K1-G10
Method BLASTX
NCBI GI g3914359
BLAST score 1877
E value 0.0e+00
Match length 382
% identity 90

NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
(PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
>gi_1928979 (U92656) phospholipase D [Vigna unguiculata]

Seq. No. 4731
Contig ID 3952_1.R1040
5'-most EST asn701138149.hl
Method BLASTX
NCBI GI g3024706
BLAST score 280
E value 2.0e-24
Match length 94
% identity 60

NCBI Description TRANSCRIPTION INITIATION FACTOR TFIID 18 KD SUBUNIT
(TAFII-18) (TAFII18) >gi_1362894_pir_S54782 PolII
transcription factor TFIID chain hTAFII18 - human
>gi_791053_emb CAA58827_ (X84003) PolII transcription
factor TFIID [Homo sapiens]

Seq. No. 4732
Contig ID 3952_2.R1040
5'-most EST LIB3051-034-Q1-K1-C10

Seq. No. 4733
Contig ID 3952_3.R1040
5'-most EST LIB3028-023-Q1-B1-G5

Seq. No. 4734
Contig ID 3953_1.R1040
5'-most EST LIB3028-023-Q1-B1-G6

Seq. No. 4735
Contig ID 3956_1.R1040
5'-most EST zhf700956881.hl
Method BLASTX
NCBI GI g2494299
BLAST score 1032
E value 1.0e-112
Match length 269
% identity 76

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT
(EIF-2-BETA) >gi_1732361 (U80269) translation initiation
factor 2 beta [Malus domestica]

Seq. No. 4736
 Contig ID 3957_1.R1040
 5'-most EST LIB3139-055-P1-N1-E11
 Method BLASTN
 NCBI GI g408793
 BLAST score 698
 E value 0.0e+00
 Match length 801
 % identity 98
 NCBI Description Glycine soja chloroplast 3-omega fatty acid desaturase (Fad3) mRNA, complete cds

Seq. No. 4737
 Contig ID 3957_2.R1040
 5'-most EST uC-gmflminsoy036a11b1
 Method BLASTN
 NCBI GI g408793
 BLAST score 235
 E value 1.0e-129
 Match length 635
 % identity 92
 NCBI Description Glycine soja chloroplast 3-omega fatty acid desaturase (Fad3) mRNA, complete cds

Seq. No. 4738
 Contig ID 3958_1.R1040
 5'-most EST LIB3028-023-Q1-B1-D4

Seq. No. 4739
 Contig ID 3961_1.R1040
 5'-most EST zsg701120931.h1
 Method BLASTX
 NCBI GI g3184061
 BLAST score 340
 E value 1.0e-31
 Match length 177
 % identity 44
 NCBI Description (AL023776) atp dependent helicase [Schizosaccharomyces pombe]

Seq. No. 4740
 Contig ID 3962_1.R1040
 5'-most EST LIB3049-025-Q1-E1-H8

Seq. No. 4741
 Contig ID 3964_1.R1040
 5'-most EST jC-gmst02400020dg12d1

Seq. No. 4742
 Contig ID 3968_1.R1040
 5'-most EST LIB3028-023-Q1-B1-E4

Seq. No. 4743
 Contig ID 3970_1.R1040
 5'-most EST jC-gmro02800029h10a1
 Method BLASTX
 NCBI GI g3329368

Method BLASTX
 NCBI GI g4406772
 BLAST score 306
 E value 2.0e-27
 Match length 119
 % identity 55
 NCBI Description (AC006836) putative nitrilase-associated protein
 [Arabidopsis thaliana]

Seq. No. 4751
 Contig ID 3983_2.R1040
 5'-most EST sat701003125.h1
 Method BLASTX
 NCBI GI g2765837
 BLAST score 279
 E value 2.0e-24
 Match length 131
 % identity 50
 NCBI Description (Z96936) NAP16kDa protein [Arabidopsis thaliana]

Seq. No. 4752
 Contig ID 3983_3.R1040
 5'-most EST jC-gmro02910061a08a1

Seq. No. 4753
 Contig ID 3983_4.R1040
 5'-most EST LIB3053-006-Q1-N1-A8
 Method BLASTX
 NCBI GI g2765837
 BLAST score 208
 E value 4.0e-16
 Match length 102
 % identity 49
 NCBI Description (Z96936) NAP16kDa protein [Arabidopsis thaliana]

Seq. No. 4754
 Contig ID 3987_1.R1040
 5'-most EST pmv700894858.h1
 Method BLASTX
 NCBI GI g3860246
 BLAST score 172
 E value 1.0e-11
 Match length 153
 % identity 36
 NCBI Description (AC005824) putative reverse-transcriptase protein
 [Arabidopsis thaliana] >gi_4510429_gb_AAD21515.1_
 (AC006929) putative reverse transcriptase [Arabidopsis
 thaliana]

Seq. No. 4755
 Contig ID 3988_1.R1040
 5'-most EST ssr700556516.h1
 Method BLASTX
 NCBI GI g2245012
 BLAST score 172
 E value 4.0e-21
 Match length 91

% identity 58
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 4756
Contig ID 3990_1.R1040
5'-most EST uC-gmropic018e11b1
Method BLASTX
NCBI GI g4107276
BLAST score 1010
E value 1.0e-137
Match length 271
% identity 85
NCBI Description (X98506) acetyl-CoA synthetase [Solanum tuberosum]

Seq. No. 4757
Contig ID 3991_1.R1040
5'-most EST g4287582
Method BLASTX
NCBI GI g4335745
BLAST score 387
E value 4.0e-37
Match length 192
% identity 42
NCBI Description (AC006284) putative hydrolase (contains an
esterase/lipase/thioesterase active site serine domain
(prosite: PS50187) [Arabidopsis thaliana]

Seq. No. 4758
Contig ID 3992_1.R1040
5'-most EST uC-gmrominsoy216h02b1
Method BLASTX
NCBI GI g2196466
BLAST score 256
E value 2.0e-21
Match length 267
% identity 44
NCBI Description (Y13673) TATA binding protein-associated factor
[Arabidopsis thaliana]

Seq. No. 4759
Contig ID 3993_1.R1040
5'-most EST LIB3028-023-Q1-B1-A2
Method BLASTX
NCBI GI g3510248
BLAST score 200
E value 2.0e-15
Match length 94
% identity 50
NCBI Description (AC005310) hypothetical protein [Arabidopsis thaliana]

Seq. No. 4760
Contig ID 4001_1.R1040
5'-most EST txt700732386.h1
Method BLASTX
NCBI GI g2911044
BLAST score 461
E value 1.0e-46

Match length	225
% identity	49
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]
Seq. No.	4761
Contig ID	4001_2.R1040
5'-most EST	LIB3170-074-Q1-J1-A6
Seq. No.	4762
Contig ID	4007_1.R1040
5'-most EST	LIB3028-022-Q1-B1-G10
Method	BLASTX
NCBI GI	g3924611
BLAST score	584
E value	1.0e-70
Match length	207
% identity	67
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana]
Seq. No.	4763
Contig ID	4011_1.R1040
5'-most EST	LIB3073-024-Q1-K1-F6
Method	BLASTN
NCBI GI	g166421
BLAST score	163
E value	3.0e-86
Match length	459
% identity	84
NCBI Description	Medicago sativa ubiquitin carrier protein mRNA, complete cds
Seq. No.	4764
Contig ID	4011_2.R1040
5'-most EST	uC-gmronoir062f10b1
Method	BLASTN
NCBI GI	g166421
BLAST score	171
E value	6.0e-91
Match length	459
% identity	84
NCBI Description	Medicago sativa ubiquitin carrier protein mRNA, complete cds
Seq. No.	4765
Contig ID	4011_3.R1040
5'-most EST	xpa700794105.h1
Method	BLASTN
NCBI GI	g166923
BLAST score	78
E value	9.0e-36
Match length	234
% identity	84
NCBI Description	Arabidopsis thaliana ubiquitin carrier protein (UBC1) mRNA, complete cds
Seq. No.	4766
Contig ID	4011_6.R1040

NCBI Description (AC002292) putative polygalacturonase [Arabidopsis thaliana]

Seq. No. 4777
Contig ID 4028_1.R1040
5'-most EST jex700908404.h1
Method BLASTX
NCBI GI g4218120
BLAST score 283
E value 4.0e-25
Match length 90
% identity 64

NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No. 4778
Contig ID 4028_2.R1040
5'-most EST LIB3030-004-Q1-B1-G8
Method BLASTX
NCBI GI g4218120
BLAST score 444
E value 4.0e-44
Match length 109
% identity 78

NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No. 4779
Contig ID 4031_1.R1040
5'-most EST wrg700788672.h1
Method BLASTX
NCBI GI g3702327
BLAST score 576
E value 3.0e-59
Match length 162
% identity 75

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 4780
Contig ID 4031_3.R1040
5'-most EST LIB3056-010-Q1-N1-H8

Seq. No. 4781
Contig ID 4037_1.R1040
5'-most EST LIB3049-042-Q1-E1-D9
Method BLASTX
NCBI GI g3342800
BLAST score 848
E value 4.0e-91
Match length 211
% identity 78

NCBI Description (AF061837) putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]

Seq. No. 4782
Contig ID 4037_2.R1040
5'-most EST LIB3028-022-Q1-B1-D5

Method BLASTX
 NCBI GI g3342802
 BLAST score 461
 E value 1.0e-45
 Match length 133
 % identity 54
 NCBI Description (AF061838) putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]

Seq. No. 4783
 Contig ID 4037_3.R1040
 5'-most EST fua701038701.h1
 Method BLASTX
 NCBI GI g3342802
 BLAST score 261
 E value 1.0e-22
 Match length 69
 % identity 75
 NCBI Description (AF061838) putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]

Seq. No. 4784
 Contig ID 4037_4.R1040
 5'-most EST uC-gmropic063f06b1
 Method BLASTX
 NCBI GI g2529229
 BLAST score 751
 E value 6.0e-80
 Match length 195
 % identity 74
 NCBI Description (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]

Seq. No. 4785
 Contig ID 4038_1.R1040
 5'-most EST LIB3139-014-P1-N1-E12
 Method BLASTX
 NCBI GI g1431629
 BLAST score 1863
 E value 0.0e+00
 Match length 399
 % identity 85
 NCBI Description (X99348) pectinacetylerase precursor [Vigna radiata]

Seq. No. 4786
 Contig ID 4038_2.R1040
 5'-most EST uC-gmflminsoyl19e06b1
 Method BLASTX
 NCBI GI g1431629
 BLAST score 754
 E value 3.0e-80
 Match length 203
 % identity 67
 NCBI Description (X99348) pectinacetylerase precursor [Vigna radiata]

Seq. No. 4787
 Contig ID 4038_3.R1040
 5'-most EST dpv701102573.h1

NCBI GI g2119933
 BLAST score 602
 E value 2.0e-62
 Match length 125
 % identity 92
 NCBI Description translation initiation factor eIF-4A.11 - common tobacco

Seq. No. 4792
 Contig ID 4040_4.R1040
 5'-most EST jC-gmst02400031b10d1
 Method BLASTX
 NCBI GI g1170508
 BLAST score 424
 E value 1.0e-41
 Match length 92
 % identity 92
 NCBI Description EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8)
 >gi_2119931_pir_S60244 translation initiation factor
 eIF-4A.8, anther-specific - common tobacco
 >gi_475219_emb_CAA55639_ (X79004) translation initiation
 factor (eIF-4A) [Nicotiana tabacum]
 >gi_475221_emb_CAA55640_ (X79005) translation initiation
 factor (eIF-4A) [Nicotiana tabacum]

Seq. No. 4793
 Contig ID 4040_5.R1040
 5'-most EST LIB3107-067-Q1-K1-C4
 Method BLASTX
 NCBI GI g2119933
 BLAST score 456
 E value 2.0e-45
 Match length 94
 % identity 93
 NCBI Description translation initiation factor eIF-4A.11 - common tobacco

Seq. No. 4794
 Contig ID 4046_1.R1040
 5'-most EST k11701206255.h1
 Method BLASTX
 NCBI GI g4406801
 BLAST score 309
 E value 6.0e-29
 Match length 121
 % identity 52
 NCBI Description (AC006304) unknown protein [Arabidopsis thaliana]

Seq. No. 4795
 Contig ID 4047_1.R1040
 5'-most EST crh700851546.h1
 Method BLASTN
 NCBI GI g22635
 BLAST score 349
 E value 0.0e+00
 Match length 617
 % identity 90
 NCBI Description P.vulgaris mRNA for 70 kD heat shock protein

Seq. No. 4796
 Contig ID 4047_2.R1040
 5'-most EST jC-gmf102220069b04d1
 Method BLASTN
 NCBI GI g22635
 BLAST score 73
 E value 7.0e-33
 Match length 160
 % identity 87
 NCBI Description P.vulgaris mRNA for 70 kD heat shock protein

Seq. No. 4797
 Contig ID 4050_1.R1040
 5'-most EST wvk700683438.h1

Seq. No. 4798
 Contig ID 4051_1.R1040
 5'-most EST LIB3028-022-Q1-B1-C6
 Method BLASTX
 NCBI GI g4388728
 BLAST score 173
 E value 1.0e-13
 Match length 84
 % identity 58
 NCBI Description (AC006413) putative grr1-like protein [Arabidopsis thaliana]

Seq. No. 4799
 Contig ID 4053_1.R1040
 5'-most EST LIB3030-003-Q1-B1-E5
 Method BLASTX
 NCBI GI g1199467
 BLAST score 707
 E value 8.0e-75
 Match length 163
 % identity 70
 NCBI Description (D64155) possible aldehyde decarboxylase [Arabidopsis thaliana]

Seq. No. 4800
 Contig ID 4054_1.R1040
 5'-most EST fC-gmle700683850f1
 Method BLASTX
 NCBI GI g2352812
 BLAST score 516
 E value 3.0e-52
 Match length 179
 % identity 56
 NCBI Description (AF008597) desacetoxyvindoline-4-hydroxylase [Catharanthus roseus]

Seq. No. 4801
 Contig ID 4055_1.R1040
 5'-most EST hrw701058906.h1
 Method BLASTN
 NCBI GI g2224732
 BLAST score 109

09684016.101000

Contig ID 4076_2.R1040
 5'-most EST zhf700958459.h1
 Method BLASTX
 NCBI GI g4127456
 BLAST score 222
 E value 5.0e-18
 Match length 87
 % identity 43
 NCBI Description (AJ010818) Cpn21 protein [Arabidopsis thaliana]

Seq. No. 4822
 Contig ID 4077_1.R1040
 5'-most EST fC-gmro700750047a2
 Method BLASTX
 NCBI GI g422337
 BLAST score 154
 E value 6.0e-10
 Match length 55
 % identity 28
 NCBI Description protein disulfide-isomerase homolog precursor - fluke
 (Schistosoma mansoni) >gi_312018_emb_CAA80520_(Z22933)
 protein disulfide isomerase homologue [Schistosoma mansoni]

Seq. No. 4823
 Contig ID 4077_2.R1040
 5'-most EST LIB3106-098-Q1-K1-G1
 Method BLASTX
 NCBI GI g422337
 BLAST score 230
 E value 6.0e-19
 Match length 67
 % identity 34
 NCBI Description protein disulfide-isomerase homolog precursor - fluke
 (Schistosoma mansoni) >gi_312018_emb_CAA80520_(Z22933)
 protein disulfide isomerase homologue [Schistosoma mansoni]

Seq. No. 4824
 Contig ID 4077_3.R1040
 5'-most EST LIB3065-012-Q1-N1-G7

Seq. No. 4825
 Contig ID 4078_1.R1040
 5'-most EST uC-gmropic060a12b1
 Method BLASTX
 NCBI GI g3522961
 BLAST score 1192
 E value 1.0e-154
 Match length 357
 % identity 79
 NCBI Description (AC004411) putative pto kinase [Arabidopsis thaliana]

Seq. No. 4826
 Contig ID 4078_2.R1040
 5'-most EST uC-gmrominsoy153c05b1
 Method BLASTN
 NCBI GI g1216483
 BLAST score 51

BLAST score 279
 E value 9.0e-25
 Match length 107
 % identity 57
 NCBI Description (AC005882) 66284 [Arabidopsis thaliana]

Seq. No. 4853
 Contig ID 4100_2.R1040
 5'-most EST vzy700754417.h1
 Method BLASTX
 NCBI GI g4508079
 BLAST score 258
 E value 2.0e-22
 Match length 96
 % identity 61
 NCBI Description (AC005882) 66284 [Arabidopsis thaliana]

Seq. No. 4854
 Contig ID 4101_1.R1040
 5'-most EST LIB3040-054-Q1-E1-G11
 Method BLASTX
 NCBI GI g541968
 BLAST score 267
 E value 6.0e-23
 Match length 91
 % identity 55
 NCBI Description HMG 1 protein - garden pea >gi_436424_emb_CAA54168_
 (X76774) HMG 1 protein [Pisum sativum]

Seq. No. 4855
 Contig ID 4103_1.R1040
 5'-most EST pmv700891270.h1
 Method BLASTX
 NCBI GI g3128168
 BLAST score 450
 E value 2.0e-44
 Match length 142
 % identity 56
 NCBI Description (AC004521) putative carboxyl-terminal peptidase
 [Arabidopsis thaliana]

Seq. No. 4856
 Contig ID 4103_2.R1040
 5'-most EST LIB3109-034-Q1-K1-F8
 Method BLASTX
 NCBI GI g3128168
 BLAST score 318
 E value 4.0e-29
 Match length 105
 % identity 52
 NCBI Description (AC004521) putative carboxyl-terminal peptidase
 [Arabidopsis thaliana]

Seq. No. 4857
 Contig ID 4104_1.R1040
 5'-most EST LIB3106-076-Q1-K1-G1
 Method BLASTX


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5'-most EST      gsv701050106.h1
Method           BLASTX
NCBI GI          g2342719
BLAST score      355
E value          2.0e-33
Match length     184
% identity       46
NCBI Description (AC002341) SF16 protein isolog [Arabidopsis thaliana]

Seq. No.         4864
Contig ID        4110_2.R1040
5'-most EST      k11701211941.h1
Method           BLASTX
NCBI GI          g2342719
BLAST score      315
E value          1.0e-28
Match length     93
% identity       66
NCBI Description (AC002341) SF16 protein isolog [Arabidopsis thaliana]

Seq. No.         4865
Contig ID        4110_3.R1040
5'-most EST      LIB3093-051-Q1-K1-C12

Seq. No.         4866
Contig ID        4110_4.R1040
5'-most EST      LIB3139-009-P1-N1-A8

Seq. No.         4867
Contig ID        4112_1.R1040
5'-most EST      k11701208153.h1
Method           BLASTX
NCBI GI          g3024022
BLAST score      779
E value          6.0e-83
Match length     159
% identity       91
NCBI Description INITIATION FACTOR 5A-5 (EIF-5A) (EIF-4D)
>gi_2225885_dbj_BAA20879_ (AB004826) eukaryotic initiation
factor 5A5 [Solanum tuberosum]

Seq. No.         4868
Contig ID        4114_2.R1040
5'-most EST      leu701150411.h1

Seq. No.         4869
Contig ID        4116_1.R1040
5'-most EST      uC-gmropic064d12b1
Method           BLASTX
NCBI GI          g3287680
BLAST score      260
E value          3.0e-22
Match length     139
% identity       50
NCBI Description (AC003979) T22J18.4 [Arabidopsis thaliana]

Seq. No.         4870

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Match length 239
 % identity 84
 NCBI Description Arabidopsis thaliana CYT1 protein (cyt1) mRNA, complete cds

Seq. No. 4876
 Contig ID 4121_5.R1040
 5'-most EST vzy700751791.h1
 Method BLASTX
 NCBI GI g4103324
 BLAST score 406
 E value 1.0e-39
 Match length 86
 % identity 94
 NCBI Description (AF022716) GDP-mannose pyrophosphorylase [Solanum tuberosum]

Seq. No. 4877
 Contig ID 4121_6.R1040
 5'-most EST uC-gmrominsoy086a10b1
 Method BLASTX
 NCBI GI g2642159
 BLAST score 261
 E value 1.0e-22
 Match length 55
 % identity 95
 NCBI Description (AC003000) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose pyrophosphorylase [Arabidopsis thaliana] >gi_4151925 (AF108660) CYT1 protein [Arabidopsis thaliana]

Seq. No. 4878
 Contig ID 4121_7.R1040
 5'-most EST zhf700959268.h1
 Method BLASTN
 NCBI GI g2642152
 BLAST score 41
 E value 8.0e-14
 Match length 101
 % identity 85
 NCBI Description Arabidopsis thaliana chromosome II BAC T517 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 4879
 Contig ID 4123_1.R1040
 5'-most EST awf700839701.h1
 Method BLASTX
 NCBI GI g2129758
 BLAST score 641
 E value 8.0e-67
 Match length 151
 % identity 78
 NCBI Description ubiquitin conjugating enzyme E2 protein - Arabidopsis thaliana >gi_992704 (U33757) UBC7 [Arabidopsis thaliana]

Seq. No. 4880
 Contig ID 4123_2.R1040
 5'-most EST LIB3049-041-Q1-E1-G12

Method BLASTX
 NCBI GI g2129758
 BLAST score 174
 E value 3.0e-12
 Match length 34
 % identity 94
 NCBI Description ubiquitin conjugating enzyme E2 protein - Arabidopsis thaliana >gi_992704 (U33757) UBC7 [Arabidopsis thaliana]

Seq. No. 4881
 Contig ID 4123_3.R1040
 5'-most EST gsv701056366.h1
 Method BLASTX
 NCBI GI g2129758
 BLAST score 659
 E value 5.0e-69
 Match length 152
 % identity 80
 NCBI Description ubiquitin conjugating enzyme E2 protein - Arabidopsis thaliana >gi_992704 (U33757) UBC7 [Arabidopsis thaliana]

Seq. No. 4882
 Contig ID 4123_4.R1040
 5'-most EST LIB3139-098-P1-N1-C5
 Method BLASTX
 NCBI GI g2129758
 BLAST score 383
 E value 5.0e-37
 Match length 88
 % identity 78
 NCBI Description ubiquitin conjugating enzyme E2 protein - Arabidopsis thaliana >gi_992704 (U33757) UBC7 [Arabidopsis thaliana]

Seq. No. 4883
 Contig ID 4123_6.R1040
 5'-most EST leu701157761.h1
 Method BLASTX
 NCBI GI g2624417
 BLAST score 174
 E value 1.0e-12
 Match length 47
 % identity 66
 NCBI Description (AJ002959) Ubiquitin carrier protein [Zea mays]

Seq. No. 4884
 Contig ID 4123_8.R1040
 5'-most EST uxk700667391.h1

Seq. No. 4885
 Contig ID 4124_1.R1040
 5'-most EST ncj700981844.h1
 Method BLASTX
 NCBI GI g1040877
 BLAST score 572
 E value 6.0e-59
 Match length 116
 % identity 86

NCBI Description (U30460) expansin S2 precursor [Cucumis sativus]

Seq. No. 4886
Contig ID 4124_2.R1040
5'-most EST jC-gmro02910046c02a1
Method BLASTX
NCBI GI g1040877
BLAST score 464
E value 2.0e-46
Match length 115
% identity 72
NCBI Description (U30460) expansin S2 precursor [Cucumis sativus]

Seq. No. 4887
Contig ID 4125_1.R1040
5'-most EST LIB3028-021-Q1-B1-D12
Method BLASTX
NCBI GI g4218991
BLAST score 217
E value 2.0e-17
Match length 82
% identity 51
NCBI Description (AF098632) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 4888
Contig ID 4125_2.R1040
5'-most EST pmv700889380.h1
Method BLASTX
NCBI GI g4218991
BLAST score 312
E value 2.0e-28
Match length 129
% identity 49
NCBI Description (AF098632) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 4889
Contig ID 4126_1.R1040
5'-most EST LIB3040-003-Q1-E1-E4
Method BLASTN
NCBI GI g407800
BLAST score 60
E value 6.0e-25
Match length 80
% identity 94
NCBI Description G.hirsutum mRNA for ribosomal protein 41, large subunit (RL41)

Seq. No. 4890
Contig ID 4126_2.R1040
5'-most EST LIB3170-013-Q1-J1-F4
Method BLASTN
NCBI GI g407800
BLAST score 60
E value 5.0e-25
Match length 80
% identity 94
NCBI Description G.hirsutum mRNA for ribosomal protein 41, large subunit

(RL41)

Seq. No. 4891
 Contig ID 4130_1.R1040
 5'-most EST LIB3028-020-Q1-B1-H8
 Method BLASTX
 NCBI GI g2098709
 BLAST score 716
 E value 7.0e-76
 Match length 182
 % identity 71
 NCBI Description (U82975) pectinesterase [Citrus sinensis]

Seq. No. 4892
 Contig ID 4133_1.R1040
 5'-most EST LIB3028-021-Q1-B1-A5
 Method BLASTX
 NCBI GI g3242079
 BLAST score 223
 E value 7.0e-18
 Match length 67
 % identity 66
 NCBI Description (AJ006984) proline-rich protein [Capsicum annuum]

Seq. No. 4893
 Contig ID 4133_2.R1040
 5'-most EST ncj700981439.h1
 Method BLASTX
 NCBI GI g3242079
 BLAST score 226
 E value 1.0e-18
 Match length 68
 % identity 65
 NCBI Description (AJ006984) proline-rich protein [Capsicum annuum]

Seq. No. 4894
 Contig ID 4135_1.R1040
 5'-most EST hyd700730983.h1
 Method BLASTX
 NCBI GI g1651904
 BLAST score 172
 E value 5.0e-12
 Match length 93
 % identity 40
 NCBI Description (D90901) hypothetical protein [Synechocystis sp.]

Seq. No. 4895
 Contig ID 4137_1.R1040
 5'-most EST zhf700964788.h1

Seq. No. 4896
 Contig ID 4141_1.R1040
 5'-most EST leu701154311.h1
 Method BLASTN
 NCBI GI g396818
 BLAST score 343
 E value 0.0e+00

09684016.101000

Match length 935
 % identity 86
 NCBI Description P.sativum pspor1 mRNA encoding porin

Seq. No. 4897
 Contig ID 4142_1.R1040
 5'-most EST ncj700981734.h1
 Method BLASTX
 NCBI GI g4006854
 BLAST score 235
 E value 2.0e-19
 Match length 102
 % identity 49
 NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 4898
 Contig ID 4142_2.R1040
 5'-most EST leu701148704.h1

Seq. No. 4899
 Contig ID 4147_1.R1040
 5'-most EST zhf700953783.h1
 Method BLASTX
 NCBI GI g3287691
 BLAST score 483
 E value 4.0e-48
 Match length 252
 % identity 45
 NCBI Description (AC003979) Contains similarity to RING zinc finger protein gb_X95455 from Gallus gallus. [Arabidopsis thaliana]

Seq. No. 4900
 Contig ID 4147_2.R1040
 5'-most EST jC-gmle01810064h11a1
 Method BLASTX
 NCBI GI g3642014
 BLAST score 173
 E value 1.0e-11
 Match length 49
 % identity 61
 NCBI Description (AL031620) similar to Zinc finger, C3HC4 type (RING finger) [Caenorhabditis elegans]

Seq. No. 4901
 Contig ID 4147_3.R1040
 5'-most EST LIB3138-012-Q1-N1-C12

Seq. No. 4902
 Contig ID 4148_1.R1040
 5'-most EST asn701138390.h1
 Method BLASTX
 NCBI GI g3377517
 BLAST score 219
 E value 2.0e-17
 Match length 99
 % identity 41
 NCBI Description (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]

Seq. No.	4903
Contig ID	4149_1.R1040
5'-most EST	leu701146016.h1
Method	BLASTX
NCBI GI	g3184289
BLAST score	334
E value	6.0e-31
Match length	160
% identity	51
NCBI Description	(AC004136) hypothetical protein [Arabidopsis thaliana]
Seq. No.	4904
Contig ID	4152_1.R1040
5'-most EST	txt700732376.h1
Seq. No.	4905
Contig ID	4153_1.R1040
5'-most EST	jC-gmle01810022h01a1
Seq. No.	4906
Contig ID	4154_1.R1040
5'-most EST	LIB3139-093-P1-N1-E3
Method	BLASTX
NCBI GI	g2982303
BLAST score	568
E value	2.0e-58
Match length	204
% identity	58
NCBI Description	(AF051236) hypothetical protein [Picea mariana]
Seq. No.	4907
Contig ID	4154_2.R1040
5'-most EST	dpv701103307.h1
Method	BLASTX
NCBI GI	g2982303
BLAST score	539
E value	3.0e-55
Match length	134
% identity	79
NCBI Description	(AF051236) hypothetical protein [Picea mariana]
Seq. No.	4908
Contig ID	4160_1.R1040
5'-most EST	LIB3087-005-Q1-K1-G5
Method	BLASTX
NCBI GI	g4454026
BLAST score	903
E value	2.0e-97
Match length	323
% identity	60
NCBI Description	(AL035394) phosphatase like protein [Arabidopsis thaliana]
Seq. No.	4909
Contig ID	4160_2.R1040
5'-most EST	uC-gmrominsoy025a07b1
Method	BLASTX

% identity 39
NCBI Description (AJ011400) NADH:ubiquinone oxidoreductase b17.2 subunit [Bos taurus]

Seq. No. 4929
Contig ID 4189_3.R1040
5'-most EST jC-gmfl02220064b02a1
Method BLASTX
NCBI GI g4580395
BLAST score 283
E value 5.0e-25
Match length 88
% identity 64
NCBI Description (AC007171) putative kinesin-related protein [Arabidopsis thaliana]

Seq. No. 4930
Contig ID 4190_1.R1040
5'-most EST vzy700753930.h1
Method BLASTX
NCBI GI g4049354
BLAST score 1999
E value 0.0e+00
Match length 452
% identity 83
NCBI Description (AL034567) glycine hydroxymethyltransferase (EC 2.1.2.1)-like protein [Arabidopsis thaliana]

Seq. No. 4931
Contig ID 4190_2.R1040
5'-most EST LIB3107-056-Q1-K1-H10

Seq. No. 4932
Contig ID 4194_1.R1040
5'-most EST uC-gmflminsoy049d03b1
Method BLASTX
NCBI GI g282994
BLAST score 1032
E value 1.0e-113
Match length 226
% identity 81
NCBI Description Sipl protein - barley >gi_167100 (M77475) seed imbibition protein [Hordeum vulgare]

Seq. No. 4933
Contig ID 4196_1.R1040
5'-most EST LIB3039-047-Q1-E1-A3
Method BLASTX
NCBI GI g4468813
BLAST score 736
E value 7.0e-78
Match length 247
% identity 53
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 4934
Contig ID 4196_2.R1040

5'-most EST fC-gmse7000751282d1

Seq. No. 4935
 Contig ID 4196_3.R1040
 5'-most EST LIB3039-028-Q1-E1-C4
 Method BLASTX
 NCBI GI g4468813
 BLAST score 369
 E value 4.0e-35
 Match length 119
 % identity 55
 NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 4936
 Contig ID 4201_1.R1040
 5'-most EST jC-gmst02400052e06a1

Seq. No. 4937
 Contig ID 4203_1.R1040
 5'-most EST uC-gmflminsoy091g11b1
 Method BLASTX
 NCBI GI g3461821
 BLAST score 522
 E value 2.0e-66
 Match length 267
 % identity 54
 NCBI Description (AC004138) putative nucleoside triphosphatase [Arabidopsis thaliana]

Seq. No. 4938
 Contig ID 4203_3.R1040
 5'-most EST xpa700793151.h1
 Method BLASTX
 NCBI GI g3461821
 BLAST score 576
 E value 2.0e-59
 Match length 173
 % identity 62
 NCBI Description (AC004138) putative nucleoside triphosphatase [Arabidopsis thaliana]

Seq. No. 4939
 Contig ID 4204_1.R1040
 5'-most EST zhf700952486.h1
 Method BLASTX
 NCBI GI g1854581
 BLAST score 886
 E value 2.0e-95
 Match length 276
 % identity 64
 NCBI Description (L24120) peroxidase precursor [Linum usitatissimum]

Seq. No. 4940
 Contig ID 4204_2.R1040
 5'-most EST LIB3106-022-Q1-K1-F10
 Method BLASTX
 NCBI GI g1518388

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BLAST score 163
 E value 3.0e-11
 Match length 65
 % identity 51
 NCBI Description (X91172) korean-radish isoperoxidase [Raphanus sativus]

Seq. No. 4941
 Contig ID 4205_1.R1040
 5'-most EST leu701146640.h1
 Method BLASTX
 NCBI GI g2129605
 BLAST score 932
 E value 1.0e-104
 Match length 210
 % identity 87
 NCBI Description GTP-binding protein 2 - Arabidopsis thaliana
 >gi_2129702_pir_S71585 Rab2 homolog GTP-binding protein
 ATGB2 - Arabidopsis thaliana >gi_1184983 (U46925) ATGB2
 [Arabidopsis thaliana] >gi_3805852_emb_CAA21472_ (AL031986)
 GTP-binding protein GB2 [Arabidopsis thaliana]

Seq. No. 4942
 Contig ID 4207_1.R1040
 5'-most EST leu701149522.h1
 Method BLASTN
 NCBI GI g603218
 BLAST score 504
 E value 0.0e+00
 Match length 884
 % identity 89
 NCBI Description Medicago sativa glucose-6-phosphate dehydrogenase mRNA,
 complete cds

Seq. No. 4943
 Contig ID 4207_2.R1040
 5'-most EST k11701215133.h1
 Method BLASTX
 NCBI GI g3617770
 BLAST score 752
 E value 1.0e-79
 Match length 183
 % identity 80
 NCBI Description (Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 4944
 Contig ID 4207_3.R1040
 5'-most EST jC-gmro02910062c06a1
 Method BLASTN
 NCBI GI g603218
 BLAST score 113
 E value 1.0e-56
 Match length 261
 % identity 86
 NCBI Description Medicago sativa glucose-6-phosphate dehydrogenase mRNA,
 complete cds

Seq. No. 4945

Contig ID 4207 4.R1040
 5'-most EST zsg701128628.h1
 Method BLASTX
 NCBI GI g3617770
 BLAST score 2232
 E value 0.0e+00
 Match length 505
 % identity 80
 NCBI Description (Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 4946
 Contig ID 4207 5.R1040
 5'-most EST LIB3170-061-Q1-K2-F9
 Method BLASTN
 NCBI GI g603218
 BLAST score 56
 E value 1.0e-22
 Match length 116
 % identity 88
 NCBI Description Medicago sativa glucose-6-phosphate dehydrogenase mRNA, complete cds

Seq. No. 4947
 Contig ID 4207 7.R1040
 5'-most EST leu701157358.h1
 Method BLASTN
 NCBI GI g603218
 BLAST score 53
 E value 5.0e-21
 Match length 77
 % identity 92
 NCBI Description Medicago sativa glucose-6-phosphate dehydrogenase mRNA, complete cds

Seq. No. 4948
 Contig ID 4208 1.R1040
 5'-most EST hyd700730986.h1
 Method BLASTX
 NCBI GI g4091806
 BLAST score 331
 E value 6.0e-34
 Match length 92
 % identity 53
 NCBI Description (AF052585) CONSTANS-like protein 2 [Malus domestica]

Seq. No. 4949
 Contig ID 4210 1.R1040
 5'-most EST LIB3049-001-Q1-E1-B5
 Method BLASTX
 NCBI GI g3599968
 BLAST score 1008
 E value 1.0e-110
 Match length 250
 % identity 77
 NCBI Description (AF032123) clp protease [Arabidopsis thaliana]

Seq. No. 4950

Contig ID 4212_1.R1040
 5'-most EST LIB3050-016-Q1-E1-C3
 Method BLASTX
 NCBI GI g4572674
 BLAST score 209
 E value 2.0e-16
 Match length 91
 % identity 56
 NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]

Seq. No. 4951
 Contig ID 4212_2.R1040
 5'-most EST LIB3050-015-Q1-E1-B8

Seq. No. 4952
 Contig ID 4214_1.R1040
 5'-most EST jC-gmst02400031f01a1
 Method BLASTX
 NCBI GI g2982465
 BLAST score 200
 E value 5.0e-15
 Match length 209
 % identity 26
 NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

Seq. No. 4953
 Contig ID 4215_1.R1040
 5'-most EST LIB3028-019-Q1-B1-F1
 Method BLASTX
 NCBI GI g4558678
 BLAST score 233
 E value 2.0e-19
 Match length 92
 % identity 47
 NCBI Description (AC006586) unknown protein [Arabidopsis thaliana]

Seq. No. 4954
 Contig ID 4215_2.R1040
 5'-most EST gsf700698478.h1
 Method BLASTX
 NCBI GI g4558678
 BLAST score 141
 E value 9.0e-09
 Match length 74
 % identity 42
 NCBI Description (AC006586) unknown protein [Arabidopsis thaliana]

Seq. No. 4955
 Contig ID 4216_1.R1040
 5'-most EST LIB3028-019-Q1-B1-F10

Seq. No. 4956
 Contig ID 4223_1.R1040
 5'-most EST LIB3028-019-Q1-B1-F8

Seq. No. 4957
 Contig ID 4224_1.R1040

% identity	69
NCBI Description	(AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana]
Seq. No.	4963
Contig ID	4229_2.R1040
5'-most EST	LIB3106-013-Q1-K1-B12
Method	BLASTX
NCBI GI	g2191138
BLAST score	439
E value	2.0e-43
Match length	131
% identity	66
NCBI Description	(AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana]
Seq. No.	4964
Contig ID	4229_3.R1040
5'-most EST	LIB3106-051-Q1-K1-E1
Seq. No.	4965
Contig ID	4230_1.R1040
5'-most EST	leu701146067.h1
Method	BLASTX
NCBI GI	g2702281
BLAST score	1132
E value	1.0e-124
Match length	276
% identity	77
NCBI Description	(AC003033) putative protein disulfide isomerase precursor [Arabidopsis thaliana]
Seq. No.	4966
Contig ID	4234_1.R1040
5'-most EST	fde700877068.h1
Method	BLASTX
NCBI GI	g1651651
BLAST score	241
E value	5.0e-41
Match length	179
% identity	53
NCBI Description	(D90899) prenyltransferase [Synechocystis sp.]
Seq. No.	4967
Contig ID	4234_2.R1040
5'-most EST	LIB3055-013-Q1-N1-E3
Seq. No.	4968
Contig ID	4237_1.R1040
5'-most EST	LIB3056-014-Q1-N1-A11
Method	BLASTX
NCBI GI	g3367534
BLAST score	1798
E value	0.0e+00
Match length	500
% identity	71
NCBI Description	(AC004392) Strong similarity to coatamer alpha subunit

(HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 4969
 Contig ID 4240_1.R1040
 5'-most EST LIB3170-082-Q1-K1-D12
 Method BLASTX
 NCBI GI g4490332
 BLAST score 380
 E value 2.0e-36
 Match length 124
 % identity 54
 NCBI Description (AL035656) putative protein [Arabidopsis thaliana]

Seq. No. 4970
 Contig ID 4240_2.R1040
 5'-most EST LIB3028-019-Q1-B1-D9
 Method BLASTX
 NCBI GI g4490332
 BLAST score 331
 E value 3.0e-37
 Match length 121
 % identity 60
 NCBI Description (AL035656) putative protein [Arabidopsis thaliana]

Seq. No. 4971
 Contig ID 4241_1.R1040
 5'-most EST hyd700730638.h1
 Method BLASTX
 NCBI GI g2257531
 BLAST score 166
 E value 8.0e-11
 Match length 165
 % identity 28
 NCBI Description (AB004537) WEB1 PROTEIN [Schizosaccharomyces pombe]
 >gi_2950507_emb_CAA17835_ (AL022072) web1 homolog; protein
 transport protein; WD-repeat protein [Schizosaccharomyces
 pombe]

Seq. No. 4972
 Contig ID 4241_2.R1040
 5'-most EST LIB3049-015-Q1-E1-G6

Seq. No. 4973
 Contig ID 4241_3.R1040
 5'-most EST leu701155661.h1
 Method BLASTX
 NCBI GI g3845237
 BLAST score 181
 E value 3.0e-13
 Match length 102
 % identity 39
 NCBI Description (AE001407) WEB-1 ortholog, WD40 [Plasmodium falciparum]

Seq. No. 4974
 Contig ID 4244_1.R1040
 5'-most EST LIB3028-019-Q1-B1-E3

0968401 in 36300

Seq. No.	4977
Contig ID	4245_2.R1040
5'-most EST	uxk700671425.h1
Method	BLASTN
NCBI GI	g287810
BLAST score	316
E value	1.0e-177
Match length	558
% identity	91
NCBI Description	M.sativa mRNA for phosphoprotein phosphatase type 2A

Seq. No.	4978
Contig ID	4245_3.R1040
5'-most EST	rlr700900452.h1
Method	BLASTN
NCBI GI	g287810
BLAST score	449
E value	0.0e+00
Match length	705
% identity	91
NCBI Description	M.sativa mRNA for phosphoprotein phosphatase type 2A

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Seq. No.          4979
Contig ID         4245_4.R1040
5'-most EST      LIB3087-012-Q1-K1-F4
Method            BLASTN
NCBI GI           g287810
BLAST score       123
E value           1.0e-62
Match length      221
% identity        90
NCBI Description  M.sativa mRNA for phosphoprotein phosphatase type 2A
```

958

NCBI Description Vigna unguiculata ferritin subunit cowpea2 precursor, mRNA,
nuclear gene encoding chloroplast protein, complete cds

Seq. No. 4986
Contig ID 4253_3.R1040
5'-most EST fde700875371.h1
Method BLASTN
NCBI GI g2970653
BLAST score 37
E value 2.0e-11
Match length 97
% identity 85

NCBI Description Vigna unguiculata ferritin subunit cowpea2 precursor, mRNA,
nuclear gene encoding chloroplast protein, complete cds

Seq. No. 4987
Contig ID 4260_1.R1040
5'-most EST LIB3028-019-Q1-B1-C2
Method BLASTX
NCBI GI g1055130
BLAST score 179
E value 4.0e-13
Match length 85
% identity 44

NCBI Description (U39998) coded for by C. elegans cDNA yk92b11.3; coded for
by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA
yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by
C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA
yk78c2.3

Seq. No. 4988
Contig ID 4269_1.R1040
5'-most EST uC-gmronoir018f07b1

Seq. No. 4989
Contig ID 4269_2.R1040
5'-most EST fde700874154.h1

Seq. No. 4990
Contig ID 4275_1.R1040
5'-most EST sat701003283.h1
Method BLASTX
NCBI GI g2129933
BLAST score 699
E value 9.0e-74
Match length 130
% identity 96

NCBI Description myb-related transcription factor TMH27 - tomato
>gi_1167484_emb_CAA64614_ (X95296) transcription factor
[Lycopersicon esculentum]

Seq. No. 4991
Contig ID 4276_1.R1040
5'-most EST crh700854095.h1

Seq. No. 4992
Contig ID 4278_1.R1040

NCBI GI g2618705
 BLAST score 1273
 E value 1.0e-141
 Match length 308
 % identity 60
 NCBI Description (AC002510) putative ABC transporter, 5' partial
 [Arabidopsis thaliana]

Seq. No. 5015
 Contig ID 4326_1.R1040
 5'-most EST LIB3028-018-Q1-B1-B7
 Method BLASTN
 NCBI GI g3702734
 BLAST score 35
 E value 7.0e-10
 Match length 147
 % identity 86
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 MNB8, complete sequence [Arabidopsis thaliana]

Seq. No. 5016
 Contig ID 4327_1.R1040
 5'-most EST rlr700896704.h1
 Method BLASTX
 NCBI GI g2688824
 BLAST score 410
 E value 9.0e-40
 Match length 124
 % identity 69
 NCBI Description (U93273) putative auxin-repressed protein [Prunus
 armeniaca]

Seq. No. 5017
 Contig ID 4327_2.R1040
 5'-most EST uC-gmrominsoy260b07b1
 Method BLASTX
 NCBI GI g2688824
 BLAST score 168
 E value 1.0e-11
 Match length 40
 % identity 78
 NCBI Description (U93273) putative auxin-repressed protein [Prunus
 armeniaca]

Seq. No. 5018
 Contig ID 4327_3.R1040
 5'-most EST g4305006
 Method BLASTX
 NCBI GI g2688824
 BLAST score 283
 E value 3.0e-31
 Match length 121
 % identity 60
 NCBI Description (U93273) putative auxin-repressed protein [Prunus
 armeniaca]

Seq. No. 5019

BLAST score 37
E value 5.0e-11
Match length 141
% identity 86
NCBI Description Arabidopsis thaliana rpoMt gene

Seq. No. 5025
Contig ID 4335_2.R1040
5'-most EST zhf700953673.h1

Seq. No. 5026
Contig ID 4340_1.R1040
5'-most EST leu701150583.h1
Method BLASTX
NCBI GI g3559805
BLAST score 363
E value 2.0e-34
Match length 79
% identity 80
NCBI Description (AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana]

Seq. No. 5027
Contig ID 4340_2.R1040
5'-most EST zzp700834154.h1

Seq. No. 5028
Contig ID 4346_1.R1040
5'-most EST hrw701059215.h1
Method BLASTX
NCBI GI g1657855
BLAST score 502
E value 2.0e-50
Match length 201
% identity 50
NCBI Description (U73216) cold acclimation protein WCOR413 [Triticum aestivum]

Seq. No. 5029
Contig ID 4346_2.R1040
5'-most EST g5607172

Seq. No. 5030
Contig ID 4346_3.R1040
5'-most EST LIB3170-086-Q1-K1-C7
Method BLASTX
NCBI GI g1657855
BLAST score 221
E value 1.0e-17
Match length 54
% identity 70
NCBI Description (U73216) cold acclimation protein WCOR413 [Triticum aestivum]

Seq. No. 5031
Contig ID 4346_4.R1040
5'-most EST LIB3093-048-Q1-K1-F5

Method BLASTX
 NCBI GI g1657855
 BLAST score 129
 E value 2.0e-20
 Match length 80
 % identity 66
 NCBI Description (U73216) cold acclimation protein WCOR413 [Triticum aestivum]

Seq. No. 5032
 Contig ID 4347_2.R1040
 5'-most EST LIB3028-017-Q1-B1-G7

Seq. No. 5033
 Contig ID 4348_1.R1040
 5'-most EST LIB3049-046-Q1-E1-A3
 Method BLASTN
 NCBI GI g3821292
 BLAST score 65
 E value 7.0e-28
 Match length 196
 % identity 84
 NCBI Description Pisum sativum cDNA fragment generated by DDRT-Alu

Seq. No. 5034
 Contig ID 4351_1.R1040
 5'-most EST LIB3040-059-Q1-E1-E6
 Method BLASTN
 NCBI GI g2565416
 BLAST score 147
 E value 2.0e-76
 Match length 511
 % identity 83
 NCBI Description Onobrychis viciifolia oxygen-evolving enhancer protein 3 precursor, mRNA, complete cds

Seq. No. 5035
 Contig ID 4351_2.R1040
 5'-most EST asn701133531.h2
 Method BLASTN
 NCBI GI g2565416
 BLAST score 42
 E value 2.0e-14
 Match length 126
 % identity 83
 NCBI Description Onobrychis viciifolia oxygen-evolving enhancer protein 3 precursor, mRNA, complete cds

Seq. No. 5036
 Contig ID 4353_1.R1040
 5'-most EST jC-gmle01810044d07d1
 Method BLASTX
 NCBI GI g2262165
 BLAST score 436
 E value 6.0e-43
 Match length 98
 % identity 87

BLAST score 181
 E value 3.0e-13
 Match length 37
 % identity 89
 NCBI Description (U93168) ribosomal protein L12 [Prunus armeniaca]

Seq. No. 5048
 Contig ID 4361_1.R1040
 5'-most EST txt700735883.h1
 Method BLASTN
 NCBI GI g1617035
 BLAST score 250
 E value 1.0e-138
 Match length 385
 % identity 92
 NCBI Description V.unguiculata mRNA for Ted2 protein

Seq. No. 5049
 Contig ID 4363_1.R1040
 5'-most EST rca700997990.h1

Seq. No. 5050
 Contig ID 4368_1.R1040
 5'-most EST sat701007339.h2
 Method BLASTX
 NCBI GI g1724114
 BLAST score 320
 E value 6.0e-29
 Match length 285
 % identity 41
 NCBI Description (U80041) Af10-protein [Avena fatua]

Seq. No. 5051
 Contig ID 4368_2.R1040
 5'-most EST jC-gmfl02220073a05d1

Seq. No. 5052
 Contig ID 4369_1.R1040
 5'-most EST dpv701097973.h1
 Method BLASTX
 NCBI GI g1407705
 BLAST score 533
 E value 1.0e-54
 Match length 150
 % identity 67
 NCBI Description (U60202) lipoxxygenase [Solanum tuberosum]

Seq. No. 5053
 Contig ID 4370_1.R1040
 5'-most EST uC-gmrominsoy029f01b1
 Method BLASTX
 NCBI GI g1899050
 BLAST score 464
 E value 2.0e-46
 Match length 141
 % identity 72
 NCBI Description (U62773) ripening-associated protein [Lycopersicon

esculentum]

Seq. No. 5054
 Contig ID 4370_2.R1040
 5'-most EST LIB3056-012-Q1-N1-B7
 Method BLASTX
 NCBI GI g1899050
 BLAST score 972
 E value 1.0e-105
 Match length 256
 % identity 72
 NCBI Description (U62773) ripening-associated protein [Lycopersicon
 esculentum]

Seq. No. 5055
 Contig ID 4371_1.R1040
 5'-most EST LIB3049-004-Q1-E1-D10

Seq. No. 5056
 Contig ID 4374_1.R1040
 5'-most EST uC-gmropic028a08b1

Seq. No. 5057
 Contig ID 4375_1.R1040
 5'-most EST jC-gmf102220137c08a1
 Method BLASTX
 NCBI GI g99809
 BLAST score 1209
 E value 1.0e-133
 Match length 326
 % identity 71
 NCBI Description gene Bp10 protein - rape >gi_17795_emb_CAA47177_ (X66608)
 Bplo [Brassica napus]

Seq. No. 5058
 Contig ID 4376_1.R1040
 5'-most EST LIB3028-017-Q1-B1-D1
 Method BLASTX
 NCBI GI g2642157
 BLAST score 223
 E value 3.0e-18
 Match length 68
 % identity 57
 NCBI Description (AC003000) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 5059
 Contig ID 4377_1.R1040
 5'-most EST kmv700742027.h1

Seq. No. 5060
 Contig ID 4379_1.R1040
 5'-most EST uC-gmrominsoy208f01b1
 Method BLASTX
 NCBI GI g4455250
 BLAST score 464
 E value 4.0e-46
 Match length 162

% identity 48
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 5061
Contig ID 4379 2.R1040
5'-most EST LIB3051-026-Q1-K1-F4
Method BLASTX
NCBI GI g4455250
BLAST score 394
E value 3.0e-38
Match length 121
% identity 50
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 5062
Contig ID 4385 1.R1040
5'-most EST ssr700559413.h1
Method BLASTN
NCBI GI g433608
BLAST score 268
E value 1.0e-148
Match length 851
% identity 83
NCBI Description R.communis mRNA for enolase

Seq. No. 5063
Contig ID 4385 2.R1040
5'-most EST LIB3028-009-Q1-B1-B2
Method BLASTN
NCBI GI g1041244
BLAST score 41
E value 1.0e-13
Match length 89
% identity 87
NCBI Description A.glutinosa mRNA for enolase

Seq. No. 5064
Contig ID 4385 3.R1040
5'-most EST zsg701118769.h1
Method BLASTX
NCBI GI g2673918
BLAST score 197
E value 6.0e-15
Match length 150
% identity 37
NCBI Description (AC002561) unknwon protein [Arabidopsis thaliana]

Seq. No. 5065
Contig ID 4389 1.R1040
5'-most EST asn701143195.h1
Method BLASTX
NCBI GI g4522008
BLAST score 463
E value 2.0e-46
Match length 149
% identity 59
NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 5066
 Contig ID 4392_1.R1040
 5'-most EST LIB3170-019-Q1-K1-G2
 Method BLASTX
 NCBI GI g3046693
 BLAST score 722
 E value 2.0e-76
 Match length 137
 % identity 92
 NCBI Description (AL022140) receptor like protein (fragment) [Arabidopsis thaliana]

Seq. No. 5067
 Contig ID 4392_2.R1040
 5'-most EST jC-gmle01810006h04a1
 Method BLASTX
 NCBI GI g3046693
 BLAST score 220
 E value 7.0e-18
 Match length 50
 % identity 80
 NCBI Description (AL022140) receptor like protein (fragment) [Arabidopsis thaliana]

Seq. No. 5068
 Contig ID 4392_3.R1040
 5'-most EST LIB3049-019-Q1-E1-A11
 Method BLASTX
 NCBI GI g3046693
 BLAST score 150
 E value 8.0e-10
 Match length 32
 % identity 84
 NCBI Description (AL022140) receptor like protein (fragment) [Arabidopsis thaliana]

Seq. No. 5069
 Contig ID 4396_1.R1040
 5'-most EST LIB3138-033-Q1-N1-D5
 Method BLASTX
 NCBI GI g3360289
 BLAST score 1017
 E value 1.0e-146
 Match length 373
 % identity 67
 NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No. 5070
 Contig ID 4396_2.R1040
 5'-most EST fC-gmle700685276b1
 Method BLASTX
 NCBI GI g3360291
 BLAST score 313
 E value 1.0e-28
 Match length 81

[Bos taurus]

Seq. No. 5075
Contig ID 4398_5.R1040
5'-most EST jC-gmst02400059b04a1
Method BLASTN
NCBI GI g3046855
BLAST score 36
E value 1.0e-10
Match length 96
% identity 84
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
MSL1, complete sequence [Arabidopsis thaliana]

Seq. No. 5076
Contig ID 4400_1.R1040
5'-most EST LIB3028-017-Q1-B1-C12
Method BLASTX
NCBI GI g3885329
BLAST score 458
E value 5.0e-53
Match length 131
% identity 84
NCBI Description (AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No. 5077
Contig ID 4408_1.R1040
5'-most EST jC-gmst02400060g09a1
Method BLASTX
NCBI GI g417256
BLAST score 159
E value 6.0e-10
Match length 164
% identity 32
NCBI Description LIPASE PRECURSOR (TRIACYLGLYCEROL LIPASE)

Seq. No. 5078
Contig ID 4408_3.R1040
5'-most EST ncj700987853.h1

Seq. No. 5079
Contig ID 4410_1.R1040
5'-most EST taw700657037.h1
Method BLASTX
NCBI GI g140739
BLAST score 283
E value 6.0e-25
Match length 169
% identity 36
NCBI Description HYPOTHETICAL 31.0 KD PROTEIN IN RNPB-SOHA INTERGENIC REGION
(ORF 2) >gi_78519_pir_JQ0613 3-hydroxyisobutyrate
dehydrogenase (EC 1.1.1.31) homolog - Escherichia coli
>gi_216632_dbj_BAA14238 (D90212) ORF2 [Escherichia coli]
>gi_606065 (U18997) ORF_f299 [Escherichia coli] >gi_1789513
(AE000394) putative dehydrogenase [Escherichia coli]

Seq. No. 5080

Contig ID 4411 1.R1040
5'-most EST LIB3028-017-Q1-B1-A2

Seq. No. 5081
Contig ID 4413 1.R1040
5'-most EST asn701132849.h1
Method BLASTX
NCBI GI g4567255
BLAST score 512
E value 5.0e-56
Match length 183
% identity 66
NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No. 5082
Contig ID 4413 2.R1040
5'-most EST LIB3106-115-Q1-K1-H2
Method BLASTN
NCBI GI g1177368
BLAST score 86
E value 2.0e-40
Match length 158
% identity 89
NCBI Description Z.mays mRNA for ribosomal protein L39

Seq. No. 5083
Contig ID 4413 3.R1040
5'-most EST jC-gmst02400053c10d1
Method BLASTN
NCBI GI g1177368
BLAST score 86
E value 1.0e-40
Match length 158
% identity 89
NCBI Description Z.mays mRNA for ribosomal protein L39

Seq. No. 5084
Contig ID 4413 5.R1040
5'-most EST g4292679
Method BLASTN
NCBI GI g1177368
BLAST score 67
E value 3.0e-29
Match length 159
% identity 86
NCBI Description Z.mays mRNA for ribosomal protein L39

Seq. No. 5085
Contig ID 4415 1.R1040
5'-most EST LIB3109-048-Q1-K1-C6
Method BLASTX
NCBI GI g1170606
BLAST score 302
E value 7.0e-34
Match length 120
% identity 59
NCBI Description ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE)

Match length 164
 % identity 92
 NCBI Description Alfalfa glucose-regulated endoplasmic reticular protein
 mRNA, complete cds

Seq. No. 5097
 Contig ID 4422_4.R1040
 5'-most EST jC-gmle01810070g05a1
 Method BLASTN
 NCBI GI g166379
 BLAST score 43
 E value 9.0e-15
 Match length 164
 % identity 87
 NCBI Description Alfalfa glucose-regulated endoplasmic reticular protein
 mRNA, complete cds

Seq. No. 5098
 Contig ID 4427_1.R1040
 5'-most EST jC-gmst02400058c09d1
 Method BLASTX
 NCBI GI g4033735
 BLAST score 209
 E value 6.0e-29
 Match length 86
 % identity 65
 NCBI Description (AF054284) spliceosomal protein SAP 155 [Homo sapiens]

Seq. No. 5099
 Contig ID 4433_1.R1040
 5'-most EST LIB3139-071-P1-N1-C7
 Method BLASTX
 NCBI GI g2129473
 BLAST score 282
 E value 1.0e-24
 Match length 145
 % identity 43
 NCBI Description arabinogalactan-like protein - loblolly pine >gi_607774
 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No. 5100
 Contig ID 4433_2.R1040
 5'-most EST jC-gmst02400002c01d1

Seq. No. 5101
 Contig ID 4436_1.R1040
 5'-most EST LIB3028-016-Q1-B1-G9
 Method BLASTX
 NCBI GI g3415113
 BLAST score 300
 E value 1.0e-34
 Match length 133
 % identity 39
 NCBI Description (AF081201) villin 1 [Arabidopsis thaliana]

Seq. No. 5102
 Contig ID 4438_1.R1040

5'-most EST sat701003234.h1
 Method BLASTX
 NCBI GI g401621
 BLAST score 245
 E value 1.0e-20
 Match length 137
 % identity 42
 NCBI Description HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION
 >gi_290561 (L10328) o188 [Escherichia coli] >gi_1790149
 (AE000448) orf, hypothetical protein [Escherichia coli]

Seq. No. 5103
 Contig ID 4440_1.R1040
 5'-most EST LIB3039-021-Q1-E1-E4
 Method BLASTX
 NCBI GI g3650368
 BLAST score 687
 E value 3.0e-72
 Match length 190
 % identity 69
 NCBI Description (AJ011398) profucosidase [Pisum sativum]

Seq. No. 5104
 Contig ID 4442_1.R1040
 5'-most EST zzp700834319.h1

Seq. No. 5105
 Contig ID 4447_1.R1040
 5'-most EST uC-gmropic009a06b1
 Method BLASTX
 NCBI GI g3522950
 BLAST score 354
 E value 2.0e-33
 Match length 115
 % identity 58
 NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No. 5106
 Contig ID 4448_1.R1040
 5'-most EST leu701157807.h1
 Method BLASTX
 NCBI GI g3402282
 BLAST score 442
 E value 1.0e-43
 Match length 155
 % identity 55
 NCBI Description (AJ000997) proline-rich protein [Solanum tuberosum]

Seq. No. 5107
 Contig ID 4450_1.R1040
 5'-most EST g4302030

Seq. No. 5108
 Contig ID 4450_2.R1040
 5'-most EST LIB3107-055-Q1-K1-C11
 Method BLASTN
 NCBI GI g170067

BLAST score 540
 E value 0.0e+00
 Match length 559
 % identity 99
 NCBI Description Soybean (G.max) proline-rich cell wall protein (SbPRP3)
 gene, complete cds

Seq. No. 5109
 Contig ID 4450_3.R1040
 5'-most EST uC-gmrominsoy086e07b1
 Method BLASTX
 NCBI GI g2760330
 BLAST score 541
 E value 3.0e-55
 Match length 139
 % identity 71
 NCBI Description (AC002130) F1N21.15 [Arabidopsis thaliana]

Seq. No. 5110
 Contig ID 4452_1.R1040
 5'-most EST jC-gmle01810061c04a1
 Method BLASTX
 NCBI GI g3292814
 BLAST score 446
 E value 5.0e-44
 Match length 101
 % identity 80
 NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 5111
 Contig ID 4453_1.R1040
 5'-most EST uC-gmrominsoy204h12b1
 Method BLASTX
 NCBI GI g4239845
 BLAST score 695
 E value 7.0e-73
 Match length 336
 % identity 46
 NCBI Description (AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No. 5112
 Contig ID 4453_3.R1040
 5'-most EST fC-gmro700869769f3
 Method BLASTX
 NCBI GI g4239845
 BLAST score 468
 E value 8.0e-47
 Match length 171
 % identity 53
 NCBI Description (AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No. 5113
 Contig ID 4455_1.R1040
 5'-most EST LIB3028-016-Q1-B1-E6
 Method BLASTN
 NCBI GI g4165340
 BLAST score 37

E value	5.0e-11
Match length	170
% identity	86
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	5114
Contig ID	4456_1.R1040
5'-most EST	LIB3039-040-Q1-E1-H1
Method	BLASTX
NCBI GI	g417148
BLAST score	743
E value	9.0e-79
Match length	226
% identity	63
NCBI Description	PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A) (G2-4) >gi_99912_pir_A33654 heat shock protein 26A - soybean >gi_169981 (M20363) Gmhsp26-A [Glycine max]
Seq. No.	5115
Contig ID	4458_1.R1040
5'-most EST	kmv700743063.h1
Method	BLASTX
NCBI GI	g3482967
BLAST score	785
E value	1.0e-83
Match length	185
% identity	75
NCBI Description	(AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.	5116
Contig ID	4459_1.R1040
5'-most EST	LIB3106-087-Q1-K1-D7
Method	BLASTX
NCBI GI	g2498732
BLAST score	603
E value	2.0e-62
Match length	169
% identity	68
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P2 >gi_1362014_pir_S57612 zeta-crystallin homolog - Arabidopsis thaliana >gi_886430_emb_CAA89262_ (Z49268) zeta-crystallin homologue [Arabidopsis thaliana]
Seq. No.	5117
Contig ID	4459_2.R1040
5'-most EST	uC-gmropic010d10b1
Method	BLASTX
NCBI GI	g2498732
BLAST score	1064
E value	1.0e-116
Match length	276
% identity	72
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P2 >gi_1362014_pir_S57612 zeta-crystallin homolog -


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% identity                68
NCBI Description          (U66424) fimbrin-like protein [Arabidopsis thaliana]

Seq. No.                  5123
Contig ID                  4467_1.R1040
5'-most EST                uaw700661776.h1

Seq. No.                  5124
Contig ID                  4467_2.R1040
5'-most EST                uC-gmflminsoy019c05b1

Seq. No.                  5125
Contig ID                  4467_3.R1040
5'-most EST                LIB3107-030-Q1-K1-B2

Seq. No.                  5126
Contig ID                  4467_4.R1040
5'-most EST                hyd700727362.h1

Seq. No.                  5127
Contig ID                  4469_1.R1040
5'-most EST                sat701009455.h1

Seq. No.                  5128
Contig ID                  4471_1.R1040
5'-most EST                LIB3028-016-Q1-B1-C10
Method                     BLASTX
NCBI GI                    g2815897
BLAST score                 177
E value                     9.0e-13
Match length                64
% identity                  59
NCBI Description          (AF043279) protein kinase 1 [Toxoplasma gondii]
                           >gi_4325070_gb_AAD17245_ (AF118099) PITSLRE-like protein
                           kinase [Toxoplasma gondii]

Seq. No.                  5129
Contig ID                  4476_1.R1040
5'-most EST                uC-gmrominsoy093dl2b1
Method                     BLASTX
NCBI GI                    g967125
BLAST score                 2482
E value                     0.0e+00
Match length                487
% identity                  98
NCBI Description          (U08140) calcium dependent protein kinase [Vigna radiata]

Seq. No.                  5130
Contig ID                  4476_2.R1040
5'-most EST                LIB3093-018-Q1-K1-C1
Method                     BLASTN
NCBI GI                    g967124
BLAST score                 465
E value                     0.0e+00
Match length                819
% identity                  90
NCBI Description          Vigna radiata Rwilcz calcium dependent protein kinase

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(CDPK) mRNA, complete cds

Seq. No. 5131
 Contig ID 4476_3.R1040
 5'-most EST LIB3109-010-Q1-K1-B6
 Method BLASTN
 NCBI GI g967124
 BLAST score 101
 E value 2.0e-49
 Match length 137
 % identity 93
 NCBI Description Vigna radiata Rwilcz calcium dependent protein kinase
 (CDPK) mRNA, complete cds

Seq. No. 5132
 Contig ID 4476_4.R1040
 5'-most EST ssr700555278.h1

Seq. No. 5133
 Contig ID 4478_1.R1040
 5'-most EST LIB3029-010-Q1-B1-B10

Seq. No. 5134
 Contig ID 4479_1.R1040
 5'-most EST gsv701049440.h1
 Method BLASTN
 NCBI GI g3204100
 BLAST score 103
 E value 3.0e-50
 Match length 407
 % identity 85
 NCBI Description Cicer arietinum mRNA for hypothetical protein, clone Can107

Seq. No. 5135
 Contig ID 4480_1.R1040
 5'-most EST leu701151508.h1
 Method BLASTX
 NCBI GI g2739279
 BLAST score 302
 E value 2.0e-27
 Match length 110
 % identity 57
 NCBI Description (AJ223177) short chain alcohol dehydrogenase [Nicotiana tabacum] >gi_2791348_emb_CAA11154_ (AJ223178) short chain alcohol dehydrogenase [Nicotiana tabacum]

Seq. No. 5136
 Contig ID 4486_1.R1040
 5'-most EST zzp700832950.h1
 Method BLASTN
 NCBI GI g1556445
 BLAST score 132
 E value 4.0e-68
 Match length 276
 % identity 87
 NCBI Description Hordeum vulgare alpha tubulin (tubA) mRNA, complete cds

Method	BLASTX
NCBI GI	g4204277
BLAST score	274
E value	3.0e-24
Match length	55
% identity	93
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	5149
Contig ID	4500_1.R1040
5'-most EST	jC-gmst02400011g06a1
Seq. No.	5150
Contig ID	4500_2.R1040
5'-most EST	LIB3107-010-Q1-K1-E8
Seq. No.	5151
Contig ID	4500_3.R1040
5'-most EST	vwf700673739.h1
Seq. No.	5152
Contig ID	4504_1.R1040
5'-most EST	uC-gmropic021c06b1
Method	BLASTN
NCBI GI	g1237085
BLAST score	480
E value	0.0e+00
Match length	1016
% identity	87
NCBI Description	P.sativum mRNA for ADP-glucose pyrophosphorylase (agpl1) >gi_1599261_gb_I18906_I18906 Sequence 1 from patent US 5498831 >gi_3972107_gb_AR014653_AR014653 Sequence 1 from patent US
Seq. No.	5153
Contig ID	4504_2.R1040
5'-most EST	rlr700896089.h1
Method	BLASTN
NCBI GI	g1237085
BLAST score	68
E value	9.0e-30
Match length	96
% identity	93
NCBI Description	P.sativum mRNA for ADP-glucose pyrophosphorylase (agpl1) >gi_1599261_gb_I18906_I18906 Sequence 1 from patent US 5498831 >gi_3972107_gb_AR014653_AR014653 Sequence 1 from patent US
Seq. No.	5154
Contig ID	4504_3.R1040
5'-most EST	uaw700663791.h1
Method	BLASTX
NCBI GI	g2625086
BLAST score	333
E value	1.0e-55
Match length	137
% identity	78

5'-most EST	fc-gmro700747787d3
Seq. No.	5170
Contig ID	4516_7.R1040
5'-most EST	LIB3170-033-Q1-K1-D11
Method	BLASTN
NCBI GI	g2832611
BLAST score	59
E value	3.0e-24
Match length	205
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSAII project)
Seq. No.	5171
Contig ID	4516_10.R1040
5'-most EST	LIB3170-033-Q1-J1-D11
Seq. No.	5172
Contig ID	4516_11.R1040
5'-most EST	gsv701056017.h1
Method	BLASTN
NCBI GI	g3790099
BLAST score	79
E value	1.0e-36
Match length	107
% identity	93
NCBI Description	Citrus X paradisi pyrophosphate-dependent phosphofructokinase beta subunit (PPi-PFKb) mRNA, complete cds
Seq. No.	5173
Contig ID	4516_12.R1040
5'-most EST	uC-gmrominsoy271d04b1
Method	BLASTX
NCBI GI	g3790100
BLAST score	278
E value	6.0e-25
Match length	71
% identity	75
NCBI Description	(AF095520) pyrophosphate-dependent phosphofructokinase beta subunit [Citrus X paradisi]
Seq. No.	5174
Contig ID	4518_1.R1040
5'-most EST	kwa701015659.h1
Method	BLASTX
NCBI GI	g4204265
BLAST score	459
E value	2.0e-91
Match length	294
% identity	59
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]
Seq. No.	5175
Contig ID	4520_1.R1040
5'-most EST	leu701147564.h1

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Seq. No. 5181
 Contig ID 4530_5.R1040
 5'-most EST awf700839714.h1
 Method BLASTX
 NCBI GI g4467158
 BLAST score 147
 E value 1.0e-09
 Match length 69
 % identity 49
 NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 5182
 Contig ID 4531_1.R1040
 5'-most EST seb700650590.h1
 Method BLASTX
 NCBI GI g1354849
 BLAST score 501
 E value 1.0e-50
 Match length 154
 % identity 61
 NCBI Description (U57350) epoxide hydrolase [Nicotiana tabacum]

Seq. No. 5183
 Contig ID 4531_3.R1040
 5'-most EST bth700849189.h1
 Method BLASTX
 NCBI GI g1354849
 BLAST score 194
 E value 5.0e-15
 Match length 62
 % identity 61
 NCBI Description (U57350) epoxide hydrolase [Nicotiana tabacum]

Seq. No. 5184
 Contig ID 4533_1.R1040
 5'-most EST wvk700686367.h1
 Method BLASTX
 NCBI GI g4455256
 BLAST score 875
 E value 4.0e-94
 Match length 228
 % identity 71
 NCBI Description (AL035523) protein-methionine-S-oxide reductase [Arabidopsis thaliana]

Seq. No. 5185
 Contig ID 4533_2.R1040
 5'-most EST LIB3170-073-Q1-K1-D2

Seq. No. 5186
 Contig ID 4533_3.R1040
 5'-most EST jC-gmle01810027e12d1
 Method BLASTX
 NCBI GI g1709690
 BLAST score 318
 E value 3.0e-29
 Match length 75

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BLAST score 421
E value 8.0e-41
Match length 228
% identity 46
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 5193
Contig ID 4552_3.R1040
5'-most EST jC-gmro02800034c03a1

Seq. No. 5194
Contig ID 4552_4.R1040
5'-most EST LIB3049-033-Q1-E1-E5

Seq. No. 5195
Contig ID 4552_5.R1040
5'-most EST LIB3139-025-P1-N1-H6

Seq. No. 5196
Contig ID 4554_1.R1040
5'-most EST hyd700728918.h1
Method BLASTN
NCBI GI g2502086
BLAST score 53
E value 1.0e-20
Match length 118
% identity 93
NCBI Description Vigna radiata adenosine triphosphatase mRNA, complete cds

Seq. No. 5197
Contig ID 4554_2.R1040
5'-most EST g5057934
Method BLASTN
NCBI GI g2502086
BLAST score 370
E value 0.0e+00
Match length 552
% identity 93
NCBI Description Vigna radiata adenosine triphosphatase mRNA, complete cds

Seq. No. 5198
Contig ID 4554_3.R1040
5'-most EST eep700868421.h1
Method BLASTN
NCBI GI g2502086
BLAST score 298
E value 1.0e-167
Match length 382
% identity 95
NCBI Description Vigna radiata adenosine triphosphatase mRNA, complete cds

Seq. No. 5199
Contig ID 4554_4.R1040
5'-most EST LIB3170-058-Q1-J1-F2
Method BLASTN
NCBI GI g2502086
BLAST score 180


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Contig ID      4560_2.R1040
5'-most EST   kl1701214579.h1
Method        BLASTX
NCBI GI       g4309734
BLAST score    163
E value       4.0e-11
Match length   63
% identity     51
NCBI Description (AC006439) putative 26S proteasome regulatory subunit 8
               [Arabidopsis thaliana]
```

Seq. No.	5206
Contig ID	4565_1.R1040
5'-most EST	LIB3170-039-01-K2-D5

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Seq. No.          5207
Contig ID         4565_2.R1040
5'-most EST      uC-gmrominsoy164h05b1
Method            BLASTX
NCBI GI           g422029
BLAST score       831
E value           8.0e-90
Match length      239
% identity        73
NCBI Description  transcription factor OBF3.2, ocs element-binding - maize
                  >gi_297018_emb_CAA48904_ (X69152) ocs-element binding
                  factor 3.2 [Zea mays]
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Seq. No.          5208
Contig ID         4565_3.R1040
5'-most EST      jC-gmro02910031a03a1
Method            BLASTX
NCBI GI           g1076782
BLAST score       717
E value           1.0e-75
Match length      277
% identity        57
NCBI Description   transcription factor HBP-1b(c1) - wheat (fragment)
```

Seq. No.	5209
Contig ID	4565_4.R1040
5'-most EST	wrg700787787.h2

Seq. No.	5210
Contig ID	4565_6.R1040
5'-most EST	LIB3051-012-01-E1-E5

```
Seq. No.          5211
Contig ID         4567_1.R1040
5'-most EST      LIB3106-099-Q1-K1-G10
Method            BLASTX
NCBI GI           g2384671
BLAST score       845
E value           2.0e-97
Match length      244
% identity         73
NCBI Description  (AF012657) putative potassium transporter AtKT2p
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Seq. No.          5217
Contig ID         4575_3.R1040
5'-most EST      hrw701058671.h1
Method            BLASTN
NCBI GI           g2443456
BLAST score       53
E value           7.0e-21
Match length      69
% identity        94
NCBI Description  Oryza sativa ethylene responsive element binding protein
                  (Os-EREBP1) mRNA, complete cds
```

Seq. No. 5218
 Contig ID 4575_4.R1040
 5'-most EST g5753147
 Method BLASTX
 NCBI GI g3122602
 BLAST score 443
 E value 1.0e-43
 Match length 168
 % identity 17
 NCBI Description PEROXISOMAL TARGETING SIGNAL 2 RECEPTOR (PTS2 RECEPTOR)
 (PEROXIN-7) >gi_1890657 (U69171) peroxisomal PTS2 receptor
 [Mus musculus]

Seq. No. 5219
 Contig ID 4577_1.R1040
 5'-most EST LIB3170-022-Q1-K1-G11
 Method BLASTN
 NCBI GI g3202041
 BLAST score 219
 E value 1.0e-119
 Match length 759
 % identity 82
 NCBI Description Mesembryanthemum crystallinum 26S proteasome regulatory
 subunit S5A mRNA, complete cds

Seq. No. 5220
 Contig ID 4577_2.R1040
 5'-most EST kl1701213417.h1
 Method BLASTX
 NCBI GI g3550985
 BLAST score 295
 E value 8.0e-27
 Match length 61
 % identity 92
 NCBI Description (AB010740) OsS5a [Oryza sativa]

Seq. No. 5221
 Contig ID 4580_1.R1040
 5'-most EST LIB3106-056-Q1-K1-H8

Seq. No. 5222
 Contig ID 4583_1.R1040
 5'-most EST LIB3138-010-Q1-N1-F12
 Method BLASTX
 NCBI GI g4324495
 BLAST score 1730
 E value 0.0e+00
 Match length 404
 % identity 85
 NCBI Description (AF105221) glutamyl-tRNA reductase precursor [Glycine max]

Seq. No. 5223
 Contig ID 4586_1.R1040
 5'-most EST jC-gmst02400023g07a1
 Method BLASTX
 NCBI GI g3142296
 BLAST score 253

Seq. No. 5242
 Contig ID 4619_1.R1040
 5'-most EST gsv701046306.h1
 Method BLASTX
 NCBI GI g1498053
 BLAST score 775
 E value 2.0e-82
 Match length 208
 % identity 74
 NCBI Description (U64436) ribosomal protein S8 [Zea mays]

Seq. No. 5243
 Contig ID 4620_1.R1040
 5'-most EST eep700863857.h1
 Method BLASTX
 NCBI GI g1710780
 BLAST score 663
 E value 2.0e-69
 Match length 173
 % identity 72
 NCBI Description 40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No. 5244
 Contig ID 4620_2.R1040
 5'-most EST leu701149795.h1
 Method BLASTX
 NCBI GI g1710780
 BLAST score 669
 E value 3.0e-70
 Match length 173
 % identity 73
 NCBI Description 40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No. 5245
 Contig ID 4620_3.R1040
 5'-most EST xpa700793723.h1
 Method BLASTX
 NCBI GI g1710780
 BLAST score 337
 E value 2.0e-31
 Match length 77
 % identity 81
 NCBI Description 40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No. 5246
 Contig ID 4620_4.R1040
 5'-most EST LIB3106-058-Q1-K1-H4
 Method BLASTX
 NCBI GI g131770
 BLAST score 132

Seq. No. 5256
 Contig ID 4638_2.R1040
 5'-most EST jC-gmfl02220093g07a1
 Method BLASTX
 NCBI GI g1931652
 BLAST score 336
 E value 3.0e-31
 Match length 113
 % identity 58
 NCBI Description (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog
 [Arabidopsis thaliana]

Seq. No. 5257
 Contig ID 4638_3.R1040
 5'-most EST LIB3065-013-Q1-N1-G11
 Method BLASTX
 NCBI GI g2739367
 BLAST score 490
 E value 3.0e-49
 Match length 142
 % identity 63
 NCBI Description (AC002505) putative phosphatidylinositol-4-phosphate
 5-kinase [Arabidopsis thaliana]

Seq. No. 5258
 Contig ID 4641_1.R1040
 5'-most EST LIB3028-013-Q1-B1-F10

Seq. No. 5259
 Contig ID 4642_1.R1040
 5'-most EST LIB3138-045-Q1-N1-D6
 Method BLASTX
 NCBI GI g3860272
 BLAST score 1296
 E value 1.0e-143
 Match length 270
 % identity 90
 NCBI Description (AC005824) putative suppressor protein [Arabidopsis
 thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1
 protein [Arabidopsis thaliana]

Seq. No. 5260
 Contig ID 4642_2.R1040
 5'-most EST uC-gmrominsoy307f06b1
 Method BLASTX
 NCBI GI g3860272
 BLAST score 1219
 E value 1.0e-134
 Match length 280
 % identity 87
 NCBI Description (AC005824) putative suppressor protein [Arabidopsis
 thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1
 protein [Arabidopsis thaliana]

Seq. No. 5261
 Contig ID 4642_3.R1040
 5'-most EST g4313953

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Method BLASTX
 NCBI GI g4107099
 BLAST score 247
 E value 2.0e-20
 Match length 149
 % identity 56
 NCBI Description (AB015141) AHP1 [Arabidopsis thaliana]
 >gi_4156245_dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis thaliana]

Seq. No. 5273
 Contig ID 4662_1.R1040
 5'-most EST wvk700681920.h1
 Method BLASTX
 NCBI GI g951449
 BLAST score 1796
 E value 0.0e+00
 Match length 507
 % identity 67
 NCBI Description (L46681) aspartic protease precursor [Lycopersicon esculentum]

Seq. No. 5274
 Contig ID 4662_2.R1040
 5'-most EST LIB3028-009-Q1-B1-B10
 Method BLASTX
 NCBI GI g951449
 BLAST score 933
 E value 1.0e-101
 Match length 249
 % identity 66
 NCBI Description (L46681) aspartic protease precursor [Lycopersicon esculentum]

Seq. No. 5275
 Contig ID 4663_1.R1040
 5'-most EST LIB3093-051-Q1-K1-A12
 Method BLASTX
 NCBI GI g4454467
 BLAST score 414
 E value 3.0e-40
 Match length 84
 % identity 85
 NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 5276
 Contig ID 4664_1.R1040
 5'-most EST leu701154408.h1
 Method BLASTX
 NCBI GI g2244732
 BLAST score 840
 E value 3.0e-90
 Match length 182
 % identity 84
 NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]

Seq. No. 5277

BLAST score	185
E value	3.0e-15
Match length	97
% identity	60
NCBI Description	(AB015315) MAP kinase kinase 4 [Arabidopsis thaliana]
Seq. No.	5284
Contig ID	4675_4.R1040
5'-most EST	jC-gmfl02220052d10d1
Method	BLASTX
NCBI GI	g1523800
BLAST score	162
E value	4.0e-11
Match length	51
% identity	57
NCBI Description	(Y07694) MAP kinase kinase alpha protein kinase [Arabidopsis thaliana]
Seq. No.	5285
Contig ID	4676_1.R1040
5'-most EST	cfl1700863656.h1
Method	BLASTX
NCBI GI	g2392895
BLAST score	1512
E value	1.0e-169
Match length	333
% identity	87
NCBI Description	(AF017056) brassinosteroid insensitive 1 [Arabidopsis thaliana]
Seq. No.	5286
Contig ID	4677_1.R1040
5'-most EST	ssr700557419.h1
Method	BLASTX
NCBI GI	g2072986
BLAST score	183
E value	2.0e-13
Match length	67
% identity	57
NCBI Description	(U95142) putative G-protein-coupled receptor [Arabidopsis thaliana] >gi_2072988 (U95143) putative G-protein-coupled receptor [Arabidopsis thaliana]
Seq. No.	5287
Contig ID	4677_2.R1040
5'-most EST	LIB3109-034-Q1-K1-F6
Method	BLASTX
NCBI GI	g2072986
BLAST score	462
E value	3.0e-46
Match length	118
% identity	74
NCBI Description	(U95142) putative G-protein-coupled receptor [Arabidopsis thaliana] >gi_2072988 (U95143) putative G-protein-coupled receptor [Arabidopsis thaliana]
Seq. No.	5288

Contig ID	4679_1.R1040
5'-most EST	leu701148521.h1
Method	BLASTX
NCBI GI	g4099833
BLAST score	559
E value	2.0e-57
Match length	186
% identity	56
NCBI Description	(U90265) bifunctional nuclease [<i>Zinnia elegans</i>]
Seq. No.	5289
Contig ID	4680_1.R1040
5'-most EST	fC-gmse700674289f1
Seq. No.	5290
Contig ID	4680_2.R1040
5'-most EST	uC-gmrominsoy227f07b1
Seq. No.	5291
Contig ID	4680_4.R1040
5'-most EST	zsg701117722.h2
Seq. No.	5292
Contig ID	4682_1.R1040
5'-most EST	LIB3028-012-Q1-B1-H1
Seq. No.	5293
Contig ID	4696_1.R1040
5'-most EST	hyd700727117.h1
Method	BLASTN
NCBI GI	g4519194
BLAST score	63
E value	1.0e-26
Match length	227
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence
Seq. No.	5294
Contig ID	4696_2.R1040
5'-most EST	LIB3051-004-Q1-E1-E3
Method	BLASTN
NCBI GI	g4519194
BLAST score	48
E value	1.0e-17
Match length	176
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence
Seq. No.	5295
Contig ID	4697_1.R1040
5'-most EST	LIB3028-010-Q1-B1-F2
Seq. No.	5296
Contig ID	4700_1.R1040
5'-most EST	LIB3074-019-Q1-E1-C2

% identity 76
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 5301
Contig ID 4710_2.R1040
5'-most EST LIB3028-012-Q1-B1-E7
Method BLASTX
NCBI GI g3877951
BLAST score 246
E value 1.0e-20
Match length 133
% identity 36
NCBI Description (Z81555) predicted using Genefinder [Caenorhabditis elegans]

Seq. No. 5302
Contig ID 4712_1.R1040
5'-most EST LIB3051-017-Q1-E1-A4

Seq. No. 5303
Contig ID 4714_1.R1040
5'-most EST LIB3109-035-Q1-K6-H10
Method BLASTX
NCBI GI g3892058
BLAST score 490
E value 9.0e-49
Match length 226
% identity 47
NCBI Description (AC002330) putative glutamate-/aspartate-binding peptide [Arabidopsis thaliana]

Seq. No. 5304
Contig ID 4714_2.R1040
5'-most EST LIB3139-030-P1-N1-B7
Method BLASTX
NCBI GI g2244904
BLAST score 181
E value 3.0e-13
Match length 85
% identity 62
NCBI Description (Z97339) similar to hypothetical protein C02F5.7 - Caenorha [Arabidopsis thaliana]

Seq. No. 5305
Contig ID 4714_3.R1040
5'-most EST uC-gmronoir030b08b1

Seq. No. 5306
Contig ID 4716_1.R1040
5'-most EST leu701154646.h1
Method BLASTX
NCBI GI g4262183
BLAST score 386
E value 3.0e-37
Match length 83
% identity 87
NCBI Description (AC005508) 51434 [Arabidopsis thaliana]

Seq. No. 5307
 Contig ID 4718_1.R1040
 5'-most EST LIB3028-012-Q1-B1-D5
 Method BLASTX
 NCBI GI g4220480
 BLAST score 242
 E value 3.0e-20
 Match length 101
 % identity 51
 NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 5308
 Contig ID 4721_1.R1040
 5'-most EST txt700734653.h1
 Method BLASTX
 NCBI GI g4454051
 BLAST score 581
 E value 6.0e-60
 Match length 208
 % identity 55
 NCBI Description (AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No. 5309
 Contig ID 4724_1.R1040
 5'-most EST jC-gmf102220115f09a1
 Method BLASTX
 NCBI GI g2739370
 BLAST score 333
 E value 4.0e-31
 Match length 128
 % identity 51
 NCBI Description (AC002505) putative pectinesterase [Arabidopsis thaliana]

Seq. No. 5310
 Contig ID 4725_1.R1040
 5'-most EST LIB3028-007-Q1-B1-G3
 Method BLASTX
 NCBI GI g602292
 BLAST score 507
 E value 3.0e-51
 Match length 208
 % identity 49
 NCBI Description (U17987) RCH2 protein [Brassica napus]

Seq. No. 5311
 Contig ID 4729_1.R1040
 5'-most EST crh700852073.h1
 Method BLASTX
 NCBI GI g4406759
 BLAST score 542
 E value 4.0e-55
 Match length 291
 % identity 44
 NCBI Description (AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	5312
Contig ID	4729_2.R1040
5'-most EST	k11701212931.h1
Method	BLASTX
NCBI GI	g4406759
BLAST score	362
E value	6.0e-34
Match length	239
% identity	36
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]
Seq. No.	5313
Contig ID	4733_1.R1040
5'-most EST	uC-gmropic019c04b1
Method	BLASTX
NCBI GI	g1350983
BLAST score	1092
E value	1.0e-119
Match length	234
% identity	88
NCBI Description	40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
Seq. No.	5314
Contig ID	4737_1.R1040
5'-most EST	LIB3028-012-Q1-B1-B12
Seq. No.	5315
Contig ID	4739_1.R1040
5'-most EST	LIB3170-025-Q1-K1-H1
Method	BLASTX
NCBI GI	g3892058
BLAST score	832
E value	4.0e-89
Match length	238
% identity	66
NCBI Description	(AC002330) putative glutamate-/aspartate-binding peptide [Arabidopsis thaliana]
Seq. No.	5316
Contig ID	4740_1.R1040
5'-most EST	zzp700834267.h1
Method	BLASTX
NCBI GI	g2392021
BLAST score	628
E value	3.0e-65
Match length	168
% identity	68
NCBI Description	(D63425) phospholipid hydroperoxide glutathione peroxidase-like protein [Spinacia oleracea]
Seq. No.	5317
Contig ID	4743_1.R1040
5'-most EST	LIB3109-019-Q1-K1-D8
Method	BLASTX
NCBI GI	g2460203
BLAST score	268
E value	1.0e-23

5'-most EST LIB3139-076-P1-N1-C2
 Method BLASTX
 NCBI GI g1841464
 BLAST score 334
 E value 5.0e-31
 Match length 75
 % identity 42
 NCBI Description (Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No. 5326
 Contig ID 4747 4.R1040
 5'-most EST sat701015226.h1

Seq. No. 5327
 Contig ID 4747 5.R1040
 5'-most EST pmv700892040.h1

Seq. No. 5328
 Contig ID 4749 1.R1040
 5'-most EST crh700852401.h1
 Method BLASTX
 NCBI GI g480618
 BLAST score 724
 E value 2.0e-76
 Match length 216
 % identity 69
 NCBI Description ATAF1 protein - Arabidopsis thaliana (fragment)
 >gi_1345506_emb_CAA52771_ (X74755) ATAF1 [Arabidopsis thaliana]

Seq. No. 5329
 Contig ID 4749 2.R1040
 5'-most EST uC-gmrominsoy245e10b1
 Method BLASTX
 NCBI GI g480618
 BLAST score 677
 E value 6.0e-71
 Match length 206
 % identity 68
 NCBI Description ATAF1 protein - Arabidopsis thaliana (fragment)
 >gi_1345506_emb_CAA52771_ (X74755) ATAF1 [Arabidopsis thaliana]

Seq. No. 5330
 Contig ID 4749 3.R1040
 5'-most EST uC-gmronoir076d10b1
 Method BLASTX
 NCBI GI g4218535
 BLAST score 446
 E value 2.0e-44
 Match length 126
 % identity 64
 NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]

Seq. No. 5331
 Contig ID 4753 1.R1040
 5'-most EST LIB3109-046-Q1-K1-D11


```
BLAST score      780
E value         8.0e-83
Match length    345
% identity      57
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
```

Seq. No.	5364
Contig ID	4806 4.R1040
5'-most EST	zsg701118740.h1

```
Seq. No.          5365
Contig ID         4809_1.R1040
5'-most EST      LIB3028-011-Q1-B1-A5
Method            BLASTX
NCBI GI           g1769895
BLAST score       803
E value           6.0e-86
Match length      228
% identity        68
NCBI Description   (X96598) CaLB protein [Arabidopsis thaliana]
```

```
Seq. No.          5366
Contig ID         4811_1.R1040
5'-most EST      uC-gmrominsoy114g12b1
Method            BLASTX
NCBI GI           g1361979
BLAST score       310
E value           5.0e-30
Match length      108
% identity        70
NCBI Description  serine O-acetyltransferase (EC 2.3.1.30) - watermelon
                  >gi_1350550_dbj_BAA12843_(D85624) serine acetyltransferase
                  [Citrullus lanatus] >gi_1841312_dbj_BAA08479_(D49535)
                  serine acetyltransferase. [Citrullus lanatus]
                  >gi_2337772_dbj_BAA21827_(AB006530) serine
                  acetyltransferase [Citrullus lanatus]
```

```
Seq. No.          5367
Contig ID         4814_1.R1040
5'-most EST      zhff700954244.h1
Method            BLASTX
NCBI GI           g3377820
BLAST score       265
E value           8.0e-37
Match length      132
% identity        62
NCBI Description  (AF076275) contains similarity to coatomer zeta chains
                  [Arabidopsis thaliana]
```

Seq. No.	5368
Contig ID	4815_1.R1040
5'-most EST	LIB3109-034-Q1-K1-E7
Method	BLASTX
NCBI GI	g2454184
BLAST score	1235
E value	1.0e-136
Match length	405

% identity	67
NCBI Description	(U80186) pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana]
Seq. No.	5369
Contig ID	4815_2.R1040
5'-most EST	seb700650890.h1
Seq. No.	5370
Contig ID	4815_3.R1040
5'-most EST	jC-gmro02910071g01d1
Seq. No.	5371
Contig ID	4816_1.R1040
5'-most EST	LIB3028-010-Q1-B1-F9
Method	BLASTX
NCBI GI	g2760324
BLAST score	322
E value	1.0e-29
Match length	104
% identity	64
NCBI Description	(AC002130) F1N21.9 [Arabidopsis thaliana]
Seq. No.	5372
Contig ID	4817_1.R1040
5'-most EST	LIB3040-054-Q1-E1-B9
Seq. No.	5373
Contig ID	4817_2.R1040
5'-most EST	LIB3072-027-Q1-E1-D9
Seq. No.	5374
Contig ID	4820_1.R1040
5'-most EST	leu701147178.h1
Method	BLASTX
NCBI GI	g4218120
BLAST score	1243
E value	1.0e-137
Match length	356
% identity	67
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]
Seq. No.	5375
Contig ID	4820_2.R1040
5'-most EST	wrg700788041.h1
Method	BLASTX
NCBI GI	g4218120
BLAST score	498
E value	3.0e-50
Match length	122
% identity	77
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]
Seq. No.	5376
Contig ID	4820_3.R1040

5'-most EST g4260376
 Method BLASTX
 NCBI GI g4218120
 BLAST score 331
 E value 8.0e-31
 Match length 79
 % identity 72
 NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No. 5377
 Contig ID 4823_1.R1040
 5'-most EST jC-gmro02800040g03d1

Seq. No. 5378
 Contig ID 4823_2.R1040
 5'-most EST uxk700672939.h1
 Method BLASTX
 NCBI GI g3650033
 BLAST score 200
 E value 2.0e-15
 Match length 81
 % identity 54
 NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]

Seq. No. 5379
 Contig ID 4823_3.R1040
 5'-most EST jC-gmf102220143c10d1

Seq. No. 5380
 Contig ID 4826_1.R1040
 5'-most EST LIB3093-007-Q1-K1-E3
 Method BLASTX
 NCBI GI g3415115
 BLAST score 498
 E value 7.0e-50
 Match length 253
 % identity 48
 NCBI Description (AF081202) villin 2 [Arabidopsis thaliana]

Seq. No. 5381
 Contig ID 4827_1.R1040
 5'-most EST LIB3028-010-Q1-B1-E6
 Method BLASTX
 NCBI GI g3618316
 BLAST score 188
 E value 4.0e-14
 Match length 100
 % identity 46
 NCBI Description (AB001886) zinc finger protein [Oryza sativa]

Seq. No. 5382
 Contig ID 4828_1.R1040
 5'-most EST wvk700680503.h1
 Method BLASTX
 NCBI GI g4539010
 BLAST score 236

E value 1.0e-19
 Match length 143
 % identity 48
 NCBI Description (AL049481) putative DNA-directed RNA polymerase [Arabidopsis thaliana]

Seq. No. 5383
 Contig ID 4830_1.R1040
 5'-most EST LIB3106-035-Q1-K1-B7
 Method BLASTX
 NCBI GI g4138916
 BLAST score 979
 E value 1.0e-106
 Match length 242
 % identity 74
 NCBI Description (AF059489) expansin precursor [Lycopersicon esculentum]

Seq. No. 5384
 Contig ID 4830_2.R1040
 5'-most EST hyd700724977.h1
 Method BLASTX
 NCBI GI g4027897
 BLAST score 452
 E value 6.0e-45
 Match length 116
 % identity 71
 NCBI Description (AF049353) alpha-expansin precursor [Nicotiana tabacum]

Seq. No. 5385
 Contig ID 4834_1.R1040
 5'-most EST LIB3138-039-Q1-N1-C11
 Method BLASTX
 NCBI GI g4468813
 BLAST score 748
 E value 3.0e-79
 Match length 200
 % identity 67
 NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 5386
 Contig ID 4836_1.R1040
 5'-most EST jC-gmro02910031e04a1

Seq. No. 5387
 Contig ID 4837_1.R1040
 5'-most EST LIB3049-053-Q1-E1-E8

Seq. No. 5388
 Contig ID 4837_2.R1040
 5'-most EST trc700566031.h1

Seq. No. 5389
 Contig ID 4840_1.R1040
 5'-most EST LIB3028-010-Q1-B1-D10

Seq. No. 5390
 Contig ID 4844_1.R1040

5'-most EST LIB3028-010-Q1-B1-B9

Seq. No. 5391
Contig ID 4845_1.R1040
5'-most EST LIB3138-126-Q1-N1-A8

Seq. No. 5392
Contig ID 4846_1.R1040
5'-most EST uC-gmropic014h09b1
Method BLASTX
NCBI GI g1546702
BLAST score 819
E value 1.0e-87
Match length 248
% identity 62
NCBI Description (X98809) peroxidase ATP5a [Arabidopsis thaliana]

Seq. No. 5393
Contig ID 4846_2.R1040
5'-most EST bth700844765.h1
Method BLASTX
NCBI GI g1546702
BLAST score 542
E value 2.0e-55
Match length 151
% identity 68
NCBI Description (X98809) peroxidase ATP5a [Arabidopsis thaliana]

Seq. No. 5394
Contig ID 4846_3.R1040
5'-most EST pmv700893877.h1
Method BLASTX
NCBI GI g2811262
BLAST score 121
E value 2.0e-11
Match length 75
% identity 56
NCBI Description (AF043234) ferriprotein porphyrin-containing peroxidase [Striga asiatica]

Seq. No. 5395
Contig ID 4848_1.R1040
5'-most EST LIB3028-010-Q1-B1-A9
Method BLASTN
NCBI GI g2746720
BLAST score 128
E value 2.0e-65
Match length 312
% identity 85
NCBI Description Capsicum annuum histone H4 mRNA, complete cds

Seq. No. 5396
Contig ID 4850_1.R1040
5'-most EST g5687831
Method BLASTN
NCBI GI g3127889
BLAST score 428

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E value 0.0e+00
Match length 760
% identity 89
NCBI Description Cicer arietinum mRNA for cysteine synthase, partial

Seq. No. 5397
Contig ID 4850_2.R1040
5'-most EST LIB3087-002-Q1-K1-A3
Method BLASTN
NCBI GI g3127889
BLAST score 149
E value 4.0e-78
Match length 193
% identity 94
NCBI Description Cicer arietinum mRNA for cysteine synthase, partial

Seq. No. 5398
Contig ID 4856_1.R1040
5'-most EST LIB3106-003-Q1-K1-F1
Method BLASTX
NCBI GI g166878
BLAST score 154
E value 4.0e-10
Match length 102
% identity 37
NCBI Description (M95796) St12p protein [Arabidopsis thaliana]

Seq. No. 5399
Contig ID 4856_2.R1040
5'-most EST LIB3138-014-Q1-N2-H8
Method BLASTX
NCBI GI g3785976
BLAST score 206
E value 4.0e-16
Match length 128
% identity 37
NCBI Description (AC005560) Sec12p-like protein [Arabidopsis thaliana]

Seq. No. 5400
Contig ID 4857_1.R1040
5'-most EST sat701011352.h1
Method BLASTX
NCBI GI g3548802
BLAST score 416
E value 2.0e-40
Match length 168
% identity 50
NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana]
>gi_4335769_gb_AAD17446_ (AC006284) putative axil protein
[Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No. 5401
Contig ID 4859_1.R1040
5'-most EST LIB3093-031-Q1-K1-F6
Method BLASTX
NCBI GI g2244924
BLAST score 324


```

E value      4.0e-30
Match length  81
% identity    73
NCBI Description (Z97339) glutaredoxin [Arabidopsis thaliana]

```

```
Seq. No.          5402
Contig ID         4859 2.R1040
5'-most EST      leu701153189.h1
Method            BLASTX
NCBI GI           g2244924
BLAST score       226
E value           1.0e-18
Match length      56
% identity        73
NCBI Description  (Z97339) glutaredoxin [Arabidopsis thaliana]
```

```
Seq. No.          5403
Contig ID         4863_1.R1040
5'-most EST      uC-gmropic113h06b1
Method            BLASTX
NCBI GI           g3776084
BLAST score       280
E value           1.0e-24
Match length      85
% identity        59
NCBI Description  (Y18251) NtN2 [Medicago truncatula]
```

```
Seq. No.          5404
Contig ID         4863 2.R1040
5'-most EST      xzm700763745.h1
Method            BLASTX
NCBI GI           g3776084
BLAST score       188
E value           1.0e-18
Match length      83
% identity        58
NCBI Description  (Y18251) NtN2 [Medicago truncatula]
```

```
Seq. No.          5405
Contig ID         4866_1.R1040
5'-most EST      LIB3049-015-Q1-E1-B1
Method            BLASTX
NCBI GI           g2136139
BLAST score       262
E value           2.0e-42
Match length      297
% identity        15
NCBI Description  sds22 protein homolog - human >gi_1085028_emb_CAA90626_
                  (Z50749) yeast sds22 homolog [Homo sapiens]
                  >gi_1585165_prf_2124310A sds22 gene [Homo sapiens]
                  >gi_4506013_ref_NP_002703.1_pPPP1R7_ protein phosphatase 1,
                  regulatory subunit
```

Seq. No.	5406
Contig ID	4867_1.R1040
5'-most EST	jC-gmst02400009d05d1
Method	BLASTX

```

NCBI GI      g2673912
BLAST score   510
E value       2.0e-51
Match length  159
% identity    63
NCBI Description (AC002561) unknown protein [Arabidopsis thaliana]

```

```

Seq. No.          5407
Contig ID         4867_2.R1040
5'-most EST      wvk700685447.h1
Method           BLASTX
NCBI GI          g2492530
BLAST score      2050
E value          0.0e+00
Match length     531
% identity       74
NCBI Description  CHLOROPLAST AMINOPEPTIDASE 1 PRECURSOR (LEUCINE
                  AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE
                  AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi_924630 (U20594)
                  leucine aminopeptidase [Solanum lycopersicum]

```

```
Seq. No.          5408
Contig ID         4867_3.R1040
5'-most EST      uC-gmropic027e08b1
Method            BLASTX
NCBI GI           g2492530
BLAST score       588
E value           1.0e-60
Match length      196
% identity        61
NCBI Description  CHLOROPLAST AMINOPEPTIDASE 1 PRECURSOR (LEUCINE
                  AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE
                  AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi_924630 (U20594)
                  leucine aminopeptidase [Solanum lycopersicum]
```

```
Seq. No.      5409
Contig ID     4867_4.R1040
5'-most EST  uC-qmrominsoy284f02b1
```

```
Seq. No.          5410
Contig ID         4867_5.R1040
5'-most EST      jC-gmle01810068e01a1
Method..         BLASTX
NCBI GI           g1483563
BLAST score       485
E value          8.0e-49
Match length      113
% identity        77
NCBI Description  (X99825) leucine aminopeptidase [Petroselinum crispum]
```

```
Seq. No.          5411
Contig ID         4867_6.R1040
5'-most EST      uC-gmropic070c01b1
Method            BLASTX
NCBI GI           g2673912
BLAST score       421
E value           2.0e-41
```

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Match length	106
% identity	75
NCBI Description	(AC002561) unknown protein [Arabidopsis thaliana]
Seq. No.	5412
Contig ID	4873_1.R1040
5'-most EST	LIB3051-043-Q1-K1-G1
Method	BLASTX
NCBI GI	g1408460
BLAST score	2168
E value	0.0e+00
Match length	514
% identity	81
NCBI Description	(U40161) type 2A protein serine/threonine phosphatase 55 kDa B regulatory subunit [Arabidopsis thaliana]
Seq. No.	5413
Contig ID	4873_2.R1040
5'-most EST	jC-gmle01810087b01d1
Seq. No.	5414
Contig ID	4873_3.R1040
5'-most EST	jC-gmro02910046a02d1
Method	BLASTX
NCBI GI	g1408460
BLAST score	341
E value	4.0e-32
Match length	76
% identity	88
NCBI Description	(U40161) type 2A protein serine/threonine phosphatase 55 kDa B regulatory subunit [Arabidopsis thaliana]
Seq. No.	5415
Contig ID	4873_4.R1040
5'-most EST	LIB3028-009-Q1-B1-F11
Method	BLASTX
NCBI GI	g3421413
BLAST score	462
E value	2.0e-46
Match length	125
% identity	73
NCBI Description	(AF081922) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa] >gi_3421415 (AF081923) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]
Seq. No.	5416
Contig ID	4875_1.R1040
5'-most EST	vzy700750750.h1
Method	BLASTX
NCBI GI	g3334323
BLAST score	966
E value	1.0e-105
Match length	193
% identity	93
NCBI Description	GTP-BINDING PROTEIN SAR1A >gi_1314860 (U56929) Sar1 homolog [Arabidopsis thaliana] >gi_2104532 gb_AAC78700.1 (AF001308) SAR1/GTP-binding secretory factor [Arabidopsis

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Seq. No. 5422
 Contig ID 4876_4.R1040
 5'-most EST epX701106549.h1
 Method BLASTX
 NCBI GI g2194137
 BLAST score 410
 E value 5.0e-40
 Match length 113
 % identity 74
 NCBI Description (AC002062) ESTs gb_R29947,gb_H76702 come from this gene.
 [Arabidopsis thaliana]

Seq. No. 5423
 Contig ID 4878_1.R1040
 5'-most EST jsh701066075.h1
 Method BLASTX
 NCBI GI g4056432
 BLAST score 1220
 E value 1.0e-134
 Match length 448
 % identity 60
 NCBI Description (AC005990) Similar to gi_2245014 glucosyltransferase
 homolog from Arabidopsis thaliana chromosome 4 contig
 gb_Z97341. ESTs gb_T20778 and gb_AA586281 come from this
 gene. [Arabidopsis thaliana]

Seq. No. 5424
 Contig ID 4878_2.R1040
 5'-most EST seb700652962.h1

Seq. No. 5425
 Contig ID 4880_1.R1040
 5'-most EST LIB3053-006-Q1-N1-G1
 Method BLASTX
 NCBI GI g543721
 BLAST score 169
 E value 1.0e-11
 Match length 142
 % identity 32
 NCBI Description PROTEIN PHOSPHATASE PP2A, 72 KD REGULATORY SUBUNIT (PR72)
 >gi_539659_pir_A47114 phosphoprotein phosphatase (EC
 3.1.3.16) 2A regulatory chain PR72 - human >gi_190222
 (L12146) protein phosphatase 2A 72 kDa regulatory subunit
 [Homo sapiens] >gi_4506021_ref_NP_002709.1_PPPP2R3 protein
 phosphatase 2 (formerly 2A), regulatory subunit B' (PR
 72), alpha isoform and (PR 130), beta isoform

Seq. No. 5426
 Contig ID 4880_2.R1040
 5'-most EST uC-gmflminsoy059f03b1

Seq. No. 5427
 Contig ID 4886_1.R1040
 5'-most EST uC-gmflminsoy058g03b1
 Method BLASTX
 NCBI GI g4126403

```
BLAST score      901
E value         4.0e-97
Match length    331
% identity      52
NCBI Description (AB011796) flavonol synthase [Citrus unshiu]
```

Seq. No.	5428
Contig ID	4889_1.R1040
5'-most EST	LIB3087-007-Q1-K1-G9

Seq. No.	5429
Contig ID	4890_1.R1040
5'-most EST	fde700874865.h1
Method	BLASTX
NCBI GI	g132717
BLAST score	250
E value	3.0e-21
Match length	92
% identity	53
NCBI Description	50S RIBOSOMAL PROTEIN L17 (BL21) >gi_71253_pir_R5BS17 ribosomal protein L17 - <i>Bacillus stearothermophilus</i>

```
Seq. No.          5430
Contig ID         4890_2.R1040
5'-most EST      bth700845664.h1
Method            BLASTX
NCBI GI           g3925782
BLAST score       138
E value           1.0e-08
Match length      49
% identity        57
NCBI Description  (AL034353) putative 60s ribosomal protein
                  [Schizosaccharomyces pombe]
```

```
Seq. No.          5431
Contig ID         4892_1.R1040
5'-most EST      dpv701102209.h1
Method            BLASTX
NCBI GI           g2281102
BLAST score       287
E value           2.0e-25
Match length      139
% identity        52
NCBI Description  (AC002333) SF16 isolog [Arabidopsis thaliana]
```

```
Seq. No.          5432
Contig ID         4894_1.R1040
5'-most EST      LIB3039-005-Q1-E1-G11
Method            BLASTN
NCBI GI           g562281
BLAST score       123
E value           1.0e-62
Match length      247
% identity        87
NCBI Description  B.oleracea mRNA for PSST subunit of NADH:ubiquinone
                  oxidoreductase
```



```

NCBI GI      g3168839
BLAST score  71
E value      1.0e-31
Match length 187
% identity   84
NCBI Description Arabidopsis thaliana copper homeostasis factor (CCH) mRNA,
                  complete cds

```

```
Seq. No.          5445
Contig ID         4905 3.R1040
5'-most EST      LIB3167-078-P1-K2-H5
Method            BLASTN
NCBI GI           g3168839
BLAST score       42
E value           5.0e-14
Match length      62
% identity        92
NCBI Description  Arabidopsis thaliana copper homeostasis factor (CCH) mRNA,
                  complete cds
```

```
Seq. No.          5446
Contig ID         4906_1.R1040
5'-most EST      jex700906490.h1
Method           BLASTX
NCBI GI          g4469008
BLAST score      177
E value          9.0e-13
Match length     62
% identity       55
NCBI Description  (AL035602) UDP rhamnose--anthocyanidin-3-glucoside
                  rhamnosyltransferase-like protein [Arabidopsis thaliana]
```

```
Seq. No.          5447
Contig ID         4908_1.R1040
5'-most EST      uC-gmflminsoy058h04b1
Method            BLASTX
NCBI GI           g2262116
BLAST score       281
E value           6.0e-25
Match length      135
% identity        35
NCBI Description  (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
```

Seq. No.	5448
Contig ID	4910_1.R1040
5'-most EST	jC-qmf102220057a11d1

```
Seq. No.          5449
Contig ID         4911_1.R1040
5'-most EST      LIB3093-033-Q1-K1-H9
Method            BLASTX
NCBI GI           g2285792
BLAST score       559
E value           4.0e-57
Match length      155
% identity        70
NCBI Description  (AB004568) cyanase [Arabidopsis thaliana]
```

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>gi_3287503_dbj_BAA31224_ (AB015748) cyanase [Arabidopsis thaliana]

Seq. No. 5450
 Contig ID 4912_1.R1040
 5'-most EST jC-gmst02400018d09a1
 Method BLASTX
 NCBI GI g3643085
 BLAST score 363
 E value 3.0e-34
 Match length 191
 % identity 41
 NCBI Description (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No. 5451
 Contig ID 4913_1.R1040
 5'-most EST uC-gmronoir025d01b1
 Method BLASTX
 NCBI GI g3335372
 BLAST score 409
 E value 1.0e-39
 Match length 112
 % identity 65
 NCBI Description (AC003028) putative SRG1 protein [Arabidopsis thaliana]

Seq. No. 5452
 Contig ID 4915_1.R1040
 5'-most EST zpv700757869.h1

Seq. No. 5453
 Contig ID 4915_2.R1040
 5'-most EST LIB3093-040-Q1-K1-F10

Seq. No. 5454
 Contig ID 4918_1.R1040
 5'-most EST g4397125

Seq. No. 5455
 Contig ID 4921_1.R1040
 5'-most EST LIB3107-059-Q1-K1-B11
 Method BLASTN
 NCBI GI g168498
 BLAST score 119
 E value 3.0e-60
 Match length 315
 % identity 84
 NCBI Description Corn histone H4 (H4C13) gene, complete cds

Seq. No. 5456
 Contig ID 4926_1.R1040
 5'-most EST jC-gmro02910066a04a1

Seq. No. 5457
 Contig ID 4926_2.R1040
 5'-most EST uC-gmflminsoy108e01b1

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Seq. No.          5465
Contig ID         4939 1.R1040
5'-most EST      pxt700944780.h1
Method            BLASTN
NCBI GI           g434342
BLAST score       144
E value           8.0e-75
Match length      464
% identity        83
NCBI Description  A.thaliana (C24) mRNA for S18 ribosomal protein
```

```
Seq. No.          5467
Contig ID         4939_3.R1040
5'-most EST      ncj700983777.h1
Method            BLASTX
NCBI GI           g3746064
BLAST score       146
E value           2.0e-09
Match length      80
```


Seq. No.	5486
Contig ID	4962_1.R1040
5'-most EST	LIB3109-022-Q1-K1-A4
Method	BLASTX
NCBI GI	g3063706
BLAST score	467
E value	2.0e-46
Match length	131
% identity	65
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]
Seq. No.	5487
Contig ID	4964_1.R1040
5'-most EST	jC-gmro02910067f08a1
Method	BLASTN
NCBI GI	g2565418
BLAST score	153
E value	2.0e-80
Match length	385
% identity	85
NCBI Description	Onobrychis viciifolia histone H3 mRNA, complete cds
Seq. No.	5488
Contig ID	4964_2.R1040
5'-most EST	leu701155595.h1
Method	BLASTN
NCBI GI	g166383
BLAST score	104
E value	2.0e-51
Match length	240
% identity	86
NCBI Description	Alfalfa histone H3 (H3-1.1) gene, complete cds
Seq. No.	5489
Contig ID	4965_1.R1040
5'-most EST	fC-gmro700845991a2
Seq. No.	5490
Contig ID	4965_2.R1040
5'-most EST	uC-gmropic020h10b1
Seq. No.	5491
Contig ID	4967_1.R1040
5'-most EST	LIB3028-008-Q1-B1-A9
Method	BLASTN
NCBI GI	g11571
BLAST score	380
E value	0.0e+00
Match length	401
% identity	98
NCBI Description	Soybean chloroplast rps12 and rps7 genes
Seq. No.	5492
Contig ID	4968_1.R1040
5'-most EST	LIB3029-011-Q1-B1-C12
Method	BLASTX

NCBI GI	g3241945
BLAST score	437
E value	5.0e-43
Match length	132
% identity	58
NCBI Description	(AC004625) unknown protein [Arabidopsis thaliana]
Seq. No.	5493
Contig ID	4968_2.R1040
5'-most EST	jex700904823.h1
Seq. No.	5494
Contig ID	4969_1.R1040
5'-most EST	LIB3028-008-Q1-B1-B10
Seq. No.	5495
Contig ID	4971_1.R1040
5'-most EST	wvk700682772.h1
Method	BLASTX
NCBI GI	g4469012
BLAST score	311
E value	1.0e-28
Match length	88
% identity	76
NCBI Description	(AL035602) hypothetical protein [Arabidopsis thaliana]
Seq. No.	5496
Contig ID	4972_1.R1040
5'-most EST	jC-gmfl02220106a08a1
Method	BLASTX
NCBI GI	g2804278
BLAST score	1861
E value	0.0e+00
Match length	414
% identity	83
NCBI Description	(AB003516) squalene epoxidase [Panax ginseng]
Seq. No.	5497
Contig ID	4972_2.R1040
5'-most EST	jC-gmfl02220086d06a1
Method	BLASTX
NCBI GI	g2804278
BLAST score	698
E value	2.0e-75
Match length	179
% identity	79
NCBI Description	(AB003516) squalene epoxidase [Panax ginseng]
Seq. No.	5498
Contig ID	4973_1.R1040
5'-most EST	gsv701050692.h1
Method	BLASTX
NCBI GI	g4262228
BLAST score	424
E value	7.0e-53
Match length	161
% identity	67

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NCBI Description (AC006200) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 5499
Contig ID 4974_1.R1040
5'-most EST LIB3040-003-Q1-E1-F10

Seq. No. 5500
Contig ID 4975_1.R1040
5'-most EST epx701105965.h1

Seq. No. 5501
Contig ID 4975_2.R1040
5'-most EST LIB3092-029-Q1-K1-F1

Seq. No. 5502
Contig ID 4980_1.R1040
5'-most EST k11701214527.h1

Seq. No. 5503
Contig ID 4980_2.R1040
5'-most EST LIB3139-047-P1-N1-D1
Method BLASTX
NCBI GI g729486
BLAST score 180
E value 4.0e-13
Match length 102
% identity 41

NCBI Description PRE-RRNA PROCESSING PROTEIN FHL1 >gi_626950_pir_S43738 transcription activator FHL1 - yeast (Saccharomyces cerevisiae) >gi_454255_emb_CAA82202_ (Z28348) Fhl1p [Saccharomyces cerevisiae] >gi_914975 (U32445) Pre-rRNA processing protein Fhl1 (Swiss Prot. accession number P39521) [Saccharomyces cerevisiae]

Seq. No. 5504
Contig ID 4983_1.R1040
5'-most EST jC-gmfl02220079h05a1
Method BLASTX
NCBI GI g577301
BLAST score 188
E value 6.0e-14
Match length 108
% identity 34

NCBI Description (D42044) The ha3523 gene product is related to S.cerevisiae gene product located in chromosome III. [Homo sapiens]

Seq. No. 5505
Contig ID 4985_1.R1040
5'-most EST zpv700758101.h1
Method BLASTX
NCBI GI g4510425
BLAST score 620
E value 2.0e-64
Match length 140
% identity 83

NCBI Description (AC006929) unknown protein [Arabidopsis thaliana]

Seq. No. 5523
 Contig ID 5012_1.R1040
 5'-most EST taw700660051.h1
 Method BLASTX
 NCBI GI g400198
 BLAST score 199
 E value 3.0e-15
 Match length 101
 % identity 50
 NCBI Description PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T)
 (LIGHT-REGULATED UNKNOWN 11 KD PROTEIN)
 >gi_99604_pir_S21023 hypothetical protein - upland cotton
 >gi_1361978_pir_A57500 photosystem II protein psbT -
 upland cotton >gi_18512_emb_CAA38027_ (X54092) unknown
 reading frame [Gossypium hirsutum]

Seq. No. 5524
 Contig ID 5012_2.R1040
 5'-most EST jC-gmst02400063f12a1
 Method BLASTX
 NCBI GI g400198
 BLAST score 190
 E value 5.0e-14
 Match length 104
 % identity 43
 NCBI Description PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T)
 (LIGHT-REGULATED UNKNOWN 11 KD PROTEIN)
 >gi_99604_pir_S21023 hypothetical protein - upland cotton
 >gi_1361978_pir_A57500 photosystem II protein psbT -
 upland cotton >gi_18512_emb_CAA38027_ (X54092) unknown
 reading frame [Gossypium hirsutum]

Seq. No. 5525
 Contig ID 5012_3.R1040
 5'-most EST LIB3074-004-Q1-K1-E8
 Method BLASTX
 NCBI GI g400198
 BLAST score 192
 E value 2.0e-14
 Match length 103
 % identity 50
 NCBI Description PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T)
 (LIGHT-REGULATED UNKNOWN 11 KD PROTEIN)
 >gi_99604_pir_S21023 hypothetical protein - upland cotton
 >gi_1361978_pir_A57500 photosystem II protein psbT -
 upland cotton >gi_18512_emb_CAA38027_ (X54092) unknown
 reading frame [Gossypium hirsutum]

Seq. No. 5526
 Contig ID 5013_1.R1040
 5'-most EST g4313283
 Method BLASTX
 NCBI GI g4262250
 BLAST score 1690
 E value 0.0e+00
 Match length 382

Contig ID 5025_1.R1040
 5'-most EST uC-gmflminsoyl18b03b1
 Method BLASTX
 NCBI GI g4567235
 BLAST score 150
 E value 9.0e-10
 Match length 81
 % identity 47
 NCBI Description (AC007119) putative phosphatidylinositol/phosphatidylcholine transfer protein [Arabidopsis thaliana]

Seq. No. 5534
 Contig ID 5026_1.R1040
 5'-most EST LIB3093-014-Q1-K1-G6

Seq. No. 5535
 Contig ID 5026_2.R1040
 5'-most EST jC-gmle01810089h07a1

Seq. No. 5536
 Contig ID 5028_1.R1040
 5'-most EST gsv701046547.h1
 Method BLASTX
 NCBI GI g2398829
 BLAST score 302
 E value 2.0e-27
 Match length 72
 % identity 39
 NCBI Description (Y11220) mitochondrial uncoupling protein [Solanum tuberosum]

Seq. No. 5537
 Contig ID 5029_1.R1040
 5'-most EST vzy700753080.h1
 Method BLASTX
 NCBI GI g1946329
 BLAST score 1014
 E value 1.0e-110
 Match length 278
 % identity 73
 NCBI Description (U69154) prohibitin [Nicotiana tabacum]

Seq. No. 5538
 Contig ID 5029_2.R1040
 5'-most EST LIB3167-027-P1-K1-E3
 Method BLASTX
 NCBI GI g1946329
 BLAST score 420
 E value 3.0e-41
 Match length 111
 % identity 72
 NCBI Description (U69154) prohibitin [Nicotiana tabacum]

Seq. No. 5539
 Contig ID 5033_1.R1040
 5'-most EST LIB3138-031-Q1-N1-D11
 Method BLASTN

0958-016-301000

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Seq. No.          5546
Contig ID         5041_6.R1040
5'-most EST      pcp700989770.h1
Method            BLASTN
NCBI GI           g1143510
BLAST score       67
E value           2.0e-29
Match length      131
% identity        88
NCBI Description  M.domestica Borkh mRNA for serine/threonine protein
                  phosphatase (PPX)
```

```
Seq. No.          5548
Contig ID         5044_1.R1040
5'-most EST      ncj700983465.h1
Method            BLASTX
NCBI GI          g1402878
BLAST score       1075
E value           1.0e-117
Match length      444
% identity        45
NCBI Description  (X98130) unknown [Arabidopsis thaliana]
```


5'-most EST uC-gmropic111d07b1
 Method BLASTN
 NCBI GI g2351064
 BLAST score 35
 E value 4.0e-10
 Match length 47
 % identity 94
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 MDJ22, complete sequence [Arabidopsis thaliana]

Seq. No. 5564
 Contig ID 5057_1.R1040
 5'-most EST LIB3028-006-Q1-B1-H10
 Method BLASTX
 NCBI GI g4559398
 BLAST score 796
 E value 6.0e-85
 Match length 229
 % identity 66
 NCBI Description (AC006526) putative mitochondrial carrier protein
 [Arabidopsis thaliana]

Seq. No. 5565
 Contig ID 5060_1.R1040
 5'-most EST LIB3139-101-P1-N1-B4
 Method BLASTX
 NCBI GI g3451068
 BLAST score 471
 E value 4.0e-47
 Match length 159
 % identity 64
 NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 5566
 Contig ID 5060_2.R1040
 5'-most EST LIB3028-008-Q1-B1-F3
 Method BLASTX
 NCBI GI g3451067
 BLAST score 306
 E value 6.0e-28
 Match length 99
 % identity 64
 NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 5567
 Contig ID 5060_3.R1040
 5'-most EST LIB3106-087-Q1-K1-A3
 Method BLASTX
 NCBI GI g3451067
 BLAST score 137
 E value 5.0e-15
 Match length 82
 % identity 59
 NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 5568
 Contig ID 5060_4.R1040

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5'-most EST LIB3106-076-Q1-K1-G6
Method BLASTX
NCBI GI g3451067
BLAST score 373
E value 1.0e-35
Match length 99
% identity 75
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 5569
Contig ID 5060_5.R1040
5'-most EST leu701155251.h1

Seq. No. 5570
Contig ID 5062_1.R1040
5'-most EST uC-gmrominsoy067f01b1
Method BLASTX
NCBI GI g4204267
BLAST score 639
E value 1.0e-66
Match length 201
% identity 67
NCBI Description (AC005223) 55585 [Arabidopsis thaliana]

Seq. No. 5571
Contig ID 5063_1.R1040
5'-most EST uC-gmrominsoy045f06b1
Method BLASTX
NCBI GI g1351856
BLAST score 1789
E value 0.0e+00
Match length 375
% identity 90
NCBI Description ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
(ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase
[Cucurbita sp.]

Seq. No. 5572
Contig ID 5063_2.R1040
5'-most EST LIB3028-001-Q1-B1-D1
Method BLASTX
NCBI GI g1351856
BLAST score 432
E value 2.0e-42
Match length 106
% identity 79
NCBI Description ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
(ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase
[Cucurbita sp.]

Seq. No. 5573
Contig ID 5065_1.R1040
5'-most EST leu701149686.h1
Method BLASTN
NCBI GI g710349
BLAST score 445
E value 0.0e+00

Seq. No. 5605
 Contig ID 5122_1.R1040
 5'-most EST LIB3106-068-P1-K1-E6
 Method BLASTN
 NCBI GI g3860330
 BLAST score 155
 E value 2.0e-81
 Match length 387
 % identity 85
 NCBI Description Cicer arietinum mRNA for hypothetical protein, clone Can106

Seq. No. 5606
 Contig ID 5122_2.R1040
 5'-most EST k11701207777.h1
 Method BLASTN
 NCBI GI g3860330
 BLAST score 112
 E value 5.0e-56
 Match length 236
 % identity 87
 NCBI Description Cicer arietinum mRNA for hypothetical protein, clone Can106

Seq. No. 5607
 Contig ID 5132_1.R1040
 5'-most EST fua701038545.h1

Seq. No. 5608
 Contig ID 5133_1.R1040
 5'-most EST LIB3138-057-Q1-N1-D4
 Method BLASTX
 NCBI GI g2129517
 BLAST score 1719
 E value 0.0e+00
 Match length 359
 % identity 86
 NCBI Description 24-sterol C-methyltransferase (EC 2.1.1.41) - Arabidopsis thaliana

Seq. No. 5609
 Contig ID 5133_2.R1040
 5'-most EST uC-gmropic067d03b1
 Method BLASTX
 NCBI GI g2129517
 BLAST score 557
 E value 3.0e-57
 Match length 124
 % identity 80
 NCBI Description 24-sterol C-methyltransferase (EC 2.1.1.41) - Arabidopsis thaliana

Seq. No. 5610
 Contig ID 5133_4.R1040
 5'-most EST LIB3092-030-Q1-K1-H5
 Method BLASTX
 NCBI GI g2129517
 BLAST score 333

E value 4.0e-31
 Match length 153
 % identity 76
 NCBI Description 24-sterol C-methyltransferase (EC 2.1.1.41) - Arabidopsis thaliana

Seq. No. 5611
 Contig ID 5134_1.R1040
 5'-most EST g5175390
 Method BLASTX
 NCBI GI g464981
 BLAST score 789
 E value 4.0e-84
 Match length 148
 % identity 99
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 5612
 Contig ID 5134_2.R1040
 5'-most EST pmv700890042.h1
 Method BLASTX
 NCBI GI g464981
 BLAST score 781
 E value 2.0e-83
 Match length 148
 % identity 97
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 5613
 Contig ID 5134_3.R1040
 5'-most EST zhf700961505.h1
 Method BLASTN
 NCBI GI g456567
 BLAST score 80
 E value 7.0e-37
 Match length 200
 % identity 85
 NCBI Description Pisum sativum ubiquitin conjugating enzyme (UBC4), complete cds

Seq. No. 5614
 Contig ID 5134_4.R1040
 5'-most EST uC-gmflminsoy056g03b1
 Method BLASTX
 NCBI GI g441457
 BLAST score 216
 E value 2.0e-17
 Match length 44
 % identity 91
 NCBI Description (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No. 5615

E value 2.0e-39
 Match length 140
 % identity 62
 NCBI Description (AB010879) chloroplast ribosomal protein L10 [Nicotiana tabacum]

Seq. No. 5620
 Contig ID 5138_2.R1040
 5'-most EST uxk700670986.h1
 Method BLASTX
 NCBI GI g3298441
 BLAST score 230
 E value 2.0e-19
 Match length 80
 % identity 62
 NCBI Description (AB010879) chloroplast ribosomal protein L10 [Nicotiana tabacum]

Seq. No. 5621
 Contig ID 5140_1.R1040
 5'-most EST LIB3051-078-Q1-K1-D12

Seq. No. 5622
 Contig ID 5144_1.R1040
 5'-most EST LIB3028-005-Q1-B1-G7

Seq. No. 5623
 Contig ID 5145_1.R1040
 5'-most EST LIB3028-005-Q1-B1-G8
 Method BLASTX
 NCBI GI g1076288
 BLAST score 355
 E value 1.0e-33
 Match length 104
 % identity 62
 NCBI Description amino acid permease AAP3 - Arabidopsis thaliana

Seq. No. 5624
 Contig ID 5149_1.R1040
 5'-most EST ssr700559066.h1
 Method BLASTX
 NCBI GI g4105794
 BLAST score 442
 E value 2.0e-43
 Match length 140
 % identity 57
 NCBI Description (AF049928) PGP224 [Petunia x hybrida]

Seq. No. 5625
 Contig ID 5152_1.R1040
 5'-most EST LIB3028-005-Q1-B1-E11

Seq. No. 5626
 Contig ID 5152_2.R1040
 5'-most EST wrq700787541.h1

Seq. No. 5627

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Seq. No.	5629
Contig ID	5162_1.R1040
5'-most EST	uC-gmrominsoy310b03b1

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Seq. No.          5631
Contig ID         5163_1.R1040
5'-most EST      zhf700955007.h1
Method           BLASTX
NCBI GI          g4567262
BLAST score      1083
E value         1.0e-118
Match length     258
% identity       79
NCBI Description  (AC006841) putative ubiquitin [Arabidopsis thaliana]
```

```
Seq. No.          5632
Contig.ID         5164_1.R1040
5'-most EST      LIB3109-007-Q1-K1-D5
Method            BLASTX
NCBI GI           g2708737
BLAST score       718
E value           9.0e-76
Match length      295
% identity        40
NCBI Description  (AC003952) putative nuclear protein [Arabidopsis thaliana]
```

1072

00684915 = J01000

00684915 = J01000

[illegible]

00684915 = **707000**

00684915 = J01000

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Seq. No.          5668
Contig ID         5235_2.R1040
5'-most EST      g4276997
Method            BLASTX
NCBI GI           g3201969
BLAST score       299
E value           6.0e-27
Match length      71
% identity        70
```


NCBI Description (AF068332) submergence induced protein 2A [Oryza sativa]

Seq. No. 5669
 Contig ID 5235_4.R1040
 5'-most EST LIB3028-047-Q1-B1-A10
 Method BLASTX
 NCBI GI g2739365
 BLAST score 423
 E value 9.0e-42
 Match length 101
 % identity 72
 NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No. 5670
 Contig ID 5239_1.R1040
 5'-most EST g4396664
 Method BLASTX
 NCBI GI g3135264
 BLAST score 359
 E value 3.0e-34
 Match length 117
 % identity 62
 NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]

Seq. No. 5671
 Contig ID 5240_1.R1040
 5'-most EST trc700563942.h1
 Method BLASTX
 NCBI GI g585338
 BLAST score 1079
 E value 1.0e-118
 Match length 225
 % identity 92
 NCBI Description ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)
 >gi_391879_dbj_BAA01181_ (D10335) adenylate kinase-b [Oryza sativa]

Seq. No. 5672
 Contig ID 5240_2.R1040
 5'-most EST zzp700831593.h1
 Method BLASTX
 NCBI GI g585338
 BLAST score 419
 E value 3.0e-41
 Match length 89
 % identity 91
 NCBI Description ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)
 >gi_391879_dbj_BAA01181_ (D10335) adenylate kinase-b [Oryza sativa]

Seq. No. 5673
 Contig ID 5242_1.R1040
 5'-most EST kl1701211937.h1

Seq. No. 5674
 Contig ID 5243_1.R1040
 5'-most EST pmv700893482.h1

NCBI GI g2465923
 BLAST score 1068
 E value 1.0e-125
 Match length 461
 % identity 54
 NCBI Description (AF024648) receptor-like serine/threonine kinase
 [Arabidopsis thaliana]

Seq. No. 5690
 Contig ID 5265_3.R1040
 5'-most EST g5057646

Seq. No. 5691
 Contig ID 5266_1.R1040
 5'-most EST LIB3107-010-Q1-K1-H3
 Method BLASTX
 NCBI GI g3292829
 BLAST score 1081
 E value 1.0e-118
 Match length 458
 % identity 62
 NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 5692
 Contig ID 5266_2.R1040
 5'-most EST LIB3030-002-Q1-B1-G9
 Method BLASTX
 NCBI GI g2697129
 BLAST score 426
 E value 4.0e-41
 Match length 415
 % identity 36
 NCBI Description (AF025654) mRNA capping enzyme [Homo sapiens]
 >gi_4506563_ref_NP_003791.1_pRNGTT_ UNKNOWN

Seq. No. 5693
 Contig ID 5269_1.R1040
 5'-most EST leu701156667.h1
 Method BLASTX
 NCBI GI g2245020
 BLAST score 184
 E value 4.0e-13
 Match length 195
 % identity 30
 NCBI Description (Z97341) growth regulator homolog [Arabidopsis thaliana]

Seq. No. 5694
 Contig ID 5269_2.R1040
 5'-most EST uaw700666916.h1

Seq. No. 5695
 Contig ID 5271_1.R1040
 5'-most EST dpv701096923.h1
 Method BLASTX
 NCBI GI g3820614
 BLAST score 480
 E value 4.0e-48

Match length 189
 % identity 55
 NCBI Description (AF094516) E1-like protein [Homo sapiens]

Seq. No. 5696
 Contig ID 5272_1.R1040
 5'-most EST jC-gmro02910016d05a1
 Method BLASTX
 NCBI GI g4539371
 BLAST score 410
 E value 1.0e-39
 Match length 199
 % identity 50
 NCBI Description (AL049525) putative protein [Arabidopsis thaliana]

Seq. No. 5697
 Contig ID 5272_2.R1040
 5'-most EST jC-gmle01810005e04a1

Seq. No. 5698
 Contig ID 5276_1.R1040
 5'-most EST jC-gmle01810082c09a1
 Method BLASTX
 NCBI GI g3043529
 BLAST score 292
 E value 3.0e-26
 Match length 92
 % identity 58
 NCBI Description (AJ002204) polyamine oxidase [Zea mays]

Seq. No. 5699
 Contig ID 5277_1.R1040
 5'-most EST hrw701063235.h1
 Method BLASTX
 NCBI GI g4063751
 BLAST score 145
 E value 2.0e-13
 Match length 118
 % identity 47
 NCBI Description (AC005851) putative white protein [Arabidopsis thaliana]
 >gi_4510409_gb_AAD21495.1 (AC006929) putative white
 protein [Arabidopsis thaliana]

Seq. No. 5700
 Contig ID 5279_1.R1040
 5'-most EST uC-gmflminsoy079g08b1
 Method BLASTX
 NCBI GI g2288997
 BLAST score 286
 E value 1.0e-25
 Match length 69
 % identity 80
 NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 5701
 Contig ID 5280_1.R1040
 5'-most EST LIB3049-002-Q1-E1-F7

E value 5.0e-58
Match length 128
% identity 85
NCBI Description (AJ009737) eukaryotic translation initiation factor 6 [Beta vulgaris]

Seq. No. 5707
Contig ID 5289 5.R1040
5'-most EST LIB3040-055-Q1-E1-H11
Method BLASTX
NCBI GI g3355311
BLAST score 278
E value 7.0e-25
Match length 59
% identity 92
NCBI Description (AJ009737) eukaryotic translation initiation factor 6 [Beta vulgaris]

Seq. No. 5708
Contig ID 5289 10.R1040
5'-most EST smc700750180.h1
Method BLASTN
NCBI GI g3355310
BLAST score 45
E value 3.0e-16
Match length 93
% identity 87
NCBI Description Beta vulgaris mRNA for eukaryotic translation initiation factor 6, partial

Seq. No. 5709
Contig ID 5290 1.R1040
5'-most EST LIB3028-003-Q1-B1-E3
Method BLASTX
NCBI GI g2252830
BLAST score 829
E value 1.0e-88
Match length 289
% identity 57
NCBI Description (AF013293) weak similarity to receptor protein kinase [Arabidopsis thaliana]

Seq. No. 5710
Contig ID 5301 1.R1040
5'-most EST LIB3170-013-Q1-K1-D5
Method BLASTX
NCBI GI g4006872
BLAST score 994
E value 1.0e-108
Match length 283
% identity 65
NCBI Description (Z99707) methionyl aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No. 5711
Contig ID 5302 1.R1040
5'-most EST wrg700789428.h2

Method BLASTX
 NCBI GI g466158
 BLAST score 219
 E value 2.0e-23
 Match length 74
 % identity 70
 NCBI Description HYPOTHETICAL 9.3 KD PROTEIN ZK652.1 IN CHROMOSOME III
 >gi_630768_pir_S44901 ZK652.1 protein - Caenorhabditis
 elegans >gi_289767 (L14429) putative [Caenorhabditis
 elegans]

Seq. No. 5723
 Contig ID 5318_1.R1040
 5'-most EST ncj700987601.h1
 Method BLASTN
 NCBI GI g3510539
 BLAST score 291
 E value 1.0e-162
 Match length 591
 % identity 87
 NCBI Description Prunus armeniaca expansin (Exp2) mRNA, complete cds

Seq. No. 5724
 Contig ID 5319_1.R1040
 5'-most EST bth700849223.h1

Seq. No. 5725
 Contig ID 5320_1.R1040
 5'-most EST LIB3028-003-Q1-B1-E10

Seq. No. 5726
 Contig ID 5324_1.R1040
 5'-most EST zsg701122415.h1

Seq. No. 5727
 Contig ID 5326_1.R1040
 5'-most EST ncj700983837.h1
 Method BLASTX
 NCBI GI g2960216
 BLAST score 1563
 E value 1.0e-174
 Match length 382
 % identity 77
 NCBI Description (AJ223384) 26S proteasome regulatory ATPase subunit 10b
 (S10b) [Manduca sexta]

Seq. No. 5728
 Contig ID 5326_2.R1040
 5'-most EST jsh701064850.h1
 Method BLASTN
 NCBI GI g3236477
 BLAST score 123
 E value 1.0e-62
 Match length 227
 % identity 89
 NCBI Description Gossypium hirsutum 26S protease regulatory subunit (PRA2)
 mRNA, partial cds

Contig ID 5363 1.R1040
 5'-most EST txt700732041.h1
 Method BLASTX
 NCBI GI g2352492
 BLAST score 310
 E value 4.0e-28
 Match length 127
 % identity 46
 NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No. 5744
 Contig ID 5363 2.R1040
 5'-most EST dpv701097370.h1
 Method BLASTX
 NCBI GI g2352492
 BLAST score 309
 E value 3.0e-28
 Match length 123
 % identity 50
 NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No. 5745
 Contig ID 5363 3.R1040
 5'-most EST gsv701046587.h1
 Method BLASTX
 NCBI GI g4262147
 BLAST score 148
 E value 9.0e-10
 Match length 44
 % identity 59
 NCBI Description (AC005275) putative homolog of transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No. 5746
 Contig ID 5364 1.R1040
 5'-most EST g5508964
 Method BLASTN
 NCBI GI g21103
 BLAST score 72
 E value 4.0e-32
 Match length 180
 % identity 85
 NCBI Description R.sativus mRNA for HMG-COA reductase (clone CRS8)

Seq. No. 5747
 Contig ID 5364 2.R1040
 5'-most EST zhf700954225.h1
 Method BLASTN
 NCBI GI g21103
 BLAST score 56
 E value 1.0e-22
 Match length 180
 % identity 83

NCBI Description R.sativus mRNA for HMG-COA reductase (clone cRS8)

Seq. No. 5748
Contig ID 5365_1.R1040
5'-most EST LIB3028-002-Q1-B1-G12

Seq. No. 5749
Contig ID 5367_1.R1040
5'-most EST LIB3028-002-Q1-B1-B6

Method BLASTX
NCBI GI g3914006
BLAST score 552
E value 2.0e-67

Match length 242
% identity 61

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi_1816588
(U85495) LON2 [Zea mays]

Seq. No. 5750
Contig ID 5372_1.R1040
5'-most EST LIB3094-054-Q1-K1-B6

Method BLASTX
NCBI GI g3023728
BLAST score 290
E value 2.0e-25

Match length 246
% identity 31

NCBI Description EXOSTOSIN-2 (PUTATIVE TUMOUR SUPPRESSOR PROTEIN EXT2)
(MULTIPLE EXOSTOSES PROTEIN 2) >gi_1619954 (U72141)
multiple exostosis 2 protein [Mus musculus]

Seq. No. 5751
Contig ID 5373_1.R1040
5'-most EST kl1701214081.h1

Method BLASTX
NCBI GI g4539335
BLAST score 1454
E value 1.0e-176

Match length 486
% identity 60

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 5752
Contig ID 5374_1.R1040
5'-most EST LIB3109-034-Q1-K1-B1

Seq. No. 5753
Contig ID 5375_1.R1040
5'-most EST LIB3028-002-Q1-B1-D9

Method BLASTX
NCBI GI g2499570
BLAST score 394
E value 4.0e-49

Match length 147
% identity 68

NCBI Description PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE
(PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN

L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN
CARBOXYL METHYLTRANSFERASE) >gi_414332 (L07941)
L-isoaspartyl methyltransferase [Triticum aestivum]

Seq. No. 5754
Contig ID 5377_1.R1040
5'-most EST leu701147682.h1
Method BLASTX
NCBI GI g2879867
BLAST score 415
E value 3.0e-40
Match length 134
% identity 62
NCBI Description (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces pombe]

Seq. No. 5755
Contig ID 5377_2.R1040
5'-most EST LIB3170-005-Q1-K1-E3
Method BLASTX
NCBI GI g2879867
BLAST score 420
E value 6.0e-41
Match length 134
% identity 63
NCBI Description (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces pombe]

Seq. No. 5756
Contig ID 5377_3.R1040
5'-most EST LIB3040-026-Q1-E1-D1
Method BLASTN
NCBI GI g2618605
BLAST score 110
E value 1.0e-54
Match length 262
% identity 85
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No. 5757
Contig ID 5377_4.R1040
5'-most EST LIB3049-054-Q1-E1-G3
Method BLASTN
NCBI GI g2618605
BLAST score 89
E value 2.0e-42
Match length 305
% identity 82
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No. 5758
Contig ID 5380_1.R1040
5'-most EST leu701148742.h1
Method BLASTX
NCBI GI g228403

BLAST score 1676
 E value 0.0e+00
 Match length 371
 % identity 89
 NCBI Description glycolate oxidase [Lens culinaris]

Seq. No. 5759
 Contig ID 5380_2.R1040
 5'-most EST LIB3093-032-Q1-K1-G8
 Method BLASTN
 NCBI GI g3435305
 BLAST score 94
 E value 4.0e-45
 Match length 266
 % identity 84
 NCBI Description Medicago sativa glycolate oxidase mRNA, partial cds

Seq. No. 5760
 Contig ID 5382_1.R1040
 5'-most EST LIB3053-005-Q1-N1-G12
 Method BLASTN
 NCBI GI g508303
 BLAST score 83
 E value 2.0e-38
 Match length 243
 % identity 84
 NCBI Description Alfalfa bimodular protein (corC) mRNA, complete cds

Seq. No. 5761
 Contig ID 5382_2.R1040
 5'-most EST LIB3106-043-Q1-K1-D1
 Method BLASTN
 NCBI GI g508303
 BLAST score 81
 E value 1.0e-37
 Match length 185
 % identity 86
 NCBI Description Alfalfa bimodular protein (corC) mRNA, complete cds

Seq. No. 5762
 Contig ID 5383_1.R1040
 5'-most EST LIB3049-051-Q1-E1-D6

Seq. No. 5763
 Contig ID 5384_1.R1040
 5'-most EST LIB3028-009-Q1-B1-E3
 Method BLASTN
 NCBI GI g563328
 BLAST score 120
 E value 1.0e-60
 Match length 316
 % identity 86
 NCBI Description A.officinalis mRNA for histone 2B

Seq. No. 5764
 Contig ID 5384_2.R1040
 5'-most EST LIB3040-058-Q1-E1-C11

03684016.101000

Method BLASTN
 NCBI GI g2935449
 BLAST score 114
 E value 4.0e-57
 Match length 278
 % identity 85
 NCBI Description Malus domestica histone H2B mRNA, partial cds

Seq. No. 5765
 Contig ID 5384_3.R1040
 5'-most EST LIB3170-001-Q1-K1-D10
 Method BLASTN
 NCBI GI g563328
 BLAST score 138
 E value 2.0e-71
 Match length 310
 % identity 88
 NCBI Description A.officinalis mRNA for histone 2B

Seq. No. 5766
 Contig ID 5384_4.R1040
 5'-most EST LIB3040-032-Q1-E1-F8
 Method BLASTN
 NCBI GI g563328
 BLAST score 136
 E value 4.0e-70
 Match length 280
 % identity 87
 NCBI Description A.officinalis mRNA for histone 2B

Seq. No. 5767
 Contig ID 5384_5.R1040
 5'-most EST LIB3106-014-Q1-K1-D4
 Method BLASTN
 NCBI GI g2558961
 BLAST score 129
 E value 6.0e-66
 Match length 265
 % identity 87
 NCBI Description Gossypium hirsutum histone H2B1 mRNA, complete cds

Seq. No. 5768
 Contig ID 5384_6.R1040
 5'-most EST jC-gmro02910069a02a1
 Method BLASTN
 NCBI GI g563328
 BLAST score 127
 E value 8.0e-65
 Match length 315
 % identity 87
 NCBI Description A.officinalis mRNA for histone 2B

Seq. No. 5769
 Contig ID 5384_7.R1040
 5'-most EST LIB3039-012-Q1-E1-E7
 Method BLASTN
 NCBI GI g2935449

Seq. No. 5781
 Contig ID 5414 1.R1040
 5'-most EST crh700854530.h1
 Method BLASTX
 NCBI GI g1944518
 BLAST score 1142
 E value 1.0e-125
 Match length 303
 % identity 73
 NCBI Description (Y07822) Shaggy-like kinase tetha [Arabidopsis thaliana]
 >gi_3047105 (AF058919) protein kinase [Arabidopsis thaliana]

Seq. No. 5782
 Contig ID 5419 1.R1040
 5'-most EST LIB3039-039-Q1-E1-D5
 Method BLASTX
 NCBI GI g3201623
 BLAST score 1864
 E value 0.0e+00
 Match length 380
 % identity 91
 NCBI Description (AC004669) shaggy-like kinase dzeta [Arabidopsis thaliana]

Seq. No. 5783
 Contig ID 5419 2.R1040
 5'-most EST LIB3093-036-Q1-K1-E5
 Method BLASTX
 NCBI GI g1877397
 BLAST score 306
 E value 1.0e-27
 Match length 102
 % identity 58
 NCBI Description (Y11591) shaggy-like kinase [Ricinus communis]

Seq. No. 5784
 Contig ID 5419 4.R1040
 5'-most EST LIB3170-006-Q1-K1-B6
 Method BLASTX
 NCBI GI g2129738
 BLAST score 484
 E value 1.0e-48
 Match length 117
 % identity 81
 NCBI Description shaggy-like kinase dzeta - Arabidopsis thaliana
 >gi_1225913_emb_CAA64408_ (X94938) shaggy-like kinase dzeta
 [Arabidopsis thaliana] >gi_1669653_emb_CAA70483_ (Y09300)
 serine/threonine kinase [Arabidopsis thaliana]

Seq. No. 5785
 Contig ID 5419 5.R1040
 5'-most EST LIB3109-041-Q1-K1-G7
 Method BLASTN
 NCBI GI g1877396
 BLAST score 106
 E value 1.0e-52

